

SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB#

52619

Requester's Full Name: _____ Examiner #: _____ Date: _____
 An Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # _____	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Orbi: _____
Date Searcher Picked Up <u>10/16/01</u>	Bibliographic _____	Dr Link _____
Date Completed <u>10/16/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>EV</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 01:44:58 ; Search time 54.72 Seconds
(without alignments)
517.853 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKQSGNRDLMNIFKL.....WLARRLKKGKSKSRMNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_68:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	98.8	385	1 A34015	L-selectin precurs
2	1992	94.1	372	2 JC5377	L-selectin precurs
3	1796	84.9	376	2 JC4892	L-selectin precurs
4	1682	79.5	370	2 S22124	L-selectin precurs
5	1653	78.1	372	2 S23936	L-selectin precurs
6	1652	78.1	323	1 S08702	L-selectin precurs
7	1651	78.0	372	1 A33375	L-selectin precurs
8	905	42.8	830	2 A30359	P-selectin precurs
9	902.5	42.7	768	2 A42755	P-selectin precurs
10	894.5	42.3	646	2 JN0473	P-selectin precurs
11	885	41.8	768	2 I53821	P-selectin - rat
12	862	40.7	610	2 A35046	E-selectin - rat
13	861	40.7	551	2 I46709	endothelial leukoc
14	857	40.5	612	2 B42755	E-selectin precurs
15	849.5	40.1	485	2 S36772	E-selectin - bovin
16	815.5	38.5	482	2 JCS092	E-selectin - pig
17	236	11.2	868	2 T20239	hypothetical prote
18	212.5	10.0	1019	2 A38738	coagulation factor
19	199.5	9.4	449	1 NBH0HS	complement factor
20	199.5	9.4	1231	1 NBH0HS	complement factor
21	175.5	8.3	2014	2 I36936	complement C3b/C4b
22	172	8.1	2489	2 I73012	complement C3b/C4b
23	171.5	8.1	597	1 S53711	C4b alpha chain p
24	170	8.0	404	2 A46274	HIV gp120-binding
25	168	7.9	2132	1 A55182	aggreccan precursor
26	167	7.9	321	1 LNHUER	IgE Fc receptor II
27	167	7.9	1234	1 LNHUER	complement factor
28	166.5	7.9	558	2 S57953	C4b protein alpha
29	166	7.8	1456	1 A36563	mannose receptor p

30	165.5	7.8	560	2 T16833	hypothetical prote
31	165.5	7.8	1479	2 T42710	mannose receptor,
32	165	7.8	311	1 LNH02A	asialoglycoprotein
33	164.5	7.8	482	2 A34924	complement C3b/C4b
34	163	7.7	669	2 S65551	factor H - bovine
35	163	7.7	2124	2 A28452	proteoglycan core
36	162.5	7.7	345	1 NBBO	apolipoprotein H p
37	162	7.7	304	2 JX0209	lectin, galactose/
38	162	7.7	1574	2 T13954	MEGF6 protein - ra
39	161	7.6	469	1 NBMS04	C4b-binding protel
40	160.5	7.6	1455	1 A48925	mannose receptor p
41	160	7.6	1091	1 PL0009	complement C3d/Eps
42	160	7.6	2415	1 A39086	aggreccan precursor
43	159	7.5	1360	2 A39808	proteoglycan core
44	159	7.5	2327	2 T42630	aggreccan - bovine
45	157	7.4	331	1 LNM5ER	IgE Fc receptor, 1

ALIGNMENTS

RESULT 1
A34015
L-selectin precursor, long splice form - human
N:Alternate names: CD62L; leucocyte cell adhesion molecule-1 (LECAM-1, LAM-1); leukoc
ral lymph node homing receptor Leu-8
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: I55333; S06798; J10104; A34015; A33912
R:Ord. D.C.: Ernst, T.J.; Zhou, L.J.; Rambaldi, A.; Spertlin, O.; Griffin, J.; Tedder
J. Biol. Chem. 265, 7760-7767, 1990
A:Title: Structure of the gene encoding the human leukocyte adhesion molecule-1 (TL1,
A:Reference number: I55333; M01D:90243637
A:Accession: I55333
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 14-385 <CONP>
A:Cross-references: GB:M32414; NID:g187259; PIDN:AA60700.1; PID:g386660
R:Cammerlin, D.; James, S.P.; Stamenkovic, I.; Seed, B.
Nature 342, 78-82, 1989
A:Title: Leu-8/TL1 is the human equivalent of the Mel-14 lymph node homing receptor.
A:Reference number: S06798; M01D:90044046
A:Accession: S06798
A:Molecule type: mRNA
A:Residues: 1-225, 'S', 227-385 <CAM>
A:Cross-references: EMBL:X17519; NID:g34344; PIDN:CA843536.1; PID:g4902829
A:Note: this translation is not annotated in Genbank entry HSL5U8, release 111.0
R:Tedder, T.F.; Isaacs, C.M.; Ernst, T.J.; Demetri, G.D.; Adler, D.A.; Distche, C.M.
J. Exp. Med. 170, 123-133, 1989
A:Title: Isolation and chromosomal localization of cDNAs encoding a novel human lymph
oteins.
A:Reference number: J10104; M01D:89310350
A:Accession: J10104
A:Molecule type: mRNA
A:Residues: 1-230, 'N', 232, 'N', 234-254, 'E', 256-385 <TEPD>
A:Cross-references: GB:X16150; NID:g34428; PIDN:CA843275.1; PID:g34429
A:Note: the translated sequence in Genbank entry HSLVAM1, release 111.0, differs from
J. Bowen, B.R.; Nguyen, T.; Lasky, L.A.
J. Cell Biol. 109, 421-427, 1989
A:Title: Characterization of a human homologue of the murine peripheral lymph node ho
A:Reference number: A34015; M01D:89308881
A:Accession: A34015
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 14-49, 'Y', 51-190, 'N', 192-205, 'V', 207-226, 'F', 228-385 <BOW>
A:Cross-references: GB:X16070; NID:g38092; PIDN:CA843203.1; PID:g38093
R:Siegelman, M.H.; Welsman, I.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 5562-5566, 1989
A:Title: Human homologue of mouse lymph node homing receptor: evolutionary conservati
A:Reference number: A33912; M01D:89315837
A:Accession: A33912
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 14-205, 'L', 207-385 <SIE>
 A:Cross-references: GB:M25280; NID:g187182; PIDN:AAC63053.1; PID:g307134
 C:Comment: For an alternative splice form, see PIR:S05702.
 C:Genetics:
 A:Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAM-1
 A:Cross-references: GDB:120157; GDB:118834; OMIM:153240
 A:Map position: 1922-1923
 A:Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 331/1; 374/1; 380/2
 C:Function:
 A:Description: binds with low affinity to oligosaccharides like heparan sulfate and sialyl
 ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutroph
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology;
 C:Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammation
 F:1-51/Domain: signal sequence #status predicted <Sig>
 F:42-168/Domain: C-type lectin homology <LCH>
 F:52-385/Product: L-selectin #status predicted <MAT>
 F:52-385/Domain: extracellular #status predicted <EXT>
 F:173-204/Domain: EGF homology <EGF>
 F:210-267/Domain: complement factor H repeat homology <FHL>
 F:272-329/Domain: complement factor H repeat homology <FHL2>
 F:344-368/Domain: transmembrane #status predicted <TM>
 F:369-385/Domain: intracellular #status predicted <INT>
 F:73,117,190,245,259/Binding site: carbonylate (Asn) (covalent) #status predicted
 F:377,380/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 98.8%; Score 2090; DB 1; Length 385;
 Best local Similarity 98.9%; Pred. No. 4,8e-148;
 Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKQSTQDRLWNIFKLMGWTMLCDFLAHGTCWTYHSEKPMNMQARRCRDN 60
 DB 14 MIFPMKQSTQDRLWNIFKLMGWTMLCDFLAHGTCWTYHSEKPMNMQARRCRDN 73
 QY 61 YTDVLAIONKAELEYEKLTPFSRSYTWGIRKIGIMTWGNTSKLTEAEWNGGEPRN 120
 DB 74 YTDVLAIONKAELEYEKLTPFSRSYTWGIRKIGIMTWGNTSKLTEAEWNGGEPRN 133
 QY 121 NKKNKEDCEIYIKRKNKAGKNNDDACHKKAALCYTASCPWSCSGHGECEIINNTTC 180
 DB 134 NKKNKEDCEIYIKRKNKAGKNNDDACHKKAALCYTASCPWSCSGHGECEIINNTTC 193
 QY 181 NCDVGYGQCQVLVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
 DB 194 NCDVGYGQCQVLVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 253
 QY 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 300
 DB 254 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 313
 QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPLFIPAVVMTAFSGLAFTIIMLARLKK 360
 DB 314 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPLFIPAVVMTAFSGLAFTIIMLARLKK 373
 QY 361 GKSKRSMDPY 372
 DB 374 GKSKRSMDPY 385

RESULT 2
 JC5377
 L-selectin precursor - hamadryas baboon
 C:Species: Papio hamadryas (hamadryas baboon)
 C:Accession: JC5377; PC4315
 C:Date: 02-Jun-1997 #sequence_revision 12-Sep-1997 #text_change 21-Jan-2000
 R:Titration: N.; Fu H.; Berg, E.L.
 A:Title: PCR cloning of the cDNA encoding baboon L-selectin.
 A:Reference number: JC5377; MUID:97128794
 A:Accession: JC5377
 A:Molecule type: mRNA
 A:Residues: 1-372 <TSU1>
 A:Cross-references: GB:U52074; NID:g1326148; PIDN:AAB40903.1; PID:g1326149

A:Accession: PC4315
 A:Molecule type: protein
 A:Residues: 37-43;142-148 <TSU2>
 C:Comment: This receptor is involved in the initial adhesive interaction between lymph
 sites of inflammation.
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
 F:1-38/Domain: signal sequence #status predicted <Sig>
 F:39-155/Domain: C-type lectin homology <LCH>
 F:39-155/Product: L-selectin #status predicted <MAT>
 F:39-157/Domain: calcium-binding #status predicted <CAB>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <FHL>
 F:259-316/Domain: complement factor H repeat homology <FHL2>
 F:333-355/Domain: transmembrane #status predicted <TM>
 F:356-372/Domain: intracellular #status predicted <INT>

Query Match 94.1%; Score 1992; DB 2; Length 372;
 Best local Similarity 93.5%; Pred. No. 8,9e-141;
 Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 MIFPMKQSTQDRLWNIFKLMGWTMLCDFLAHGTCWTYHSEKPMNMQARRCRDN 60
 DB 1 MIFPMKQSTQDRLWNIFKLMGWTMLCDFLAHGTCWTYHSEKPMNMQARRCRDN 60
 QY 61 YTDVLAIONKAELEYEKLTPFSRSYTWGIRKIGIMTWGNTSKLTEAEWNGGEPRN 120
 DB 61 YTDVLAIONKAELEYEKLTPFSRSYTWGIRKIGIMTWGNTSKLTEAEWNGGEPRN 120
 QY 121 NKKNKEDCEIYIKRKNKAGKNNDDACHKKAALCYTASCPWSCSGHGECEIINNTTC 180
 DB 121 NKKNKEDCEIYIKRKNKAGKNNDDACHKKAALCYTASCPWSCSGHGECEIINNTTC 180
 QY 181 NCDVGYGQCQVLVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
 DB 181 NCDVGYGQCQVLVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
 QY 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 300
 DB 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 300
 QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPLFIPAVVMTAFSGLAFTIIMLARLKK 360
 DB 301 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPLFIPAVVMTAFSGLAFTIIMLARLKK 360
 QY 361 GKSKRSMDPY 372
 DB 361 GKSKRSMDPY 372

RESULT 3
 JC4892
 L-selectin precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Accession: JC4892
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
 R:Olan, J.; Huang, X.; Marks, R.M.
 A:Title: Cloning of the cDNA for rabbit L-selectin and expression of recombinant prot
 A:Reference number: JC4892; MUID:96354800
 A:Accession: JC4892
 A:Molecule type: mRNA
 A:Residues: 1-376 <QIA>
 A:Cross-references: GB:U26335; NID:g847787; PIDN:AA67896.1; PID:g847788
 C:Comment: This protein involved in leukocyte-endothelial adhesion; it mediates adhes
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
 F:1-37/Domain: signal sequence #status predicted <Sig>
 F:29-155/Domain: C-type lectin homology <LCH>
 F:38-376/Product: L-selectin #status predicted <MAT>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <FHL>
 F:259-316/Domain: transmembrane #status predicted <TM>


```

Db      1 MLCIFKKCQNAAGSLNNVFELMWIMLCCDFRHHGHTDCMTYHSKRPRMWEKARAFCHEN 60
Oy      61 YTDVAIAIONKAIEYLEKTLPFSRSYWIIGIKIGIWTWGTNKSLTLEAENMGDEBN 120
Db      61 YTDVAIAIONKGEIEYLNTKLTPFSRTYYWIGIRKYGVGWTVGTNKSLTLEAKNAGABPN 120
Oy      121 NKKNKEDCEVETIKRNKNAGKWNDDACHKRLKALCYTASCPWSSGGEGCEVEITINNHC 180
Db      121 NKKSKEDCEVETIKRNKSGKWNDDACHRAKATLCYTASCKPSCSGHQCEVINNTVC 180
Oy      181 NCDVGAYGPOCOLVIQCPELLEAPELGTMDCTHPFNFSFSSOCASFSEGTNLTIIEETT 240
Db      181 NCDDLGYGEECOFYVQCVPLEAPKLGTACTRPLGNFSMSCAANGSKGIDMIGEETT 240
Oy      241 CGPFNGWSSPEPTCOVIOCEPLSADPLDGLIMNCSDHPLASFSFTSACTFTICSEGTDLGRKK 300
Db      241 CAPFGNWSSPEPTCRVIOCEPLTEPDLDGMDCNHPLVDYGFSSSTCFSCSEBAELTGEEK 300
Oy      301 TPCESGSITSNSPICOKIDKSFMIKEGDYNPFLTPAVAVMTAFSGLAFTILMLARRLK 360
Db      301 TICGSLGNWSSPSPPCOKINRTISINESDYNDPLPIPAVMVTAFSGLAFTILMLARK- 359
Oy      361 GKSKR 366
Db      360 -RKSK 364

RESULT 5
S23936
L-selectin precursor - rat
N:Alternate names: Leucocyte cell adhesion molecule 1 (LECAM-1)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
C:Accession: S23936
R:Matanabe, T.; Song, Y.; Hirayama, Y.; Tamateani, T.; Kuida, K.; Miyasaka, M.
Biochim. Biophys. Acta 1131, 321-324, 1992
A>Title: Sequence and expression of a rat cDNA for LECAM-1.
A:Reference number: S23936; MUID:92329548
A:Accession: S23936
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-372 <MAT>
A:Cross-references: GB:D10831; NID:g220801; PIDN:BAA01613.1; PID:g220802
C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
C:Keywords: transmembrane protein
E:29-155/Domain: C-type lectin homology <LCH>
F:160-191/Domain: EGF homology <EGF>
F:197-254/Domain: complement factor H repeat homology <FH>
F:259-316/Domain: complement factor H repeat homology <FH2>

Query Match          78.1%; Score 1653; DB 2; Length 372;
Best Local Similarity 76.9%; Pred. No. 1.3e-115;
Matches 286; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

Oy      1 MTFPKCOSTQDNLNINKLMGWTMLCCDFLAHGTCMYTHYSKPNNQRRARFCRDN 60
Db      1 MVFPNRCSAQNGSMSPLKMTIRTLCCDLLPHGHGCMTHYHSRSMNWEARFCRH 60
Oy      61 YTDVAIAIONKAIEYLEKTLPFSRSYWIIGIRKIGIWTWGTNKSLTLEAENMGDEBN 120
Db      61 YTDVAIAIONKREIEYLEKTLPKNPYYWIGIRIKTKTWGTNKTLLKEANMGDTGBPN 120
Oy      121 NKKNKEDCEVETIKRNKNAGKWNDDACHKRLKALCYTASCPWSSGGEGCEVEITINNHC 180
Db      121 NKKSKEDCEVETIKRNKSGKWNDDACHKRRKALCYTASCOPESCNRHGEVETINNNTC 180
Oy      181 NCDVGAYGPOCOLVIQCPELLEAPELGTMDCTHPFNFSFSSOCASFSEGTNLTIIEETT 240
Db      181 ICDDPYGYGQQCVYIQCEPLKRAPELGTMCNIHPLDGDFSGOSCAPANCSEGBSLGNATE 240
Oy      241 CGPFNGWSSPEPTCOVIOCEPLSADPLDIMNCSDHPLASFSFTSACTFTICSEGTDLGRKK 300
Db      241 CGPFNGWSSPEPTCOVIOCEPLSADPLDIMNCSDHPLASFSFTSACTFTICSEGTDLGRKK 300

```

Db 241 CGASGNWYLEPIQVIOCMPLADLGTMECSHPLANSFTSACTFTCTSEEDLIGERK 300
 QY 301 TICESSGIMNSPICKOKLDKSFMSIKSGDYNPFTPAVWVWTAARSGAFTIWLARRKK 360
 Db 301 TYCRSSGMSWSSPICKOKTKRSFSKIKSGDYNPFTPAVWVWTAARSGAFTIWLARRKK 360
 QY 361 GKSKSRSMNDPY 372
 Db 361 GKSKSRSMNDPY 372

RESULT 6

L-selectin precursor, short splice form - human
 N:Alternate names: CD62L; leucocyte cell adhesion molecule-1 (LFCAM-1, LAM-1); leukocyte
 tal lymph node homing receptor Leu-8
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 26-May-2000
 C:Accession: S09702
 R:Cammerlin, D.; James, S.P.; Stamenkovic, I.; Seed, B.
 Nature 342, 78-82, 1989
 A:Title: Leu-8/701 is the human equivalent of the Mel-14 lymph node homing receptor.
 A:Reference number: S06798; MUID:90044046
 A:Accession: S09702
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-323 <CAM>
 A:Cross-references: EMBL:X17519; NID:934344
 A:Note: this translation is not annotated in GenBank entry HSEU8, release 111.0
 C:Comment: For an alternative splice form, see PIR:A34015.
 C:Genetics:
 A:Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAN-1
 A:Cross-references: GDB:120157; GDB:118834; OMIM:153240
 A:Map position: 1922-1923
 A:Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 303/2
 A:Function:
 A:Description: binds with low affinity to oligosaccharides like heparan sulfate and sialy
 ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutroph
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology;
 C:Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammation
 F:1-51/Domain: signal sequence #status predicted <SIG>
 F:42-168/Domain: C-type lectin homology <LCH>
 F:52-323/Product: L-selectin #status predicted <EXT>
 F:52-300/Domain: extracellular #status predicted <EXT>
 F:173-204/Domain: BGF homology <EGF>
 F:210-267/Domain: complement factor H repeat homology <PH1>
 F:272-323/Domain: complement factor H repeat homology #status atypical <FH2>
 F:301-318/Domain: transmembrane #status predicted <TM>
 F:319-323/Domain: intracellular #status predicted <INT>
 F:713,117,190,245,259/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:322/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 78.1%; Score 1652; DB 1; Length 323;
 Best Local Similarity 98.3%; Pred. No. 1.4e-115;
 Matches 285; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKCGSTQDRLNMFILMGWMLCDPLAHGHTYCTYHYSEKPMWQARRPFCRDN 60
 Db 14 MIFPMKCGSTQDRLNMFILMGWMLCDPLAHGHTYCTYHYSEKPMWQARRPFCRDN 73
 QY 61 YTDVLAIONKAELEYLEKTLPSRSYTWGIRKIGIWTWGTNKSLEAEANMGDGEPN 120
 Db 74 YTDVLAIONKAELEYLEKTLPSRSYTWGIRKIGIWTWGTNKSLEAEANMGDGEPN 133
 QY 121 NKKNEDECEYIYIKRNKDGKWNDDACHKRLKALCYTASCPWMSGGECVEIINNNTC 180
 Db 134 NKKNEDECEYIYIKRNKDGKWNDDACHKRLKALCYTASCPWMSGGECVEIINNNTC 193
 QY 181 NCDVGYYPQCOVLVQCEPLAEPLGTMDCTHPFGNFSFSSQCAFCSEGTNLGTIEETT 240
 Db 194 NCDVGYYPQCOVLVQCEPLAEPLGTMDCTHPFGNFSFSSQCAFCSEGTNLGTIEETT 253

QY 241 CGPGRNWSPEPTCOYIQCEPLASAPDLGTMCNCHPLASFTSACTFTCS 290
 Db 254 CGPGRNWSPEPTCOYIQCEPLASAPDLGTMCNCHPLASFTSACTFTCS 303

RESULT 7

L-selectin precursor - mouse
 N:Alternate names: lymph node homing receptor MEL-14; lymphocyte surface antigen Ly-2
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
 C:Accession: A32375; A35102; A40167; A60906
 R:Laskey, L.A.; Singer, M.S.; Yednock, T.A.; Dowbenko, D.; Fennie, C.; Rodriguez, H.;
 Cell 56, 1045-1055, 1989
 A:Title: Cloning of a lymphocyte homing receptor reveals a lectin domain.
 A:Reference number: A32375; MUID:89168433
 A:Accession: A32375
 A:Molecule type: mRNA
 A:Residues: 1-372 <LAS>
 A:Cross-references: GB:M25324; NID:9198803; PIDN:AAA39431.1; PID:9198804
 R:Siegelman, M.H.; Cheng, I.C.; Weissman, I.L.; Wakeland, E.K.
 Cell 61, 611-622, 1990
 A:Title: The mouse lymph node homing receptor is identical with the lymphocyte cell s
 A:Reference number: A35102; MUID:90263086
 A:Accession: A35102
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-372 <SEL>
 A:Cross-references: GB:M36005; NID:9199735; PIDN:AAA39722.1; PID:9199736; GB:M36058;
 R:Siegelman, M.H.; van de Rijn, M.; Weissman, I.L.
 Science 243, 1165-1172, 1989
 A:Title: Mouse lymph node homing receptor cDNA clone encodes a glycoprotein revealing
 A:Reference number: A40167; MUID:89162048
 A:Accession: A40167
 A:Molecule type: mRNA
 A:Residues: 1-372 <SID>
 A:Cross-references: GB:X14772; NID:952942; PIDN:CAA32880.1; PID:952943
 A:Note: part of this sequence, including the amino end of the mature protein, was con
 R:Siegelman, M.; Bond, M.W.; Gallatin, W.M.; St. John, T.; Smolth, H.T.; Fried, V.A.; W
 Science 231, 823-829, 1986
 A:Title: Cell surface molecule associated with lymphocyte homing is a ubiquitinated b
 A:Reference number: A60906; MUID:86122900
 A:Accession: A60906
 A:Molecule type: protein
 A:Residues: 'X', '40', 'X', '42', 'XXX', '46', 'X', '48', 'XXXXXX', '55-56', 'X', '58', 'XXXXXX', '65', 'V', '67', 'X
 C:Comment: This protein is ubiquitinated.
 C:Function:
 A:Description: binds with low affinity to oligosaccharides like heparan sulfate and si
 ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutr
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homolog
 C:Keywords: cell adhesion; duplication; glycoprotein; inflammation; phosphoprotein; s
 F:1-38/Domain: signal sequence #status predicted <SIG>
 F:29-155/Domain: C-type lectin homology <LCH>
 F:39-372/Product: L-selectin #status experimental <NAT>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <PH1>
 F:259-316/Domain: complement factor H repeat homology <PH2>
 F:332-355/Domain: transmembrane #status predicted <TM>
 F:356-372/Domain: intracellular #status predicted <INT>
 F:60,104,216,246,278,308,320/Binding site: carboxylate (Asn) (covalent) #status pred
 F:364/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 78.0%; Score 1651; DB 1; Length 372;
 Best Local Similarity 76.1%; Pred. No. 1.9e-115;
 Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MIFPMKCGSTQDRLNMFILMGWMLCDPLAHGHTYCTYHYSEKPMWQARRPFCRDN 60
 Db 1 MIFPMKCGSTQDRLNMFILMGWMLCDPLAHGHTYCTYHYSEKPMWQARRPFCRDN 60
 QY 61 YTDVLAIONKAELEYLEKTLPSRSYTWGIRKIGIWTWGTNKSLEAEANMGDGEPN 120

```
Db 61 YTDLVAIQNKRELEYLENTLPKSPYIYWGIRKGMWVGNKTLTKEAENMGACEPN 120
|||||
Qy 121 NKRKEDCEVIYIKRNKADGWMDACHKLKALCYTASCPWSCSGHGECEIINNHTC 180
|||||
Db 121 NKRKEDCEVIYIKRNKADGWMDACHKLKALCYTASCPWSCSGHGECEIINNHTC 180
|||||
Qy 181 NCDVGYIQCQVLYOCEPLEAPELGTMDCTHPPGNFSFSQCAFSCSEGTNLGIEETT 240
|||||
Db 181 ICAGYGYPCQVYVOCPELEAPELGTMDCIHPLGNFSFQSCAFNCSSEGTNLGIEETQ 240
|||||
Qy 241 CGPFGNMSDEPTQVOCPELEAPDLGIMNCSHPLASFSTSCFTSCGTELGICKK 300
|||||
Db 241 CGASGNMSSPEPTICQVYVOCPELEAPELGTMDCIHPLGNFSFQSCAFNCSSEGTNLGIEETQ 300
|||||
Qy 301 TICSSGIMNSPFCOKLDRSEFMKEGDNPLFIPAVAVTAAGSLAFIIMLARLKK 360
|||||
Db 301 TCGGASGNMSSPEPTICQVYVOCPELEAPELGTMDCIHPLGNFSFQSCAFNCSSEGTNLGIEETQ 360
|||||
Qy 361 GKRSKRSMDPY 372
|||||
Db 361 GKRSKRSMDPY 372
|||||

RESULT 8
A30359
P-selectin precursor - human
N:Alternate names: CD62 antigen; granule membrane protein 140
C:Species: Homo sapiens (man)
C>Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 19-May-2000
C:Accession: A30359
R:Johnson, G.I.; Cook, R.G.; McEwen, R.P.
Cell 56, 1033-1044, 1989
A>Title: Cloning of GMP-140, a granule membrane protein of platelets and endothelium: se
A:Reference number: A30359; MUID:89168432
A:Accession: A30359
A:Molecule type: mRNA
A:Residues: 1-830 <TOH>
A:Cross-references: GB:M25322
A>Note: parts of this sequence, including the amino end of the mature protein, were conf
C:Genetics:
A:Gene: GDB:SELP; GRMP
A:Cross-references: GDB:120018; OMIM:173610
A:Map position: 1q22-1q25
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology; EGF
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; surface anti
F:1-41/Domain: signal sequence #status predicted <Sig>
F:42-630/Product: P-selectin #status experimental <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FH01>
F:262-319/Domain: complement factor H repeat homology <FH02>
F:324-381/Domain: complement factor H repeat homology <FH03>
F:386-443/Domain: complement factor H repeat homology <FH04>
F:448-505/Domain: complement factor H repeat homology <FH05>
F:510-567/Domain: complement factor H repeat homology <FH06>
F:572-629/Domain: complement factor H repeat homology <FH07>
F:642-699/Domain: complement factor H repeat homology <FH08>
F:704-761/Domain: complement factor H repeat homology <FH09>
F:772-795/Domain: transmembrane #status predicted <TMN>
F:796-830/Domain: intracellular #status predicted <CYT>
F:54,98,180,212,219,411,460,518,665,716,723,741/Binding site: carbohydrate (Asn) (coval
```

```
Db 71 QNKNEIDYLNKVLPHYSSYYWIGIRKNNKTTWTYGTAKALTNENADNEPNKRNED 130
|||||
Qy 128 CVELIYIKRNKADGWMDACHKLKALCYTASCPWSCSGHGECEIINNHTCNDVGY 187
|||||
Db 131 CVELIYIKRNKADGWMDACHKLKALCYTASCPWSCSGHGECEIINNHTCNDVGY 190
|||||
Qy 188 GPCQVLYOCEPLEAPELGTMDCTHPPGNFSFSQCAFSCSEGTNLGIEETTGPFGNM 247
|||||
Db 191 GPECEYVREGGELELPQVHVMNCSHPLGNFSFQSCAFNCSSEGTNLGIEETTGPFGNM 250
|||||
Qy 248 SDEPTQVOCPELEAPDLGIMNCSHPLASFSTSCFTSCGTELGICKKTCESG 307
|||||
Db 251 TKNPQCLAQCPPLKPEGNMCLHSAKAFQHOSSCSCEBGFADVGPVYQCTASG 310
|||||
Qy 308 TWSNPSPIQ 317
|||||
Db 311 VWPAPAPVC 320
|||||

RESULT 9
A42755
P-selectin precursor - mouse
N:Alternate names: CD62; granule membrane protein 140; PADGEM
C:Species: Mus musculus (house mouse)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 19-May-2000
C:Accession: A42755; A44899
R:Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A>Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-sele
A:Reference number: A42755; MUID:92340571
A:Accession: A42755
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-768 <MBL>
A:Cross-references: GB:M8761; NID:g200552; PIDN:AAA0008.1; PID:g200553
A:Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBIP:10967)
R:Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L.
Blood 80, 795-800, 1992
A>Title: Molecular cloning and analysis of in vivo expression of murine P-selectin.
A:Reference number: A44899; MUID:92345617
A:Accession: A44899
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-723, 'E', 725-768 <SAN>
A:Cross-references: GB:M72332; NID:g193565; PIDN:AAA3712.1; PID:g193566
A>Note: sequence extracted from NCBI backbone (NCBIP:109900)
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology;
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; transmembr
F:1-41/Domain: signal sequence #status predicted <Sig>
F:42-768/Product: P-selectin #status predicted <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FH01>
F:262-319/Domain: complement factor H repeat homology <FH02>
F:324-381/Domain: complement factor H repeat homology <FH03>
F:386-443/Domain: complement factor H repeat homology <FH04>
F:448-505/Domain: complement factor H repeat homology <FH05>
F:510-567/Domain: complement factor H repeat homology <FH06>
F:580-637/Domain: complement factor H repeat homology <FH07>
F:642-699/Domain: complement factor H repeat homology <FH08>
F:710-733/Domain: transmembrane #status predicted <TMN>
F:734-768/Domain: intracellular #status predicted <INT>
F:45,54,107,212,347,398,456,467,603,654,661,679/Binding site: carbohydrate (Asn) (cov
```

OY	LPFSASYWIGIRKJGGIMTWGNTNKSLLTEEAENNDGSPNNKKRKEDEVETIYIRNKKA	139
Db	IPFNSYIWIGIRKJNNKNKTWTGNKTLTEEAENNADNEPNNKKNNODCVETIYIKSNSAP	142
OY	KWMNDACHKRLKALCYTASCPMCSGSGHGEVEIINNHTCQMDVGYYPQCOLATOCBP	199
Db	GKMNDPECFKRFRALCYTASCQDMCSMGECIEITIGSYTCGYFGYPCBEVEYKECK	202
OY	LEAPBLGTMDCHPRPGNSFSFSQCAFSCSEGINLTGIEETTCCPRGMMSPEPTQVIOC	259
Db	VNIPIHVLMINSHPJGEERSFSNQCFPSCAEGEYLDEGPBLOCLAGIWTNNPKDAVOQ	262
OY	EPLSAPDLGINNCSHPLASFSTACTFCISGBTELICKKKTICSSGIWSNPDIOTKL	319
Db	QSLEAPPHGTMACMPILAFAYDSECKFECCOPGIYAARSNTLHCTGSCGMSBDLPJTCEAI	322

RESULT 10
JN0473
P-selectin precursor - bovine
N:Alternate names: granule membrane protein-140
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jan-2000
C:Accession: JN0473
R:Strubel, N.A.; Nguyen, M.; Kansas, G.S.; Tedder, T.F.; Bischoff, J.
Biochem. Biophys. Res. Commun. 192, 338-344, 1993
A:Title: Isolation and characterization of a bovine cDNA encoding a functional homolog
A:Reference number: JN0473; MUID:93249394
A:Accession: JN0473
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-646 <STR>
A:Cross-references: GB:J12041; NID:g304246; PIR:AAA30743.1; PID:g304247
C:Comment: This protein is a Ca2+ dependent receptor for myeloid cells.
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology; EGF
F:1-41/Domain: signal sequence
F:42-646/Product: P-selectin status predicted <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FH1>
F:262-319/Domain: complement factor H repeat homology <FH2>
F:324-381/Domain: complement factor H repeat homology <FH3>
F:386-443/Domain: complement factor H repeat homology <FH4>
F:458-515/Domain: complement factor H repeat homology <FH5>
F:520-577/Domain: complement factor H repeat homology <FH6>
F:588-611/Domain: transmembrane
F:612-646/Domain: intracellular #status predicted <CYT>

Query Match	42.3%	Score 894.5	DB 2	length 646
Best Local Similarity	48.7%	Pred. No. 5,2e-59		
Matches 155	Conservative 51	Mismatches 109	Indels 3	Gaps 1
QY	* 2	IFPWKCSTORDIMNIFKLMGWTMLCDDFLAHGHGYCMTYHYSEKPEPMWQBARFCHDNY	61	
Db	8	IMNWR---PQRAAFRTVOLLCSFVLFEVINOKEVSAWTFHNSKTYSWMYSAFCCKEY	64	
QY	62	TDVAIONKAKEIYLEKTELPFSRSYYWIGIRKIGATWGTWTKSLTEPEENNDDGDPNN	121	
Db	65	TDVVAIONKKEIAYLMTETIYYNSYWIGIRKINNNKWTWGTCKTLEELENNADNDEPN	124	
QY	122	KKKKECVETIYIKRKNDDACHKIKLAKALCYTASCPMCSGHEGCEVETIINHTCN	181	
Db	125	KRNNQCVETIYIKSLSAPGKGMNDPCWKRRAKCYTASCDMCSKQGEIETIGNTCS	184	
QY	182	CDVGYPCOCOLVIOCEPLEAPELGTMDCTHPRGNFSFSSQCAFSCSEGTNLGIEBTTTC	241	
Db	185	CYPGFYGPECEYRECGEGEDLPQHVMHNSCHPLGNFSFNHSCFHCAEGYALNGPELEEC	244	
QY	242	GPGGNSSPEPCQVYIOCEPLSAPDGLIMNCHPLLSFSTSACTYICSEGTLLIGKKT	301	
Db	245	IASGIIWNSPPOCVAAOCPALKSPBQGSMSCVASADAFHOSSCSFCEGEGFALVPEVAV	304	

```
QY      302 ICESGWSNPSPICQKL 319
          | : |:| : |:| :| :|
Db      305 HCTALGVWTAFTPVCKAL 322
```

RESULT 11
153821
p-selectin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C:Accession: 153821
R:Anchupach, J.A.; Oliver, M.G.; Anderson, D.C.; Manning, A.M.
Gene 145, 251-255, 1994
A:Title: Cloning, sequence comparison and in vivo expression of the gene encoding rat
A:Reference number: 153821; MUID:94333817
A:Accession: 153821
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-768 <RES>
A:Cross-references: GB:I23086; NID:g349552; PIDN:AAA60325.1; PID:g349553
C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement fa
F:32-158/Domain: C-type lectin homology <LCH>
F:163-194/Domain: EGF homology <EGF>
F:262-319/Domain: complement factor H repeat homology <FHR>
F:510-567/Domain: complement factor H repeat homology <FHO6>
F:642-699/Domain: complement factor H repeat homology <FHO7>
F:642-699/Domain: complement factor H repeat homology <FHO8>

[illegible]

RESULT 12
A35046
E-selectin precursor - human
W:Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1); LECAM-2
C:Species: Homo sapiens (man)
C:Date: 27-Jul-1990 #sequence, revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: A38615; A35046; A32606
J:R. Collins, T.; Williams, A.; Johnston, G.I.; Kim, J.; Eddy, R.; Shows, T.; Gimbrone J
J. Biol. Chem. 266, 2466-2473, 1991
A:Title: Structure and chromosomal location of the gene for endothelial-leukocyte adhesion molecule
A:Reference number: A38615; M01D:91115870
A:Accession: A38615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-610 <COL>
A:Cross-references: GB:61893; GB:M56017; M1D:g182043; P1D:AAA52375.1; P1D:g182046
R:Hennessy, C.; Osborn, L.; Goff, D.; Chi-Rosso, G.; Vassallo, C.; Pasek, M.; Pittack, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 1673-1677, 1990
Title: Endothelial leukocyte adhesion molecule 1: direct expression cloning and fun

```

A:Cross-references: GB:M91005; NID:g165006; PIDN:AAA31244.1; PID:g165007
A:Accession: I46708
A>Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-307,'T', 309-327,'T', 329-490,'A',492-551 <LAN2>
A:Cross-references: GB:M91004; NID:g165004; PIDN:AAA31243.1; PID:g165005
C:Genetics:
A:Gene: ELAM1
A:Map position: 1q22-q25
A:Introns: 13/1; 143/1; 179/1; 241/1; 303/1; 366/1; 429/1; 488/1; 525/1; 533/2
C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement factor F14-140/Domains: C-type lectin homology <LCH>
F:182-239/Domains: complement factor H repeat homology <FH>
F:244-301/Domains: complement factor H repeat homology <FH>
F:306-364/Domains: complement factor H repeat homology <FH>
F:369-427/Domains: complement factor H repeat homology <FH>
F:433-486/Domains: complement factor H repeat homology <FH>
F:32,45,201,314,321,466/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match      40.7%; Score 861; DB 2; Length 551;
Best Local Similarity 51.8%; Pred. No. 1,4e+56;
Matches 146; Conservative 41; Mismatches 95; Indels 0; Gaps 0;
Oy      36 TGCCTGTHYSEKMNNOARRRCECDNYDTDLVAIONAAEIELEKTLPSFSYYWIGIRKG 95
| | | | | : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db      21 TSTWTIHFSAEKMTYDEDSAYCOQNTYHLVIAONKEEDIDLNSILDYSPSYTWIGIRKVN 80
Oy      96 GTATWGVTNKSLTEBAEWMDGEPEPNKKKNKEDCEVIITIKRNKDAGKWDDACHIKLAALC 155
| | | | | : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db      81 NWMIIVGTGRHKPLTEGAKKMWADPEEPNNKKONNECCVEIYTIKRPDGTGMWNDERCSKKRIALC 140

```

B

Db Qy Db Qy Db	 161 YTAAGTAAACSCSGHGGICIEIINNYSCCKCPGPGSLKCEADVYVCEADVPQHGSILNCTHPLG 200 216 NFSBSOCACFSCSESTNLGTDEITTCGPFGMNSPEPPCOYIQCEPLSAPDLGINCSNP 275 201 NFNYSNCSSVSVCERYELPSSFTETTWCTSSGEASAPPAACKVECCPMKGKPANGDVKCSPS 260 276 LASFSFTSACTPTFCSEGTLELIGKKRTIKCESSGIWENPSPICO 317 261 QGSAPMNNTCTCFDCEEGFTLLGARSLQCTSSSMWNEMKNPTCK 302
--	---

C

RESULT B42755 N:Alternate names: C:Species: C>Date: C:Accession:	 14 E-selectin precursor - mouse Mus musculus (house mouse) 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000 S53174; B42755
---	---

D

Eur. A>Title: Reference number:	 J. Blochm, M.; van Huijsdunjen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J. Murine endothelial leukocyte-adhesion molecule 1 is a close structural and f 92283265
---------------------------------------	---

A:Molecule type: DNA
A:Residues: 1-612 <BEC>
A:Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
R:Weller, A.; Iseemann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A:Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-selectin in mouse endothelial cells.
A:Reference number: A42755; MUID:92340571
A:Accession: B42755
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'MKATGV', 1-389, 391-612 <MEL>
A:Cross-references: GB:M87862; NID:g193107
A:Experimental source: endothelial cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109470)

A/Note: the sequence in GenBank entry MUSELEEC, release 117.0, (PID:AAA37577.1; PID:q1
 A/Note: It is uncertain whether the initiator is Met-1 or the AUG codon preceding that
 C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement fact
 C/Keywords: glycoprotein; transmembrane protein
 F:1-21/Domain: signal sequence homology <LCH>
 F:12-138/Domain: C-type lectin homology <LCH>
 F:22-612/Product: P-selectin #status predicted <MAT>
 F:143-174/Domain: EGF homology <EGF>
 F:180-238/Domain: complement factor H repeat homology <FH1>
 F:243-300/Domain: complement factor H repeat homology <FH2>
 F:305-363/Domain: complement factor H repeat homology <FH3>
 F:368-426/Domain: complement factor H repeat homology <FH4>
 F:431-489/Domain: complement factor H repeat homology <FH5>
 F:494-548/Domain: complement factor H repeat homology <FH6>
 F:525,528/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.5%; Score 857; DB 2; Length 612;
 Best Local Similarity 51.4%; Pred. No. 3e-56;
 Matches 148; Conservative 42; Mismatches 96; Indels 2; Gaps 2;

QY 31 LAHGYTCWTHYSEKPMNQRRRCRDNYTLVAIONKAETLEYLTKLPFSRSTYWG 90
 DB 15 LAGEST-AMTYNASSSELMTYDEASACQRDYTHLVAIONKEELYNLSNLKHSPTYYWG 73
 QY 91 IRKIGIMTWGTVNKSILTEEAENMGDEPNKKKEDCVETIYIKRNKAGKNDACIKL 150
 DB 74 IRKYNVNWIMVIGKPLTEBAQNAWAPERNKKRNEDCVETIYIORTKDSGMWDERCNKK 133
 QY 151 KAALCYTASCQPMSCSGHGECVEIINNHTCNCVGYGQCQLVIOCEPLAELGTMDC 210
 DB 134 KIALCYTASCTNASCSGHGECITFINSYCKCHPGLFPCNCEQAVCKPOEHPDYSIAC 193
 QY 211 THPEGNFSSQCAFCSSETNLTGIEET-CGPFNMSSPEPTCOVIOCEPLSAPDLGI 269
 DB 194 SHPEGPFSTNSSCSFGCKRGLPDSMETTYRCSSGEMWAPACHAVECEALTHPAHGI 253
 QY 270 MNCSHPLASFSTACTFICSEGTETLIGKKKTICESSGIWNSPPIQ 317
 DB 254 RRCSSNPGSYPMWNTCTCFPCVEGRRVGAQNLCTSSGIMDNFTPSCK 301

RESULT 15
 S36772
 E-selectin - bovine
 C:Species: Bos primigenius taurus (catle)
 C>Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
 C:Accession: S36772
 R:Nguyen, M.; Strudel, N.A.; Bischoff, J.
 Nature 365, 267-269, 1993
 A>Title: A role for sialyl Lewis-X/A glycoconjugates in capillary morphogenesis.
 A:Reference number: S36772; MUID:93382537
 A:Accession: S36772
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-485 <NGD>
 A/Cross-references: GB:U12039; NID:9402913; PID:AAA02991.1; PID:9402914
 C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement facto
 F:13-139/Domain: C-type lectin homology <LCH>
 F:181-237/Domain: complement factor H repeat homology <FH1>
 F:242-299/Domain: complement factor H repeat homology <FH2>
 F:304-362/Domain: complement factor H repeat homology <FH3>
 F:367-421/Domain: complement factor H repeat homology <FH4>

Query Match 40.1%; Score 849.5; DB 2; Length 485;
 Best Local Similarity 53.0%; Pred. No. 8.6e-56;
 Matches 148; Conservative 40; Mismatches 90; Indels 1; Gaps 1;

QY 39 WTHYSEKPMNQRRRCRDNYTLVAIONKAETLEYLTKLPFSRSTYWGIRKIGTW 98
 DB 23 WSHYHSTEMTTEARDYCOCKTYTALVAIONDEBELYNSTSYSPSYWIGIRKIGTW 82

Search completed: October 13, 2001, 02:55:06
 Job time: 4208 sec

QY 99 TWVGTNKSILTEEAENMGDEPNKKKEDCVETIYIKRNKAGKNDACIKLKAALCYTA 158
 DB 83 TWIGTNSLTKKATNNAPGEPNNKQSDCEVEIYIKREKDSGMWDERCKTKALACTYA 142
 QY 159 SCQPMSCSGHGEVEIINNHTCNCVGYGQCQLVIOCEPLAELGTMDCTHPGNFS 218
 DB 143 ACNPTGCGSHGECVEIINNHTYTCCHGFGKLCQEVVTCPAQKHPBGHLVC-NPLGKFT 201
 QY 219 FSSQCAFCSSEGTNLGIEETGPPGNSSPEPTCOVIOCEPLSAPDLGIWNSHPLAS 278
 DB 202 YNSSCSISCAEGYLPSTETATRCMSSGEMWSTPLKCNVVCDAISLMDNGVWNCSPNHS 261
 QY 279 FSFTSACTFICSEGTETLIGKKKTICESSGIWNSPPIQ 317
 DB 262 LPWNTTCTFPCQBGYKLTGPQHLCITSSGIMDNKOPFCR 300

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:54:03 ; Search time 53.96 Seconds
(without alignments)
236.157 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKQOSTGRDLMNIFKL.....WLARRLKKGKSKSRMNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	98.8	372	1	LEM1_HUMAN
2	2085	98.5	372	1	LEM1_PANTR
3	2062	97.4	372	1	LEM1_PONPY
4	1996	94.3	372	1	LEM1_MNCMU
5	1992	94.1	372	1	LEM1_PAPHA
6	1682	79.5	370	1	LEM1_BOVIN
7	1653	78.1	372	1	LEM1_RAT
8	1651	78.0	372	1	LEM1_MOUSE
9	919.5	43.5	769	1	LEM3_SHEEP
10	905	42.8	830	1	LEM3_HUMAN
11	902.5	42.7	768	1	LEM3_MOUSE
12	894.5	42.3	646	1	LEM3_BOVIN
13	885	41.8	768	1	LEM3_RAT
14	862	40.7	610	1	LEM2_HUMAN
15	861	40.7	551	1	LEM2_RABIT
16	860	40.6	611	1	LEM2_CANFA
17	858.5	40.6	549	1	LEM2_RAT
18	857	40.5	612	1	LEM2_MOUSE
19	849.5	40.1	485	1	LEM2_BOVIN
20	814.5	38.5	484	1	LEM2_PIG
21	212.5	10.0	1019	1	LFC_TACTR
22	199.5	9.4	1231	1	CFAH_HUMAN
23	195	9.2	858	1	HIG_DROME
24	189.5	9.0	1019	1	LFC_CARRO
25	172	8.1	2039	1	CRI_HUMAN
26	171	8.1	2333	1	PGCA_CANFA
27	168	7.9	2132	1	PGCA_HUMAN
28	167	7.9	331	1	FCE2_HUMAN
29	167	7.9	1234	1	CFAB_MOUSE
30	166.5	7.9	558	1	C4BP_MOUSE
31	166	7.8	390	1	DARF_MOUSE
32	166	7.8	1456	1	MANR_HUMAN
33	166	7.8	2364	1	PGCA_BOVIN

34	165	7.8	311	1	LECI_HUMAN	P07307	homo sapien
35	165	7.8	548	1	KUCR_MOUSE	P70194	rattus musculu
36	163	7.7	2124	1	PGCA_RAT	P07897	rattus norv
37	162.5	7.7	345	1	APOH_BOVIN	P17650	bos taurus
38	162	7.7	304	1	MGGL_MOUSE	P49300	mus musculu
39	160	7.6	2415	1	PGCA_HUMAN	P16112	homo sapien
40	157	7.4	331	1	FCE2_MOUSE	P20693	mus musculu
41	157	7.4	469	1	C4BP_MOUSE	P08607	mus musculu
42	157	7.4	610	1	C4BP_BOVIN	P28065	bos taurus
43	156.5	7.4	207	1	LECH_CHICK	P02707	gallus gall
44	156.5	7.4	1025	1	CR2_MOUSE	P19070	mus musculu
45	156	7.4	258	1	C4BP_RAT	P06315	rattus norv

ALIGNMENTS

RESULT	1	STANDARD	PRT	372 AA.
LEM1_HUMAN				
ID	LEM1_HUMAN			
AC	P14151; P15023;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR)			
DE	MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL)			
DE	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LFCAM1) (CD62L).			
GN	SEL1 OR LYAM1 OR LNH1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89315837; PubMed=2664786;			
RA	Siegelman M.H., Weissman I.L.;			
RT	"Human homologue of mouse lymph node homing receptor: evolutionary			
RT	conservation at tandem cell interaction domains.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:5562-5566(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=tonsil;			
RX	MEDLINE=89310350; PubMed=2473156;			
RA	Tedder T.F., Isaacs C.M., Ernst T.J., Demetri G.D., Adler D.A.,			
RT	"Isolation and chromosomal localization of cDNAs encoding a novel			
RT	human lymphocyte cell surface molecule, LAM-1. Homology with the			
RT	mouse lymphocyte homing receptor and other human adhesion proteins.";			
RL	J. Exp. Med. 170:123-133(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90044046; PubMed=2509939;			
RA	Camerini D., James S.P., Stamenkovic I., Seed B.;			
RT	"Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing			
RT	receptor.";			
RL	Nature 342:78-82(1989).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89308881; PubMed=2663882;			
RA	Bowen B.R., Nguyen T., Lasky L.A.;			
RT	"Characterization of a human homologue of the murine peripheral lymph			
RT	node homing receptor.";			
RL	J. Cell Biol. 109:421-427(1989).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90243637; PubMed=1692315;			
RA	Ord D.C., Ernst T.J., Zhou L.J., Rambaldi A., Spertini O.,			
RT	Griffith J., Tedder T.F.;			
RT	"Structure of the gene encoding the human leukocyte adhesion			
RT	molecule-1 (TQ1, Leu-8) of lymphocytes and neutrophils.";			
RL	J. Biol. Chem. 265:7760-7767(1990).			
RN	[6]			
RP	3D-STRUCTURE MODELING.			

RA Tsurushita N.;
 RU Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE
 CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
 CC VENTILES IN PERIPHERAL LYMPH NODES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U73728; AAB18248.1; -
 CC HSSP: P14151; IKJB.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -
 DR InterPro: IPR002396; -
 DR Pfam: PF00008; EGF_1;
 DR Pfam: PF00059; lectin_c; 1.
 DR Pfam: PF00084; sush1; 2.
 DR PRINTS: PR00343; SELECTIN.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
 DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 KW Selectin; Signal; Sush1; Repeat.
 FT SIGNAL 1 28
 FT PROPEP 29 38
 FT CHAIN 39 372
 FT DOMAIN 39 332
 FT TRANSMEM 333 355
 FT DOMAIN 356 372
 FT DOMAIN 55 155
 FT DOMAIN 156 192
 FT DOMAIN 196 317
 FT DOMAIN 196 255
 FT DOMAIN 258 317
 FT DISULFID 57 155
 FT DISULFID 128 147
 FT DISULFID 160 171
 FT DISULFID 165 180
 FT DISULFID 182 191
 FT DISULFID 197 241
 FT DISULFID 227 254
 FT DISULFID 259 303
 FT CARBOHYD 289 316
 FT CARBOHYD 60 60
 FT CARBOHYD 104 104
 FT CARBOHYD 117 177
 FT CARBOHYD 216 216
 FT CARBOHYD 232 232
 FT CARBOHYD 246 246
 FT CARBOHYD 271 271
 SQ SEQUENCE 372 AA: 42188 MW: 6EA991802A2D3643 CRC64;

Query Match 98.5%; Score 2085; DB 1; Length 372;
 Best Local Similarity 98.7%; Pred No. 1e-162;
 Matches 367; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MFEPMKCGSTORDLWNIIFKLGWTLMLCDFLAHGTYCWTYHYSEKPMNQARRECRDN 60
 DB 1 MFEPMKCGSTORDLWNIIFKLGWTLMLCDFLAHGTYCWTYHYSEKPMNQARRECRDN 60

OY 61 YTDVLAIQNAKLEIEYKTLPSRSYYWIGIRKIGGIWTVGNKSLTEBAEMNGDEPN 120
 DB 61 YTDVLAIQNAKLEIEYKTLPSRSYYWIGIRKIGGIWTVGNKSLTEBAEMNGDEPN 120
 OY 121 NKKNKEDCEVETIYKRNKDAGKAMDACCHKLKAALCTYASCPMSGSGHCEVEIINHTC 180
 DB 121 NKKNKEDCEVETIYKRNKDAGKAMDACCHKLKAALCTYASCPMSGSGHCEVEIINHTC 180
 OY 181 NCDVGYGPGCQVLVIOCEPLEDELGTMDCTHPFGNFSSSGCAFCSEGTNLGTJETT 240
 DB 181 NCDVGYGPGCQVLVIOCEPLEDELGTMDCTHPFGNFSSSGCAFCSEGTNLGTJETT 240
 OY 241 CGPFGMWSSPEPTCOYVQCCEPLSAPDLGTNCSHPLASFSFACPTFISEGTNLGKKK 300
 DB 241 CGPFGMWSSPEPTCOYVQCCEPLSAPDLGTNCSHPLASFSFACPTFISEGTNLGKKK 300
 OY 301 TIESSGIMSNPSPICOKLDKSFMKEGDYNFLTPVAWYAFSGLAFTIWLARLKK 360
 DB 301 TIESSGIMSNPSPICOKLDKSFMKEGDYNFLTPVAWYAFSGLAFTIWLARLKK 360
 OY 361 GKSKRSMDPY 372
 DB 361 GKSKRSMDPY 372
 RESULT 3
 LEM1_PONPY STANDARD; PRT; 372 AA.
 AC 095235;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION
 DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1)
 DE (LECAM1) (CD62L).
 GN SELL.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,
 RA Tsurushita N.;
 RU Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE
 CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
 CC VENTILES IN PERIPHERAL LYMPH NODES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U73729; AAB18247.1; -
 CC HSSP: P14151; IKJB.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -
 DR InterPro: IPR002396; -
 DR Pfam: PF00008; EGF_1;
 DR Pfam: PF00059; lectin_c; 1.
 DR Pfam: PF00084; sush1; 2.
 DR PRINTS: PR00343; SELECTIN.
 DR PROSITE: PS00022; EGF_1; 1.

```

DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
FT SIGNAL; 1
FT PROPEP; 29
FT CHAIN; 39
FT DOMAIN; 39
FT TRANSMEM; 333
FT DOMAIN; 356
FT DOMAIN; 55
FT DOMAIN; 156
FT DOMAIN; 196
FT DOMAIN; 196
FT DOMAIN; 255
FT DOMAIN; 258
FT DISULFID; 57
FT DISULFID; 128
FT DISULFID; 160
FT DISULFID; 171
FT DISULFID; 180
FT DISULFID; 182
FT DISULFID; 197
FT DISULFID; 227
FT DISULFID; 227
FT DISULFID; 259
FT CARBOHYD; 289
FT CARBOHYD; 60
FT CARBOHYD; 104
FT CARBOHYD; 177
FT CARBOHYD; 216
FT CARBOHYD; 226
FT CARBOHYD; 232
FT CARBOHYD; 246
FT CARBOHYD; 271
SQ SEQUENCE; 372 AA; 42118 MW; 6517DD22213FF15E CRC64;

```

```

Query Match      97.4%; Score 2062; DB 1; Length 372;
Best Local Similarity 97.6%; Pred. No. 7, 5e-161;
Matches 363; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIEPWKCSOTQRDLMNFKLGMWMLCCPFLAHGTYCWTYHSEKPMNORARRCRON 60
DB 1 MIEPWKCSOTQRDLCNFKLGMWMLCCPFLAHGTYCWTYHSEKPMNORARRCRON 60
QY 61 YTPDLVIAONKAELEYLEKTLPEFSRSTYWGIRKIGIMTWGTVNKSLEAEWNGDGEPN 120
DB 61 YTPDLVIAONKAELEYLEKTLPEFSRSTYWGIRKIGIMTWGTVNKSLEAEWNGDGEPN 120
QY 121 NKKNKEDCEVIYIKRNKDKGNWDACHLKAALCYTASCOPWSCSGHGECEIINNHTC 180
DB 121 NKKNKEDCEVIYIKRNKDKGNWDACHLKAALCYTASCOPWSCSGHGECEIINNHTC 180
QY 181 NCOVGYGQCQULVIOCEPLEAPELCTMDCTHPFGNFSSQCAFSCSEGTNLTGIEETT 240
DB 181 NCOVGYGQCQULVIOCEPLEAPELCTMDCTHPFGNFSSQCAFSCSEGTNLTGIEETT 240
QY 241 CGPFGNMSSPEPTQVIOCEPLSAPDLGIMNCSHPLASFSFSACTFICSEBTELGKCK 300
DB 241 CGPFGNMSSPEPTQVIOCEPLSAPDLGIMNCSHPLASFSFSACTFICSEBTELGKCK 300
QY 301 TICSSGGLWNSPPTQKIDKSFMSIKEGDYNPLPIPAVAVWTASGLAFITWLARRKK 360
DB 301 TICSSGGLWNSPPTQKIDKSFMSIKEGDYNPLPIPAVAVWTASGLAFITWLARRKK 360
QY 361 GKSKRSNMDDPY 372
DB 361 GKSKRSNMDDPY 372

```

```

RESULT 4
LEML_MACMU STANDARD; PRT; 372 AA.
AC 095198;

```

```

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LMA-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
DE DE SEL.
GN Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,
RA Teurushita N.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -! FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE
CC OF LYMPHOCTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
CC VENULES IN PERIPHERAL LYMPH NODES.
CC -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -! SIMILARITY: TO OTHER SELECTINS/LECAMS.
CC -! SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -! SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -! SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U73730; AAB18246.1; -
DR HSSP; P1451; IKJB.
DR InterPro; IPR000436; -
DR InterPro; IPR000561; -
DR InterPro; IPR001304; -
DR InterPro; IPR002396; -
DR Pfam; PF00008; EGF_1;
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sush1; 2.
DR PRINTS; PRO0343; SELECTIN.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL; 1
FT PROPEP; 29
FT CHAIN; 39
FT DOMAIN; 39
FT TRANSMEM; 333
FT DOMAIN; 356
FT DOMAIN; 372
FT DOMAIN; 55
FT DOMAIN; 156
FT DOMAIN; 196
FT DOMAIN; 196
FT DOMAIN; 255
FT DISULFID; 57
FT DISULFID; 128
FT DISULFID; 160
FT DISULFID; 171
FT DISULFID; 180
FT DISULFID; 182
FT DISULFID; 191
FT DISULFID; 197
FT DISULFID; 227
FT DISULFID; 227
FT DISULFID; 259
FT CARBOHYD; 289
FT CARBOHYD; 60
FT CARBOHYD; 104
FT CARBOHYD; 177

```

```
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA; 42109 MW; 08BD7DD5AC549D6D CRC64;

Query Match 94.3%; Score 1996; DB 1; Length 372;
Best Local Similarity 93.8%; Pred. No. 1,8e-155;
Matches 349; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

OY 1 MIRPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTWCYTHYSEKPMNQARRFCRDN 60
D 1 MIRPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTWCYTHYSEKPMNQARRFCRDN 60
OY 61 YTDLVAIQNKAIELEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
D 61 YTDLVAIQNKAIELEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
OY 121 NKNKKEDCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCVEIINNHTC 180
D 121 NKNKKEDCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCVEIINNHTC 180
OY 181 NCDVGYGPOCOLVIOCEPLEAPDLGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
D 181 NCDVGYGPOCOLVIOCEPLEAPDLGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
OY 241 CGPFGNMSSPEPTCOYIQCEPLAPDLGIMNCSHPLASFSTACPTICSEGTLLIGKKK 300
D 241 CGPFGNMSSPEPTCOYIQCEPLAPDLGIMNCSHPLASFSTACPTICSEGTLLIGKKK 300
OY 301 TIESSGINSNPICQKLDKSMIKEGDYNFLFPAVAVTAFAFLAIIIMLARLKK 360
D 301 TIESSGINSNPICQKLDKSMIKEGDYNFLFPAVAVTAFAFLAIIIMLARLKK 360
OY 361 GKSKRSMDPY 372
D 361 GKSKRSMDPY 372
Db 361 GKSKRSMDPY 372

RESULT 5
LEML_PAPHA STANDARD; PRT; 372 AA.
ID LEML_PAPHA 028768;
AC 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
GN SEL.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97128794; PubMed=8973334;
RA Tsurushita N., Fu H., Berg E.L.;
RT PCR cloning of the cDNA encoding baboon L-selectin."
RL Gene 181:219-220(1996).
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
CC VENELES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
```

```
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U52074; ABA0903.1; -.
DR HSSP: P14151; 1KJB.
DR InterPro: IPR000436; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR001304; -.
DR InterPro: IPR002396; -.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00059; lectin_C; 1.
DR Pfam: PF00084; sushi; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS0041; C-TYPE LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 335
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT DOMAIN 196 255
FT DOMAIN 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 60
FT CARBOHYD 104 104
FT CARBOHYD 177 177
FT CARBOHYD 226 226
FT CARBOHYD 232 232
FT CARBOHYD 246 246
FT CARBOHYD 271 271
SQ SEQUENCE 372 AA; 42091 MW; 64E7BD5AC549D69 CRC64;

Query Match 94.1%; Score 1992; DB 1; Length 372;
Best Local Similarity 93.5%; Pred. No. 3,8e-155;
Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

OY 1 MIRPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTWCYTHYSEKPMNQARRFCRDN 60
D 1 MIRPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTWCYTHYSEKPMNQARRFCRDN 60
OY 61 YTDLVAIQNKAIELEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
D 61 YTDLVAIQNKAIELEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
OY 121 NKNKKEDCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCVEIINNHTC 180
D 121 NKNKKEDCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCVEIINNHTC 180
OY 181 NCDVGYGPOCOLVIOCEPLEAPDLGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
D 181 NCDVGYGPOCOLVIOCEPLEAPDLGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
OY 241 CGPFGNMSSPEPTCOYIQCEPLAPDLGIMNCSHPLASFSTACPTICSEGTLLIGKKK 300
```

```

Db 241 CCEFGNMSPEPTQVYQCEPLAPDLGIMNSHPLASFSFSACTFSCSETEIGEKK 300
OY 301 TICESSGIMNSPITQCKDKFSMTKBDYNPLFIPAVVMYTAESGLAFITWLARLKK 360
Db 301 TICESSGIMNSPITQCKDKFSMTKBDYNPLFIPAVVMYTAESGLAFITWLARLKK 360
OY 361 GKRSKSMNDPY 372
Db 361 GKRSKSMNDPY 372

RESULT 6
LEMI_BOVIN STANDARD; PRT; 370 AA.
AC P98131;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
DE SEL.
GN Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=92164727; PubMed=1371468;
RA Walcheck B., White M., Kurk S., Kishimoto T.K., Jutila M.A.;
RT "Characterization of the bovine peripheral lymph node homing receptor: a lectin cell adhesion molecule (LECAM).";
RL Eur. J. Immunol. 22:469-476(1992).
RN 12;
RP SEQUENCE FROM N.A.
RX MEDLINE=9405053; PubMed=7694420;
RA Bosworth B.T., Dowbenko D., Shuster D.E., Harp J.A.;
RT "Bovine L-selectin: a peripheral lymphocyte homing receptor.";
RL Vet. Immunol. Immunopathol. 37:201-215(1993).
CC 1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.
CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC 1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC 1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC 1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC 1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licenses@sib-sib.ch).
CC -----
CC EMBL: X62882; CAA44676.1;
DR HSSP: P14151, 1KXB.
DR InterPro: IPR000436;
DR InterPro: IPR000561;
DR InterPro: IPR001304;
DR InterPro: IPR002396;
DR Pfam: PF00008; EGF_1;
DR Pfam: PF00059; lectin_C_1;
DR Pfam: PF00084; sushi_2;
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1;
DR PROSITE: PS01186; EGF_2;
DR PROSITE: PS00615; C-TYPE LECTIN_1;
DR PROSITE: PS00041; C-TYPE LECTIN_2;
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;

```

```

KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38 POTENTIAL.
FT CHAIN 39 370 L-SELECTIN.
FT DOMAIN 39 333 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 334 354 POTENTIAL.
FT DOMAIN 355 370 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 55 155 C-TYPE LECTIN (SHORT FORM).
FT DOMAIN 156 192 EGF-LIKE.
FT DOMAIN 196 255 2 x SUSHI (SCR) REPEATS.
FT DOMAIN 196 255 SUSHI 1.
FT DOMAIN 258 317 SUSHI 2.
FT DISULFID 57 155 BY SIMILARITY.
FT DISULFID 128 147 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 197 241 BY SIMILARITY.
FT DISULFID 227 254 BY SIMILARITY.
FT DISULFID 259 303 BY SIMILARITY.
FT DISULFID 289 316 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 370 AA; 41971 MW; 92168F8116A9E9228 CRC64;

```

Query Match 79.5%; Score 1682; DB 1; Length 370;
 Best Local Similarity 77.0%; Pred. No. 6,5e-130;
 Matches 282; Conservative 42; Mismatches 40; Indels 2; Gaps 1;

```

OY 1 MIFPKCOSTORDLNNIFKLMGWMTCODFLAHGTCWYHYSEKPMNQARARFCRDN 60
Db 1 MIFPKCQNAORGLNNVYKLMWVIMLCODEFAHHGTCTWYHYSKRPMPEKARAFCDREN 60
OY 61 YTDVAIONKKAIEYELEKTLPEFSRYYWIGIRKIGITWVGTGKSLTEAEWNGDEPN 120
Db 61 YTDVAIONKKEIEYELKTLPEFSRYYWIGIRKIGITWVGTGKSLTEAEWNGDEPN 120
OY 121 NKKKEDCEVEIYIKRNDAGKWNDDACHKALCYTASQCPWSCGSGECVEIINNHTC 180
Db 121 NKKSEDCVEIYIKRNDSCGMNDACHKAKTALCYTASCPWSCGSGHGCVEIINNHTC 180
OY 181 NCDVGYGPOCOLYQCEPLAPDLGIMNSHPLASFSFSACTFSCSETEIGEETT 240
Db 181 NCDVGYGPEQFVYQCEPLAPDLGIMNSHPLASFSFSACTFSCSETEIGEETT 240
OY 241 CGEPGNMSPEPTQVYQCEPLAPDLGIMNSHPLASFSFSACTFSCSETEIGEETT 300
Db 241 CAPGNMSPEPTQVYQCEPLAPDLGIMNSHPLASFSFSACTFSCSETEIGEETT 300
OY 301 TICESSGIMNSPITQCKDKFSMTKBDYNPLFIPAVVMYTAESGLAFITWLARLKK 360
Db 301 TICESSGIMNSPITQCKDKFSMTKBDYNPLFIPAVVMYTAESGLAFITWLARLKK 360
OY 361 GKRSK 366
Db 360 -RKSK 364

RESULT 7
LEMI_RAT STANDARD; PRT; 372 AA.
AC P30836;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)

```

DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION
MOLECULE-1) (LAM-1) (LY-22) (LYMPHOCYTE SURFACE MEL-14 ANTIGEN)
DE (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
GN SELL OR LNH OR LY-22.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92329548; PubMed=1378303;
RA Watanabe T., Song Y., Hirayama Y., Tamatani T., Kuida K., Miyasaka M.;
RT "Sequence and expression of a rat cDNA for LECAM-1.";
RL Blochm. Biophys. Acta 1131:321-324 (1992).
CC - FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE
OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
VENULES IN PERIPHERAL LYMPH NODES.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC - SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC - SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D10831; BAA01613.1; -
DR PIR: S23936; S23936.
DR HSSP: P14151; IKJB.
DR Interpro: IPR000436; -
DR Interpro: IPR000561; -
DR Interpro: IPR001304; -
DR Interpro: IPR002396; -
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00059; LECTIN_C_1.
DR Pfam: PF00084; SUSHI_2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE-LECTIN_1; 1.
DR PROSITE: PS00041; C-TYPE-LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 372
FT TRANSMEM 33 355
FT DOMAIN 335 372
FT DOMAIN 355 372
FT DOMAIN 156 155
FT DOMAIN 196 317
FT DOMAIN 196 317
FT DOMAIN 255 255
FT DOMAIN 317 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 60
FT CARBOHYD 104 104
FT CARBOHYD 177 177
FT CARBOHYD 226 226
FT CARBOHYD 246 246
FT CARBOHYD 246 246

FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA: 42441 MW: 38884E0F1EAD191A CRC64;
Query Match 78.1%; Score 1653; DB 1; Length 372;
Best Local Similarity 76.9%; Pred. No. 1.5e-127;
Matches 286; Conservative 35; Mismatches 51; Indels 0; Gaps 0;
QY 1 MIFPWWQSTQORDLWNTFKLMGWTMLCCDFLANHGTYCTWYHYSEKMMNQRRARFCRDN 60
DB 1 MIFPWWQSTQORDLWNTFKLMGWTMLCCDFLANHGTYCTWYHYSEKMMNQRRARFCRDN 60
QY 61 YTPDVAIONAKREIELEKTLPEFSRYWIGIRKIGIWTWGNKSLTEBAENMGDCEPN 120
DB 61 YTPDVAIONAKREIELEKTLPEFSRYWIGIRKIGIWTWGNKSLTEBAENMGDCEPN 120
QY 121 NKRKEDCEVETIKRNKADKAMDACHKLAALCYTASQCPSCSGHGEVETIINHTC 180
DB 121 NKRKEDCEVETIKRNKADKAMDACHKLAALCYTASQCPSCSGHGEVETIINHTC 180
QY 181 NCDVGYGPOCQVLYOCEPLEAPELGTMDCTHPGNSFSSQCAFSCSEGTNLGTIEET 240
DB 181 NCDVGYGPOCQVLYOCEPLEAPELGTMDCTHPGNSFSSQCAFSCSEGTNLGTIEET 240
QY 241 CGPFGWNSPEPCOVYTOCEPLASAPDLGIMNCSHPLASFSTSCPTGSEGTIELGKK 300
DB 241 CGPFGWNSPEPCOVYTOCEPLASAPDLGIMNCSHPLASFSTSCPTGSEGTIELGKK 300
QY 301 TIGSSGINSNPSPICCKLKDSESMKEGDNPLFIPAAVWTAFAFSLARLIWLARLKK 360
DB 301 TIGSSGINSNPSPICCKLKDSESMKEGDNPLFIPAAVWTAFAFSLARLIWLARLKK 360
QY 361 GKRSKRSMDPY 372
DB 361 GKRSKRSMDPY 372
QY 361 GKRSKRSMDPY 372
DB 361 GKRSKRSMDPY 372
RESULT 8
LEMI_MOUSE STANDARD; PRT; 372 AA.
ID LEMI_MOUSE
AC P18337;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION
MOLECULE-1) (LAM-1) (LY-22) (LYMPHOCYTE SURFACE MEL-14 ANTIGEN)
DE (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
GN SELL OR LNH OR LY-22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89162048; PubMed=2646713;
RA Siegelman M.H., van de Rijn M., Weissman I.L.;
RT "Mouse lymph node homing receptor cDNA clone encodes a glycoprotein
revealing tandem interaction domains.";
RT Science 243:1165-1172 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90263086; PubMed=1693096;
RA Siegelman M.H., Cheng I.C., Weissman I.L., Wakeland E.K.;
RT "The mouse lymph node homing receptor is identical with the
lymphocyte cell surface marker Ly-22: role of the EGF domain in
endothelial binding.";
RT Cell 61:611-622 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168433; PubMed=2647302;
RA Lasky L.A., Singer M.S., Yednock T.A., Dowbenko D., Fennie C.,
Rodriguez H., Nguyen T., Stachel S., Rosen S.D.;
RT "Cloning of a lymphocyte homing receptor reveals a lectin domain.";

```

RL Cell 56:1045-1055(1989).
RN [4]
RP SEQUENCE OF 1-360 FROM N.A.
RX MEDLINE-91169529; Pubmed-2004776;
RA Dovenko D.J., Diep A., Taylor B.A., Lusis A.J., Lasky L.A.;
RT "Characterization of the murine homing receptor gene reveals
RT correspondence between protein domains and coding exons.";
RT Genomics 9:270-277(1991).
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDATE THE ADHERENCE
CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
CC VENUES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X14772; CAA32880.1; -
DR EMBL: M36005; AAA39722.1; -
DR EMBL: M36058; AAA39723.1; -
DR EMBL: M25324; -; NOT ANNOTATED_CDS.
DR EMBL: M64549; AA75651.1; -
DR EMBL: M64440; AA75651.1; JOINED.
DR EMBL: M64345; AA75651.1; JOINED.
DR EMBL: M64548; AA75651.1; JOINED.
DR PIR: A33375; A32375.
DR HSSP: P14151; 1KJb.
DR MGD: MGT:98279; Se11.
DR InterPro: IPR000436; -
DR InterPro: IPR000361; -
DR InterPro: IPR001304; -
DR InterPro: IPR002396; -
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00059; lectin_C_1.
DR Pfam: PF00084; sush1_2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00615; C-TYPE-LECTIN_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00041; C-TYPE-LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT DOMAIN 196 255
FT DOMAIN 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 104
FT CARBOHYD 104 177
FT CARBOHYD 177 177

```

```

FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 32 32 I -> T (IN REF. 4).
SQ SEQUENCE 372 AA; 42288 MW; 4433EDF64CB2B78 CRC64;

Query Match 78.0%; Score 1651; DB 1; Length 372;
Best Local Similarity 76.1%; Pred. No. 2,2e-127;
Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MFPWKCOSTORDLWNIIFLWGTWMLCCDFLAHGHGYCTHYSEKPMWQARFRCNDN 60
Dy 1 MFPWKEGTYWMSRNILKLTWTLCCDFLIHGHCHTTHYSEKPMWQARFRCNDN 60
QY / 61 YPDVAIQKAELEYELKLPFSRSTYWGIRKIGIWTWGTNKSLTDEANMGDGEPN 120
Dy 61 YPDVAIQKAELEYELKLPFSRSTYWGIRKIGIWTWGTNKSLTDEANMGDGEPN 120
QY 121 NKKNKEDCEYIYIKRNKDGKWNDDACHKKAALCYTASCOFSGSCGEGCEIINNHC 180
Dy 121 NKKSKEDCEYIYIKRERDGSKNDDACHKKAALCYTASCOFSGSCGEGCEIINNHC 180
QY 181 NCDVGYGPOCOLVIOCEPLEAPELGTMDCTHPFNFSFSCAFSCSEGTNLGIEETT 240
Dy 181 IDAGYGPQCOYVOCPELEAPELGTMDCTHPFNFSFSCAFSCSEGTNLGIEETT 240
QY 241 CGPFGWSSPEPTCOVIOCEPLSAPDLGIMNSHPLASFPSACTFICSSTELIGKK 300
Dy 241 CGASGWSPEPTCOVIOCEPLSAPDLGIMNSHPLASFPSACTFICSSTELIGKK 300
QY 301 TIJESSGIWNSNPICOKLIDKFSMIKEGDYNPLETPAVWVTFSGIATFIWLRRLK 360
Dy 301 TCGASGWSPEPTCOVIOCEPLSAPDLGIMNSHPLASFPSACTFICSSTELIGKK 360
QY 361 GKSKRSNDPT 372
Dy 361 GKSKRSNDPT 372
Db 361 GKSKRSNDPT 372

RESULT 9
LEMS3_SHEEP STANDARD; PRT; 769 AA.
ID LEMS3_SHEEP
AC P98109;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Burns S.A., Neufeld E.J., Donady J.J.;
RT Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUCOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.

```

FT	CARBOHYD	655	655	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT <td>CARBOHYD <td>662 <td>662 <td>N-LINKED (GLCNAC. . .) <td>(POTENTIAL). </td></td></td></td></td>	CARBOHYD <td>662 <td>662 <td>N-LINKED (GLCNAC. . .) <td>(POTENTIAL). </td></td></td></td>	662 <td>662 <td>N-LINKED (GLCNAC. . .) <td>(POTENTIAL). </td></td></td>	662 <td>N-LINKED (GLCNAC. . .) <td>(POTENTIAL). </td></td>	N-LINKED (GLCNAC. . .) <td>(POTENTIAL). </td>	(POTENTIAL).
		666	666	N-LINKED (GLCNAC. . .) <td>(POTENTIAL). </td>	(POTENTIAL).

RT "Structure and function of the epidermal growth factor domain of p-selectin."

RT selectin"; structure and function of the epidermal growth factor domain of F


```

RN [4]
RP 3D-STRUCTURE MODELING OF 42-161.
RX MEDLINE=94033388; PubMed=7505680;
RA Bajorath J., Stenkamp R., Aruffo A.;
RT Knowledge-based model building of proteins: concepts and examples.";
RL Protein Sci. 2:1798-1810(1993).
RN [5]
RP VARIANTS ASN-331; ASP-603; VAL-640 AND PRO-756.
RX MEDLINE=98334547; PubMed=9668170;
RA Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,
RA Riddaers J.B., Arveiller D., Luc G., Cambien F.;
RT "The P-selectin gene is highly polymorphic: reduced frequency of the
RT Pro715 allele carriers in patients with myocardial infarction.";
RL Hum. Mol. Genet. 7:1277-1284(1998).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUCOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 9 SUSII (SCR) REPEATS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD62p entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M60217; AAA35910.1; JOINED.
DR EMBL, M60217; AAA35910.1; JOINED.
DR EMBL, M60218; AAA35910.1; JOINED.
DR EMBL, M60219; AAA35910.1; JOINED.
DR EMBL, M60222; AAA35910.1; JOINED.
DR EMBL, M60223; AAA35910.1; JOINED.
DR EMBL, M60224; AAA35910.1; JOINED.
DR EMBL, M60225; AAA35910.1; JOINED.
DR EMBL, M60226; AAA35910.1; JOINED.
DR EMBL, M60227; AAA35910.1; JOINED.
DR EMBL, M60228; AAA35910.1; JOINED.
DR EMBL, M60229; AAA35910.1; JOINED.
DR EMBL, M60231; AAA35910.1; JOINED.
DR EMBL, M60232; AAA35910.1; JOINED.
DR EMBL, M60233; AAA35910.1; JOINED.
DR EMBL, M25322; -. NOT ANNOTATED_CDS.
DR PIR, A30359; A30359.
DR PDB, 1FSB; 01-APR-97.
DR PDB, 1KJD; 03-APR-96.
DR MIM, 173610; -.
DR InterPro; IPR000436; -.
DR InterPro; IPR000561; -.
DR InterPro; IPR001304; -.
DR InterPro; IPR002396; -.
DR Pfam; PF00008; EGF_1;
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; sushi; 9.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS0186; EGF_2; 1.
DR PROSITE; PS50615; C-TYPE_LECTIN_2; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
RW Selectin; Signal; Sushi; Repeat; Lipoprotein; Palmitate; Polymorphism;
RW 3D-structure.

```

[illegible]

QY 68 QNKAETLEYLKTLPFSKSYWIGRTGTMVGTNKSLTTEENNGDGPNNKKKED 127
DB 71 QNKNEDIDYLNKVPYSSYYWIGIRKNNKNTWGTGKTKALTEENWADENPNKRNED 130
QY 128 CVELIYKRNNDACKGKNDACDKLKAALCYTASCOVSCSGCEVELIYNNHTCCDVGYY 187
DB 131 CVELIYKSPAPGKNDDEHLKKAALCYTASCOVSCSGCEVELIYNNHTCCDVGYY 190
QY 188 GPQCQVLYQCEPLEAPBLGTMDCVTHPGRNFSFSCAFSCSEGTNLGIEETTCGPGNW 247
DB 191 GPCEVYRECGEDELPHVYVLMNSCHPLGNFSNQCSCFHCCTDGYVNGPCKLECLAGIWM 250
QY 248 SSEPPTQVLYQCEPLEAPBLGTMDCVTHPGRNFSFSCAFSCSEGTNLGIEETTCGPGNW 307
DB 251 TNNPPOCLAQCPPLKIPERGNNICLHSAKAFHOSSCSFCEGFAVPEVVOCTASG 310
QY 308 TMSNPSPICQ 317
DB 311 VMTAPAPVCK 320

RESULT 11
LEW3 MOUSE STANDARD; PRT: 768 AA.
AC Q01102;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP OR GRMP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92340571; PubMed=1378846;
RA Weller A., Isenmann S., Vestweber D.;
RT "Cloning of the mouse endothelial selectins. Expression of both E-
and P-selectin is inducible by tumor necrosis factor alpha.";
RT J. Biol. Chem. 267:15176-15183(1992).
RL [2]
RN SEQUENCE FROM N.A.
RA MEDLINE=92345617; PubMed=1379089;
RA Sanders W.E., Jr., Wilson R.W., Ballantyne C.M., Beaudet A.L.;
RT "Molecular cloning and analysis of in vivo expression of murine P-
selectin.";
RT Blood 80:795-800(1992).
RL -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STORED IN ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECTINS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
CC THE HUMAN SUSHI-2 EQUIVALENT.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL: M87861; AAA40008.1; -;
DR EMBL: M72332; AAA37712.1; -;
DR PIR: A42755; A42755.
DR HSSP: P16109; IFSB.
DR MGD: MGI:98280; Selp.
DR InterPro: IPR000436; -;
DR InterPro: IPR000561; -;
DR InterPro: IPR001304; -;
DR InterPro: IPR002396; -;
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00059; lectin_C; 1.
DR Pfam: PF00084; sush1; 8.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat; Lipoprotein; Palmitate.
FT SIGNAL 1 41
FT CHAIN 42 768
FT DOMAIN 42 709
FT TRANSMEM 710 733
FT DOMAIN 734 768
FT DOMAIN 58 158
FT DOMAIN 159 195
FT DOMAIN 199 700
FT DOMAIN 199 258
FT DOMAIN 261 320
FT DOMAIN 323 382
FT DOMAIN 385 444
FT DOMAIN 447 506
FT DOMAIN 509 568
FT DOMAIN 579 638
FT DOMAIN 641 700
FT DISULFID 60 158
FT DISULFID 131 150
FT DISULFID 163 174
FT DISULFID 168 183
FT DISULFID 185 194
FT DISULFID 200 244
FT DISULFID 230 257
FT DISULFID 262 306
FT DISULFID 292 319
FT DISULFID 324 368
FT DISULFID 354 381
FT DISULFID 386 430
FT DISULFID 416 443
FT DISULFID 448 492
FT DISULFID 478 505
FT DISULFID 510 554
FT DISULFID 540 567
FT DISULFID 580 624
FT DISULFID 610 637
FT DISULFID 642 686
FT DISULFID 672 699
FT CARBOHYD 398 398
FT CARBOHYD 603 603
FT CARBOHYD 654 654
FT CARBOHYD 661 661
FT CARBOHYD 679 679
FT LIPID 745 745
FT SITE 756 759
FT CONFLICT 724 724
FT SEQUENCE 768 AA; 83098 MW; E5173074D2F66E8 CRC64;

QY 20 LMGWTMLCCPFLAHNGYVCTYHSEKPMNQRARRCRONTYDVAIQNKAETLEYLKT 79
Query Match 42.7%; Score 902.5; DB 1; Length 768;
Best Local Similarity 52.0%; Pred. No. 4.3e-66;
Matches 156; Conservative 40; Mismatches 103; Indels 1; Gaps 1;

```

Db 24 1W-FSALISELVNOKVEVAAATYNTSKAYSWANNSRVEFCRRHFTDVALIONKNEIHLNDV 82
QY 80 LPEFSRYSYIGIRKIGITWTGNSLPEEANGDGPNNKKRKECVETIYIRKMDA 139
Db 83 IPEFNSYVIGIRKINNKWTWGTNKTLEENADNEPNKKNOCCEVETIYIRKSNAP 142
QY 140 GWRNDACRKLKALCYTASCPMSCSGHCEVEIINNHTCNDVGYGPOCOLVIOCEP 199
Db 143 GWRNDEPCRRKRALCYTASCPMSCSGHCEVEIINNHTCNDVGYGPOCOLVIOCEP 202
QY 200 LEAPELGTMDCTHPRGNSFSSCAFSCSEGNLTGIEETCGPRGNSSPEPTCOVITQC 259
Db 203 VAIIPHVLHNCNCHPLGEFSFNSQCFSCAEGVELDPELQCLASGIVTNNPKDAVOC 262
QY 260 EPLSAPDGIINCSHPLASFSFTNACTPFCSEGTLEICKRTICESGIGWNSPDIQOKL 319
Db 263 OSLEAPRPGTMACHPIAFAVYDSSCKRCECPGYRARSNTLHCTGSGQSEPLPTCEAI 322

```

RESULT 12

LEM3_BOVIN STANDARD; PRT; 646 AA.

AC P42201;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE P-SELECTIN RECEPTOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).

GN SELP.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RC SEQUENCE FROM N.A.

RP TISSUE=Capillary endothelium;

RX MEDLINE=93249394; Pubmed=7683458;

RA Strubel N.A., Nguyen M., Kansas G.S., Tedder T.F., Bischoff J.;

RT "Isolation and characterization of a bovine cDNA encoding a

functional homolog of human P-selectin."

RL Biochem. Biophys. Res. Commun. 192:338-344(1993).

CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUCOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO THE CELL SURFACE.

CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMS.

CC -1- SIMILARITY: CONTRAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

CC -1- SIMILARITY: CONTRAINS 6 SUSHI (SCR) REPEATS; BOVINE P-LECTIN LACKS THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

CC EMBL: L12041; AAA30743.1; -

DR HSSP: P16109; 15SB.

DR InterPro: IPR000436; -

DR InterPro: IPR000561; -

DR InterPro: IPR001304; -

DR InterPro: IPR002396; -

DR Pfam: PF00008; EGF_1.

```

DR Pfam: PF00059; lectin_c; 1.
DR Pfam: PF00084; sushi; 6.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 41
FT CHAIN 42 646
FT DOMAIN 42 587
FT TRANSMEM 588 611
FT DOMAIN 612 646
FT DOMAIN 38 158
FT DOMAIN 159 195
FT DOMAIN 199 578
FT DOMAIN 199 258
FT DOMAIN 261 320
FT DOMAIN 323 382
FT DOMAIN 385 444
FT DOMAIN 457 516
FT DOMAIN 519 578
FT DISULFID 60 158
FT DISULFID 131 150
FT DISULFID 163 174
FT DISULFID 168 183
FT DISULFID 185 194
FT DISULFID 200 244
FT DISULFID 230 257
FT DISULFID 262 306
FT DISULFID 292 319
FT DISULFID 324 368
FT DISULFID 354 381
FT DISULFID 386 430
FT DISULFID 416 443
FT DISULFID 458 502
FT DISULFID 488 515
FT DISULFID 520 564
FT DISULFID 550 577
FT CARBOHYD 48 48
FT CARBOHYD 54 54
FT CARBOHYD 80 80
FT CARBOHYD 180 180
FT CARBOHYD 212 212
FT CARBOHYD 219 219
FT CARBOHYD 336 336
FT CARBOHYD 481 481
FT CARBOHYD 532 532
FT CARBOHYD 539 539
FT CARBOHYD 557 557
FT SITE 634 637
SQ SEQUENCE 646 AA; 71229 MW; 573912A4627A6ACA CRC64;

```

Query Match 42.3%; Score 894.5; DB 1; Length 646;
Best Local Similarity 48.7%; Pred. No. 1.6e-65;
Matches 155; Conservative 51; Mismatches 109; Indels 3; Gaps 1;

```

QY 2 IFPKCOOSTRODLAMNFKLMGWTMLCCDFLAHGYTCWYHSEKPMKQRRARRCRONY 61
Db 8 IIMNR---TQRAVFRVQLCTSVLFEVINQEVSAWYHNSNTYSMNYSRAFCQRY 64
QY 62 TDVAIONKAEIYELEKTLPEFSRYSYVIGIRKIGITWTGNSLPEEANGDGPNN 121
Db 65 TDVAIONKNEIAYLNETIPYNSYVIGIRKINNKWTWGTNKTLEENADNEPN 124
QY 122 KKKKECVETIYIRKNDACKRNDACRKLKALCYTASCPMSCSGHCEVEIINNHTCN 181
Db 125 KRNNOCEVEIYIKSSAPKWNDEPCRRKRALCYRASCQDMSCSKQEGCEIETIGNYCS 184
QY 182 CDVGYGPOCOLVIOCEPLPELGTMDCTHPRGNSFSSCAFSCSEGNLTGIEETC 241

```



```

RESULT 14
LEM2_HUMAN STANDARD: PRT: 610 AA.
ID LEM2_HUMAN
AC P16581; P16111.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
DE (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
DE (CD62E).
GN SELE OR ELAM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90175359; PubMed=1689848;
RA Hession C., Osborn L., Goff D., Chi-Rosso G., Vassallo C.,
RA Passak M., Pittack C., Tizard R., Goelz S., McCarthy K., Hopple S.,
RA Lobb R.;
RT "endothelial leukocyte adhesion molecule 1: direct expression cloning
RT and functional interactions.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:1673-1677(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89162047; PubMed=2466335;
RA Bevilacqua M.P., Stengelin S., Gimbrone M.A. Jr., Seed B.;
RT "endothelial leukocyte adhesion molecule 1: an inducible receptor for
RT neutrophils related to complement regulatory proteins and lectins.";
RL Science 243:1160-1165(1989).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91115870; PubMed=1703529;
RA Collins T., Williams A., Johnston G.I., Kim J., Eddy R., Shows T.,
RA Gimbrone M.A. Jr., Bevilacqua M.P.;
RT "Structure and chromosomal location of the gene for endothelial-
RT leukocyte adhesion molecule 1.";
RL J. Biol. Chem. 266:2466-2473(1991).
[4]
RP LIGAND.
RX MEDLINE=91068005; PubMed=1701274;
RA Phillips M.L., Nudelmann E., Gaeta F.C., Perez M., Singhal A.K.,
RA Hakomori S., Paulson J.C.;
RT "ELAM-1 mediates cell adhesion by recognition of a carbohydrate
RT ligand, sialyl-Lex.";
RL Science 250:1130-1132(1990).
[5]
RP 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RX MEDLINE=93202275; PubMed=7681016;
RA Mills A.;
RT "Modelling the carbohydrate recognition domain of human E-selectin.";
RL FEBS Lett. 319:5-11(1993).
[6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 22-178.
RX MEDLINE=94150646; PubMed=7509040;
RA Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li S.,
RA Huang K.-S., Prekry D.H., Familletti P.C., Wollitzky B.A., Burns D.K.;
RT "Insight into E-selectin/ligand interaction from the crystal
RT structure and mutagenesis of the lec/EGF domains.";
RL Nature 367:533-538(1994).
[7]
RP VARIANT ARG-149.
RX MEDLINE=95179107; PubMed=7533025;
RA Wenzel K., Felix S., Kleber F.X., Brachold R., Menke T., Schatke S.,
RA Schulte K.L., Glaser C., Rohde K., Baumann G., Speer A.;
RT "E-selectin polymorphism and atherosclerosis: an association study.";
RL Hum. Mol. Genet. 3:1935-1937(1994).
[8]
RP VARIANT ARG-149.
RX MEDLINE=99134508; PubMed=9933738;
RA Ye S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Gupta R.;
RT "A psci polymorphism detects the mutation of serine-128 to arginine in

```

```

RT CD 62E gene - a risk factor for coronary artery disease.";
RL J. Biomed. Sci. 6:18-21(1999).
CC -1- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
CC MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY
CC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCCOSYLATED DERIVATIVES OF
CC POLYACETOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
CC GLYCOLIPIDS).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH A
CC HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFICANTLY
CC HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIENTS WITH
CC ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED WITH AN
CC UNSELECTED POPULATION (SER-149).
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD62e entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd62e.htm".
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
-----
DR EMBL; M30640; AAA52377.1; -
DR EMBL; M61893; AAA52375.1; JOINED.
DR EMBL; M61895; AAA52375.1; JOINED.
DR EMBL; M61887; AAA52375.1; JOINED.
DR EMBL; M61888; AAA52375.1; JOINED.
DR EMBL; M61890; AAA52375.1; JOINED.
DR EMBL; M61891; AAA52375.1; JOINED.
DR EMBL; M61892; AAA52375.1; JOINED.
DR EMBL; M24736; AAA52376.1; -
DR PIR; A32606; A32606.
DR PIR; A35046; A35046.
DR PIR; A38615; A38615.
DR PDB; 1ESL; 31-APR-94.
DR PDB; 1KJA; 03-APR-96.
DR MIM; 131210; -
DR InterPro; IPR000436; -
DR InterPro; IPR000561; -
DR InterPro; IPR001304; -
DR InterPro; IPR002396; -
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 6.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat; Polymorphism; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 610
FT DOMAIN 22 556 E-SELECTIN.
FT TRANSMEM 557 578 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 579 610 POTENTIAL.
FT DOMAIN 38 138 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 139 175 EGF-LIKE.
FT DOMAIN 179 548 6 X SUSHI (SCR) REPEATS.
FT DOMAIN 179 238 SUSHI 1.
FT DOMAIN 241 300 SUSHI 2.
FT DOMAIN 303 363 SUSHI 3.
FT DOMAIN 366 426 SUSHI 4.
FT DOMAIN 429 489 SUSHI 5.
FT DOMAIN 492 548 SUSHI 6.
FT DISULFID 40 138
FT 111 130

```


Query Match	40.7%;	Score 861;	DB 1;	Length 551;
Best Local Similarity	51.8%;	Pred. No. 7.2e-63;		
Matches 146;	Conservative 41;	Mismatches 95;	Indels 0;	Gaps 0;

```
Search completed: October 13, 2001, 02:59:38
Job time: 335 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:55:12 ; Search time 85 Seconds
(without alignments)
579.029 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKOSTQORDLMNIFKL.....MLARRKKGKSKSRMNDPY 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.16:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.unclassified:*
13: sp.vertebrate:*
14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	98.8	385	6 Q9UJ43	Q9UJ43 homo sapien
2	1796	84.9	376	4 Q28629	Q28629 oryctolagus
3	1667	78.8	372	11 Q63762	Q63762 rattus norv
4	911	43.1	616	4 Q95509	Q95509 homo sapien
5	909	43.0	740	4 Q95507	Q95507 homo sapien
6	898	42.4	740	4 Q95508	Q95508 homo sapien
7	884	41.8	754	6 Q28290	Q28290 canis faml
8	876.5	41.4	646	6 Q28097	Q28097 sus scrofa
9	860.5	40.7	649	6 Q28657	Q28657 oryctolagus
10	860	40.6	609	6 Q9GLF0	Q9GLF0 canis faml
11	815.5	38.5	382	6 Q28982	Q28982 sus scrofa
12	248.5	11.7	3567	11 Q9ES77	Q9ES77 mus musculu
13	247.5	11.7	1124	5 Q9VYR4	Q9VYR4 drosophila
14	237.5	11.2	974	5 P91658	P91658 drosophila
15	236	11.2	868	5 Q18849	Q18849 caenorhabd
16	216	10.2	1061	5 Q9VXX7	Q9VXX7 drosophila
17	199.5	9.4	449	4 Q14570	Q14570 homo sapien
18	199.5	9.4	449	4 Q9NU86	Q9NU86 homo sapien
19	199.5	9.4	1172	4 Q9NU87	Q9NU87 homo sapien

20	195	9.2	866	5 Q917E3	Q917E3 drosophila
21	195	9.2	933	5 Q917E4	Q917E4 drosophila
22	195	9.2	958	5 Q9V560	Q9V560 drosophila
23	192.5	9.1	481	4 Q9H284	Q9H284 homo sapien
24	189.5	9.0	1083	5 Q26423	Q26423 carcinoscor
25	183	8.6	328	4 Q9UJ71	Q9UJ71 homo sapien
26	176	8.3	378	6 Q62837	Q62837 sagittinus oe
27	175.5	8.3	2014	6 Q29530	Q29530 pan troglod
28	173	8.2	1653	5 Q9VIT9	Q9VIT9 drosophila
29	172	8.1	2039	4 Q16745	Q16745 homo sapien
30	172	8.1	2489	4 Q16744	Q16744 homo sapien
31	171.5	8.1	395	14 Q9J2M6	Q9J2M6 macaca mula
32	171	8.1	354	5 Q9U611	Q9U611 drosophila
33	171	8.1	359	5 Q9V0X3	Q9V0X3 drosophila
34	170	8.0	314	6 Q62835	Q62835 sagittinus oe
35	170	8.0	404	4 Q9NNX6	Q9NNX6 homo sapien
36	169.5	8.0	559	4 Q9UQV2	Q9UQV2 homo sapien
37	168	7.9	292	4 Q14538	Q14538 homo sapien
38	168	7.9	533	11 Q08569	Q08569 cavla porce
39	166	7.8	1911	6 Q29528	Q29528 papio hamad
40	165.5	7.8	560	5 Q22328	Q22328 caenorhabd
41	165.5	7.8	1479	11 Q64449	Q64449 mus musculu
42	165	7.8	287	4 Q03969	Q03969 homo sapien
43	165	7.8	292	4 Q00448	Q00448 homo sapien
44	164.5	7.8	377	6 Q62838	Q62838 sagittinus oe
45	164	7.8	214	11 Q9R0Q8	Q9R0Q8 mus musculu

ALIGNMENTS

RESULT 1	Q9UJ43	PRELIMINARY;	PRT;	385 AA.
AC	Q9UJ43;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	L-SELECTIN PRECURSOR.			
GN	L-SELECTIN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEMATOPOIETIC (B LYMPHOCYTE);			
RA	Fleiger C.B.;			
RU	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEMATOPOIETIC (B LYMPHOCYTE);			
RA	Fleiger C.B.;			
RU	Thesis (1998), Freie Universitaet Berlin, Fachbereich Chemie.			
DR	EMBL: AJ246000; CAB5486.1; -.			
DR	HSSP: P14151; IKCB.			
DR	InterPro: IPR000436; -.			
DR	InterPro: IPR000561; -.			
DR	InterPro: IPR001304; -.			
DR	InterPro: IPR002396; -.			
DR	Pfam: PR00008; EGF_1.			
DR	Pfam: PR00059; EGF_1.			
DR	Pfam: PR00084; sushi; 2.			
DR	PRINTS: PR00343; SELECTIN.			
DR	PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.			
DR	PROSITE: PS00041; C-TYPE_LLECTIN_2; 1.			
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE: PS01186; EGF_2; 1.			
DR	SMART: SM00032; CCP; 1.			
DR	EGF-like domain; Glycoprotein; Lectin; Selectin; Signal.			
FT	POTENTIAL.			
FT	CHAIN 1 51 L-SELECTIN.			
FT	SEQUENCE 385 AA; 43617 MW; 1205F691BA638EF1 CRC64;			

Query Match 98.8%; Score 2090; DB 4; Length 385;
Best Local Similarity 98.9%; Pred. No. 1.6e-197;
Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 MIFPMKCSOTQORDLWNTFKLMGWTMLCCDFLAHGTGTCWYHYSEKPMNORARFCRDN 60
    |||||||
DB 14 MIFPMKCSOTQORDLWNTFKLMGWTMLCCDFLAHGTGTCWYHYSEKPMNORARFCRDN 73
    |||||||
QY 61 YTDLVAIONKAEIYELEKTLPEFSRSYYWIGIRKIGIWTWVGNTKSLTEAENMGDEPN 120
    |||||||
DB 74 YTDLVAIONKAEIYELEKTLPEFSRSYYWIGIRKIGIWTWVGNTKSLTEAENMGDEPN 133
    |||||||
QY 121 NKKKKECEVEIYIKRNKDAGKNDACHKLKALCTYASCPWCSGHECEVEIINNHTC 180
    |||||||
DB 134 NKKKKECEVEIYIKRNKDAGKNDACHKLKALCTYASCPWCSGHECEVEIINNHTC 193
    |||||||
QY 181 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 240
    |||||||
DB 194 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 253
    |||||||
QY 241 CGPFGWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTGSEGTLLGKKK 300
    |||||||
DB 254 CGPFGWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTGSEGTLLGKKK 313
    |||||||
QY 301 TIGESSGIMSNPSPIQKLDKSFMSIKEGDYNPLFTIPVAVMTAFSGLAFTIWLARLKK 360
    |||||||
DB 314 TIGESSGIMSNPSPIQKLDKSFMSIKEGDYNPLFTIPVAVMTAFSGLAFTIWLARLKK 373
    |||||||
QY 361 GKSKRSMDPY 372
    |||||||
DB 374 GKSKRSMDPY 385
```

RESULT 2 PRELIMINARY: PRT; 376 AA.

```
ID 028629
AC 028629; PRELIMINARY: PRT; 376 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE L-SELECTIN PRECURSOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, CORTEX;
RA Qian J., Marks R.M.;
RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL: U26535; AAA67896.1;
DR HSSP: P14151; IKTJ.
DR InterPro: IPR000436;
DR InterPro: IPR000561;
DR InterPro: IPR001304;
DR InterPro: IPR002396;
DR Pfam: PF00008; EGF_1;
DR Pfam: PF00059; lectin_C_1;
DR Pfam: PF00084; sushi_2;
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00615; C_TYPE_LECTIN_1;
DR PROSITE: PS00615; C_TYPE_LECTIN_2;
DR PROSITE: PS00622; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2;
DR SMART: SM00032; CCP_1;
DR EGF-like domain; Glycoprotein; Lectin; Signal.
FT SIGNAL 1
FT CHAIN 39 376 POTENTIAL.
SQ SEQUENCE 376 AA; 42346 MM; 59F6AD530F490947 CRC64;
```

Query Match 84.9%; Score 1796; DB 6; Length 376;
Best Local Similarity 84.1%; Pred. No. 1.3e-168;
Matches 311; Conservative 24; Mismatches 35; Indels 0; Gaps 0;

```
QY 1 MIFPMKCSOTQORDLWNTFKLMGWTMLCCDFLAHGTGTCWYHYSEKPMNORARFCRDN 60
    |||||||
DB 1 MIFPMKCSOTQORDLWNTFKLMGWTMLCCDFLAHGTGTCWYHYSEKPMNORARFCRDN 60
    |||||||
QY 61 YTDLVAIONKAEIYELEKTLPEFSRSYYWIGIRKIGIWTWVGNTKSLTEAENMGDEPN 120
    |||||||
DB 61 YTDLVAIONKAEIYELEKTLPEFSRSYYWIGIRKIGIWTWVGNTKSLTEAENMGDEPN 120
    |||||||
QY 121 NKKKKECEVEIYIKRNKDAGKNDACHKLKALCTYASCPWCSGHECEVEIINNHTC 180
    |||||||
DB 121 NKKKKECEVEIYIKRNKDAGKNDACHKLKALCTYASCPWCSGHECEVEIINNHTC 180
    |||||||
QY 181 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 240
    |||||||
DB 181 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 240
    |||||||
QY 241 CGPFGWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTGSEGTLLGKKK 300
    |||||||
DB 241 CGPFGWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTGSEGTLLGKKK 300
    |||||||
QY 301 TIGESSGIMSNPSPIQKLDKSFMSIKEGDYNPLFTIPVAVMTAFSGLAFTIWLARLKK 360
    |||||||
DB 301 TIGESSGIMSNPSPIQKLDKSFMSIKEGDYNPLFTIPVAVMTAFSGLAFTIWLARLKK 360
    |||||||
QY 361 GKSKRSMD 370
    |||||||
DB 361 GKSKRSMD 370
```

RESULT 3

ID 063762 PRELIMINARY: PRT; 372 AA.

```
AC 063762;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE LYMPHOCTE MEMBRANE PROTEIN A.11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=95369821; PubMed=7543874;
RT Sackstein R., Meng L., Xu X.M., Chin Y.H.;
RT "Evidence of post-transcriptional regulation of L-selectin gene
    expression in rat lymphoid cells.";
RL Immunology 85:198-204(1995).
DR EMBL: S79523; AAC60710.2;
DR HSSP: P14151; IKTJ.
DR InterPro: IPR000436;
DR InterPro: IPR000561;
DR InterPro: IPR001304;
DR InterPro: IPR002396;
DR Pfam: PF00008; EGF_1;
DR Pfam: PF00059; lectin_C_1;
DR Pfam: PF00084; sushi_2;
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00615; C_TYPE_LECTIN_1;
DR PROSITE: PS00615; C_TYPE_LECTIN_2;
DR PROSITE: PS00622; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2;
DR SMART: SM00032; CCP_1;
DR EGF-like domain; Glycoprotein.
SQ SEQUENCE 372 AA; 42471 MM; 7DFD125610DD6E4A CRC64;
```

Query Match 78.8%; Score 1667; DB 11; Length 372;

Best Local Similarity 77.2%; Pred. No. 6,5e-156;
Matches 287; Conservative 35; Mismatches 50; Indels 0; Gaps 0;

Oy	1	MIIPKQCSOTRODLNIFIKLGMWIMLCCDFLAHHGTCSWTHYSEKEMNQARAFRCRD	60
Db	1	WVEPFRCSAGRGSMSFKLIMTWLCCDILLPHGHGTCHWTYHYSEKEMENAKRPFCKH	60
Oy	61	YTDVAIONKRAIEIELEKTLPEFRSRYWIGIRIGGWTWGTAKSLTEAEAKNGDCEPN	120
Db	61	YTDVAIONKKEIEIELEKTLPEKNPTYYWIGIRIKGKWTWWTGKTKLTERENNGTCEPN	120
Oy	121	NKKNKEDCEVEIYIKRNKDAGKAMDACHKHLKALCYTASCPMSCSGHGECEVLINHTC	180
Db	121	NKSKEDCEVEIYIKRERDSGKAMDACHKRAALCYTASCPRESCNRHGECEVLINHTC	180
Oy	181	NCDNGYTPQCQOLVYQCEPRLAPELGTMDCTHPRGNFSSFOCAFSCSEGTNLGTIEET	240
Db	181	ICDPGYTPQCQOLVYQCEPRLAPELGTMDCTHPRGNFSSFOCAFSCSEGTNLGTIEET	240
Oy	241	CGPFGMSSEPTECOVIOCEPRLAPDLGINMCSHPLASFSTSCAPTEICSGEFTLICKK	300
Db	241	CGASGNMYYLEITCIVDIOCMPLAPDLGTMCSHPLANFSTSCACTTCSEEDLIGERK	300
Oy	301	TICESSGTISNPSPIQCKLDRKSFEMIKEGEDNPNPIFVAWVTAFFSGLAFITLARLKK	360
Db	301	TYCRSSGSSMSPSPIQCKLDRKSFEMIKEGEDNPNPIFVAWVTAFFSGLAFITLARLKK	360
Oy	361	GKSKRSRNDPY 372	
Db	361	GKSKQERMDPY 372	

RESULT	4			
095509				
ID	095509	PRELIMINARY;	PRT;	616 AA.
AC	095509;			
DT	01-MAY-1999 (TREMBLrel, 10, Created)			
DT	01-MAY-1999 (TREMBLrel, 10, last sequence update)			
DT	01-MAY-2001 (TREMBLrel, 16, last annotation update)			
DE	DJ780M13.1.3 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN			
DE	CD62, GMF140)) (ISOFORM 3) (FRAGMENT)).			
GN	SELp.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Howden P.;			
RL	Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AL022146; CAAL8144.1; -.			
DR	HSSP: P16109; 1KID.			
DR	InterPro: IPR000436; -.			
DR	InterPro: IPR000561; -.			
DR	InterPro: IPR001304; -.			
DR	InterPro: IPR002396; -.			
DR	Pfam: PF00008; EGF_1.			
DR	Pfam: PF00059; lectin_C; 1.			
DR	Pfam: PF00084; sushi_6.			
DR	PRINTS: PR00343; SELECTIN.			
DR	PROSITE: PS00615; C_type_LECTIN_1; 1.			
DR	PROSITE: PS50041; C_type_LECTIN_2; 1.			
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE: PS01186; EGF_2; 1.			
DR	SMART: SM00032; CCP; 1.			
KW	EGF-like domain; Glycoprotein.			
FT	NON_TER	616		
SQ	SEQUENCE	616 AA; 67735 MW; 35CD4BFAD61D724 CRC64;		

Query Match 43.1%; Score 911; DB 4; Length 616;
Best Local Similarity 50.6%; Pred. No. 3e-81;
Matches 158; Conservative 47; Mismatches 107; Indels 0; Gaps 0;

[illegible]

```

RESULT      5
ID           095507      PRELIMINARY;      PRT;      740 AA.
AC           095507;
DT           01-MAY-1999 (TREMBLrel, 10, Created)
DT           01-MAY-1999 (TREMBLrel, 10, last sequence update)
DT           01-MAR-2001 (TREMBLrel, 16, last annotation update)
DE           D/J780M13.1.1 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN
DE           CD62, GMP140)) (ISOFORM 1) (FRAGMENT).
GN           SELP.
OS           Homo sapiens (Human).
OC           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX           NCBI_TaxID=9606;
RN           [1]
RP           SEQUENCE FROM N.A.
RA           Howden P.;
RL           Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR           EMBL: AL022146; CA18142.1; -.
DR           HSSP: P16109; 1KJD.
DR           InterPro: IPR000436; -.
DR           InterPro: IPR000561; -.
DR           InterPro: IPR001304; -.
DR           InterPro: IPR001396; -.
DR           Pfam: PF00008; EGF_1.
DR           Pfam: PF00059; lectin_C.1.
DR           Pfam: PF00084; sushi_8.
DR           PRINTS: PR00343; SELECTIN.
DR           PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR           PROSITE: PS00041; C_TYPE_LLECTIN_2; 1.
DR           PROSITE: PS00022; EGF_1; UNKNOWNW_1.
DR           PROSITE: PS01186; EGF_2; 1.
DR           SMART: SM00032; CCP_1.
DR           Egf-like domain; Glycoprotein.
FT           NON_TER      740
SQ           SEQUENCE      740 AA;      81095 MW;      3B5F70A45B1A3C4D CRC64;

```

	Query Match	43.0%	Score 909;	DB 4;	Length 740;
	Best Local Similarity	50.3%;	Pred No 5.9e-81;		
	Matches 157;	Conservative 48;	Mismatches 107;	Indels 0;	Gaps 0;
OY	8	OSTGDDLNIEFLKMTWMLCCDFLAHHGYCTTYHSEKPMNQRRRCRDNYDVAI	67		
Db	11	QRFORVFESLLOCFASLISLTNQEVAATYTHSTAYSAWMNSIRKKCQRHYTDVAI	70		
OY	68	QKAKELEYLEKLFPERSRYTWIGIRKGITMNVGTNTSLTEAEENMGDGEPNNKNKD	127		

	Query Match Best Local Similarity	42.44; 50.66;	Score 898; Pred. No. 7.2e-80;	DB 4; Matches 158;	Length 740; Conservative 45;	Mismatches 109;	Indels 0;	Gaps
QY	8	QSTORDIMNIRKILGWMLCCDFLAHHGTCYMTYHSEKPNMORARPCNDYTDVAI	67					
DB	11	QRFPRVYVFIQGLLCFSAIIISLNLQKEVAAWMTYHTSKAYSMWISKRYCQNRITDVAI	70					
QY	68	QNKREIYELEKTLFFSNYYWIGIRKTGGIMTWYGVNKSILTEEAENGDEEPNNKKKK	127					
DB	71	QNKNEIDYLNKLVLPYSSYYWIGIRKNNKKTWMTWGTAKALTNEAENADNEPNKKRND	130					
QY	128	QVEYLIRKNDAGWMDACIKLKAALCYTASQPMWCSGSHGEVLEINNHCTCMCDVGY	187					
DB	131	QVEYLIRSPAPGKWNDEHCKLKKHNAICYTASQDMSCSKGGELELTIGYVTSQCVGY	190					

Query Match	41.8%	Score 884	DB 6	Length 754
Best Local Similarity	50.5%	Pred. No. 1,76-78		
Matches 151	Conservative 46	Mismatches 102	Indels 0	Gaps 0
QY	19	KLNGWMLCCDFLAHHGTCVHTYHSKRPMMQRRARFCRDNYTDLYAIQNAKIEIYLEK	78	
Db	7	KLCCFLVLELLKQEVAGWYTNSTAYSWNSRLEFCOHHYDVAIQNKKEIYLYND	66	
QY	79	TLEPSSRYWIGIRKIGGIWTVGNTKSLTEAEAWMGDEBPNNKKNKEDCEVEIYIRKND	138	
Db	67	VIPYNSYRWIGIRKINDKWTWVGTRKPLTEAEAWMAENBPNNKKNKQDCEVEIYIRSLA	126	
QY	139	AGKWDNDACHKLKAALCTYASQCPMSSCGHDECVIINNHTCNDGVGYYPQQLYIQE	198	
Db	127	PGAWNDPQWKKRRALCTYASQDMSCKSGOECEIETIGNYTCSCFPEYGSDEEYRREGC	186	
QY	199	PLEAPLEIGTMDCTHPGNGNFSGQAFCSGEGTNLTGIEETGCPFGGMSSEPTTCQVIO	258	

Db 187 DEDPQHVLNMCNCHPLGNFSPNSECSPFYCTEGVELNGPNSKLECLASGNTWTKPPRCVATQ 246

QY 259 CEPISADLDGIMNCNHPPLASFSTFSACTFICSECTELIGKKTKTCSSGATWSNPSPICQ 317

Db 247 CPLLKTEQSGMNCMLHSEAFQYOSCHFCSEGFALVGEVVOCTSGMWTAAAPVCE 305

RESULT 8

Q29097 PRELIMINARY; PRT; 646 AA.

ID Q29097; AC Q29097; DT 01-NOV-1996 (Tremblrel. 01, Created) DT 01-NOV-1996 (Tremblrel. 01, Last sequence update) DT 01-MAR-2001 (Tremblrel. 16, Last annotation update) DE P-SELECTIN PRECURSOR. OS Sus scrofa (Pig). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus. NCBI_TaxID=9823; RN [1] RP SEQUENCE FROM N.A. RC TISSUE-AORTA; RA Rollins S.A., Johnson K.K., Birks C.W., Mattis L.A., Rother R.P.; RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases. [2]

RP SEQUENCE FROM N.A. RC TISSUE-AORTA; RA MEDLINE=20171534; PubMed=10706724; RA Stocker C.J., Sugars K.L., Harari O.A., Landis R.C., Morley B.J., Hasard D.O.; RT "NF-alpha, IL-4, and IFN-gamma regulate differential expression of P- and E-selectin expression by porcine aortic endothelial cells."; RL J. Immunol. 164:3309-3315(2000).

DR EMBL: L39075; AAA/9007.1; -. DR HSSP: P16109; IFSB. DR InterPro: IPR000436; -. DR InterPro: IPR000561; -. DR InterPro: IPR001304; -. DR Pfam: PF00008; EGF_1. DR Pfam: PF00059; Lectin_C; 1. DR PRINTS: PR00343; SELECTIN. DR PROSITE: PS00615; C-TYPE_LECTIN_1; UNKNOWN_1. DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1. DR PROSITE: PS00022; EGF_1; UNKNOWN_1. DR PROSITE: PS01186; EGF_2; 1. DR SMART: SM00032; CCP; 1. DR EGF-like domain; Glycoprotein; Lectin; Selectin; Signal. FT SIGNAL 1 41 POTENTIAL. FT CHAIN 42 646 P-SELECTIN. SQ SEQUENCE 646 AA; 71127 MW; 3863F4AFE09F0BB6 CRC64;

Query Match 41.4%; Score 876.5; DB 6; Length 646; Best Local Similarity 46.3%; Pred. No. 8e-78; Matches 158; Conservative 48; Mismatches 124; Indels 11; Gaps 2;

QY 11 ORDLNFIKLMGTMCCDFLAHNGTCWTYHSEKPMNORARRPRDNYTDVAIONK 70

Db 14 QRSFRTVQLLFVALISDLNOKGVAAMTYNSTAYSMNTSHVFCQRYFTDLVALIQNK 73

QY 71 AETLELEKTPFSRSYWGIRKIGIWTWGTNKSITBEAENMGDEPNKKKNECDVE 130

Db 74 KELATYLVNDVPIYSSYVWIMRKINNKWTWVGTRKTLTQEAENNAKKNPNESNQCVE 133

QY 131 IYTRNKDACKNDADCHKLKALCYTASQPMSCSGHGECEVEIINNHTCNCDVGYTGPQ 190

Db 134 MYTKSLPAPKWNDEPCVKKRRALCYTASQSTSCSKQGECEETIGNYTSCSYSGFYGPR 193

QY 191 COLVIOCEPLEADELGMDCTHPFGNFSFSCQAFSCSEGTNLGIEETTCGPRGNMSSP 250

Db 194 CEYKCEGEFRLPOLVVLNCSHPLGNFNSQCSFHCAEGYTLNGPSELCLASGNTWTHP 253

QY 251 EPTCOVIOCEPLSADLDGIMNCNHPPLASFSTFSACTFICSECTELIGKKTKTCSSGATWS 310

Db 254 PPOCVAAVQCPLKSPKPEKNMACHSEKAFQYOSSCNFCEGEGYALVGEVVOCAQSGMWT 313

QY 311 NSPICKLCKSFMKEGQYNPLEIPAVAVWTAFA-SGLAF 350

Db 314 APVPCRAI-----TCEPLESPVYSGMDCFPSSRAF 344

RESULT 9

Q28657 PRELIMINARY; PRT; 649 AA.

ID Q28657; AC Q28657; DT 01-NOV-1996 (Tremblrel. 01, Created) DT 01-NOV-1996 (Tremblrel. 01, Last sequence update) DT 01-MAR-2001 (Tremblrel. 16, Last annotation update) DE P-SELECTIN. OS Oryctolagus cuniculus (Rabbit). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID=9986; RN [1] RP SEQUENCE FROM N.A. RA Vora D.K., Fang Z., Liva S.M., Parhami F., Watson A.D., Drake T.A., Territo M.C., Berliner J.A.; RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases. [2]

RP SEQUENCE FROM N.A. RA Warden C.H.; RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases. DR EMBL: U39446; AAA81385.1; -. DR HSSP: P16109; IFSB. DR InterPro: IPR000436; -. DR InterPro: IPR000561; -. DR InterPro: IPR001304; -. DR InterPro: IPR002396; -. DR Pfam: PF00008; EGF_1. DR Pfam: PF00059; Lectin_C; 1. DR PRINTS: PR00343; SELECTIN. DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1. DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1. DR PROSITE: PS00022; EGF_1; UNKNOWN_1. DR PROSITE: PS01186; EGF_2; 1. DR SMART: SM00032; CCP; 1. DR EGF-like domain; Glycoprotein; Lectin. SQ SEQUENCE 649 AA; 71755 MW; ECCD8C847B84BC31 CRC64;

Query Match 40.7%; Score 860.5; DB 6; Length 649; Best Local Similarity 48.3%; Pred. No. 3e-76; Matches 155; Conservative 53; Mismatches 104; Indels 9; Gaps 4;

QY 2 IEPWKCSTORDLNFIKLMGTMCCDFLAHNGTCWTYHSEKPMNORARRPRDNY 61

Db 8 IWNMR---FORAVERTVQLLCFSVLIFEVINQKEVSAMTYHNSKTYSMNYSRAFCQKY 64

QY 62 TDVAIONKAEIELEKTPFSRSYWGIRKIGIWTWGTNKSITBEAENMGDE 118

Db 65 TDVAIONKNEIDLVLEITPYNSYWGIRKDOQING--TWVG--NNKLTBEAENMGDNE 121

QY 119 PNKNKNEDECEIYIKRNKNDAGKNNDACHKLKALCYTASQPMSCSGHGECEVEIINN 178

Db 122 PNKNRNNDQCEIYIKLSAPGKNWDEPCVKKRRALCYRASQPMSCSKQGECEIETIGNY 181

QY 179 TNCNDVGYGPOCOLVIOCEPLEADELGMDCTHPFGNFSFSCQAFSCSEGTNLGIEE 238

Db 182 TCSQCPGYEGCEYVREWMSLDLPQHVHNMCSHPLGNFNSHCSFHACADGYALNPSE 241

QY 239 TTGCPFNWSSPEPTCOVIOCEPLSADLDGIMNCNHPPLASFSTFSACTFICSECTELIGK 298

Db 242 LBCLASGIWNSPPOCAVAVCPALSKPEQSGMSVCVSAFAFQHOSSCSFCEGFEIYGP 301
 QY 299 KKTICSSGIMNSPICOGL 319
 Db 302 EYVHCATGACVWTAFTPTVCAL 322

RESULT 10

09GLF0 PRELIMINARY; PRT: 609 AA.
 AC 09GLF0:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE E-SELECTIN.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RX NCBI_TaxID=9615;
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOTHELIUM.
 RA Zheng L., Shi Y., Wu H., Zhang G.;
 RT "Cloning and sequencing of beagle E-selectin genomic DNA and
 comparison with other species."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF287257; AAG10039.1; -
 KW Lectin; Selectin.
 SQ SEQUENCE 609 AA; 66073 MW; 41E62D1F4D23881F CRC64;

Query Match 40.6%; Score 860; DB 6; Length 609;
 Best Local Similarity 52.0%; Pred. No. 3.1e-76;
 Matches 145; Conservative 43; Mismatches 91; Indels 0; Gaps 0;

QY 39 WTYHSEKPMNORARFCRDNYTDVAIONKAEIETLEKTPESRSTYWGIRKIGTW 98
 Db 23 WSYNASTEATPTPEASAYCOQRTTHVAIONDEIETLMSFSTYPTTWIGIRKNKKW 82
 QY 99 TWVGTNKSLEEBENMGDGEPPNKKKKEDCEVEIYIKRNKDAGKNDACHKLAALCYTA 158
 Db 83 TWIGTKLLEAKNNAPGEPNNKQNDCEVEIYIKRKDSGKNDERDCKKLAALCYTA 142
 QY 159 SCQPMSCSGHGECEVETIINNHTCNCVGYGPOCOVIOCEPLAPLGTMDCTHPGANS 218
 Db 143 ACTPTSCSGHGECEVETIINNHTCNCVGYGPOCOVIOCEPLAPLGTMDCTHPGANS 202
 QY 219 FSSQCAFSCSEGTNLGIEETTCGPPGNWSPPTCOVIOCEPLAPLGTMDCTHPGANS 278
 Db 203 YNSSCFVSCDKGILPSTETATCTSTGEMASBPACNVCECSALTNPCGVMDCLQSSGN 262
 QY 279 FSTTACTFICSGTELLIGKKTKTICSSGIMNSPICO 317
 Db 263 FPMNMTCTPECBEGFELMGPKRLQCTSSGWNDRKPTCK 301

RESULT 11

028982 PRELIMINARY; PRT: 482 AA.
 AC 028982:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE E-SELECTIN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NCBI_TaxID=9623;
 RX NCBI_TaxID=9623;
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97075911; PubMed=8918234;
 RA Winkler H., Brostjan C., Csizmadia V., Nataraajan G., Anrather J.,
 Bach F.H.;

RT "The intron-exon structure of the porcine E-selectin-encoding gene."
 RL Gene 176:67-72(1996).
 DR EMBL: U37521; AAC48680.1; -
 DR HSP; P16581; 1ESL.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -
 DR InterPro: IPR002396; -
 DR Pfam: PF00008; EGF_1.
 DR Pfam: PF00059; Lectin_C_1.
 DR Pfam: PF00084; sushi_4.
 DR PRINTS: PR00343; SELECTIN.
 DR PROSITE: PS00615; C-TYPE-LECTIN_1; 1.
 DR PROSITE: PS00441; C-TYPE-LECTIN_2; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR SMART: SM00032; CCP; 1.
 KW EGF-like domain; Glycoprotein; Lectin.
 SQ SEQUENCE 482 AA; 52341 MW; 97DCSD70BFI15944 CRC64;

Query Match 38.5%; Score 815.5; DB 6; Length 482;
 Best Local Similarity 36.1%; Pred. No. 5.7e-72;
 Matches 159; Conservative 56; Mismatches 109; Indels 117; Gaps 7;

QY 39 WTYHSEKPMNORARFCRDNYTDVAIONKAEIETLEKTPESRSTYWGIRKIGTW 98
 Db 23 WSYNASTEATPTPEASAYCOQRTTHVAIONHAEIETLNSFNSASYSYWGIRKNGTW 82
 QY 99 TWVGTNKSLEEBENMGDGEPPNKKKKEDCEVEIYIKRNKDAGKNDACHKLAALCYTA 158
 Db 83 TWIGTKLLEAKNNAPGEPNNKQNDCEVEIYIKRKDSGKNDERDCKKLAALCYTA 142
 QY 159 SCQPMSCSGHGECEVETIINNHTCNCVGYGPOCOVIOCEPLAPLGTMDCT----- 211
 Db 143 ACTPTSCSGHGECEVETIINNHTCNCVGYGPOCOVIOCEPLAPLGTMDCT----- 202
 QY 212 -----HP-----FGNES 218
 Db 203 TCAFECKGFEIPEHLOCTSSGSMGKKPTCAVYCDTVGHQNDGVCNHSSTGEFA 262
 QY 219 FSSQCAFSCSEGTNLGIEETTCGPPGNWSPPTCOVIOCEPLAPLGTMDCTHPGANS 277
 Db 263 YKSTCHFCAEGFGLQGAQIECTAOGCOMTQOAPYCAVCAVPSQPKNLVFTHSPIG 322
 QY 278 SESPTACTFICSGTELLIGKKTKTICSSGIMNSPICO-----KLDKSFMTKEGD 330
 Db 323 EFTYKSSCAFSCEBGEFELRGSALACTSGQWTOEVPSCQVOCSSLEVPREIMSCSGE 382
 QY 331 YNPLF-----IPAVVWTA----- 344
 Db 383 --PVFAGVCTPACPEGMVNGSVALTGGATGHSGLPTCEAPAESKITPLAMGLAAGVS 440
 QY 345 -FSGLATIINLARKLKGGKS 364
 Db 441 FMTSASFLLMLKRLKRAKN 461

RESULT 12

09ES77 PRELIMINARY; PRT: 3567 AA.
 AC 09ES77:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE POLYOM PROTEIN PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HENSIC;

Query March	1.2%	Score 237.5	DB 5	Length 974
Best Local Similarity	25.2%	Pred. No. 1e-14		
Matches 85, Conservative	39	Mismatches 124	Indels 89	Gaps 18

RESULT 15

RA Parsons. J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Query Match	11.2%;	Score 236;	DB 5;	Length 868;
Best Local Similarity	22.3%;	Pred. No. 1.3e-14;		
Matches	84;	Conservative	48;	Mismatches 128;
			Indels	116;
			Gaps	18

```
Search completed: October 13, 2001, 03:02:16
Job time: 424 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:49:05 ; Search time 189.31 Seconds
(without alignments)
7492.630 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259
Sequence: 1 GAATTCACAGTGTCTGCTT.....CCGCCACACACTGGAAATTC 2259

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_0601.*
1: /cgnl_9/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgnl_9/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /cgnl_9/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /cgnl_9/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgnl_9/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /cgnl_9/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /cgnl_9/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /cgnl_9/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /cgnl_9/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /cgnl_9/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /cgnl_9/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /cgnl_9/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /cgnl_9/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /cgnl_9/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /cgnl_9/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /cgnl_9/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /cgnl_9/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /cgnl_9/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /cgnl_9/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /cgnl_9/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgnl_9/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /cgnl_9/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2259	100.0	2259	20	AAV08321 Human lymphocyte h
2	2255.8	99.9	2259	14	AAO44243 HULHR DNA. Homo s
3	2255.8	99.9	2259	16	AAO92802 Human LHR CDNA. H
4	2255.8	99.9	2259	16	AAT05869 Human LHR CDNA. H
5	2255.8	99.9	2259	17	AAT30003 Human lymphocyte c
6	2255.8	99.9	2259	19	AAV19012 Homo sapiens lymph
7	2254.2	99.8	2259	14	AAO43154 Human lymphocyte h
8	2251.6	99.7	2259	13	AAO12118 Sequence encoding
9	2241.6	99.2	2262	13	AAO24987 Human lymphocyte h
10	2241.2	99.2	2262	13	AAO24987 Sequence encoding
11	2127.8	94.2	2350	17	AAT14723 Human Leu8 antigen

12	2127.8	94.2	2350	21	AA50596 Human T-cell spect
13	2126.2	94.1	2350	13	AAO21184 Encodes T lymphocy
14	2126.2	94.1	2350	19	AAV63460 Human Leu8 antigen
15	2126.2	94.1	2350	20	AAV81217 Human Leu8 antigen
16	2087.6	92.4	2330	15	AAO31006 L-selectin CDNA.
17	2086	92.3	2330	14	AAO35142 LAM-1 B125 CDNA c1
18	2076.4	91.9	2330	14	AAO38839 Sequence of LAM-1
19	2076.4	91.9	2330	18	AAT72270 Human lymphocyte-a
20	2074.8	91.8	2330	14	AAO37304 LAM-1 CDNA from pl
21	2058.8	91.1	2337	11	AAO05871 Sequence encoding
22	2033.4	90.0	2330	13	AAO31767 Human LAM-1. Homo
23	1273.4	56.4	1914	21	AA50632 Human T-cell spect
24	1271.5	56.3	1914	13	AAO25500 Encodes T lymphocy
25	970.2	42.9	138169	21	AAA34791 Human adenosine re
26	970.2	42.9	141589	21	AAE20913 Human ELAM-1 poly
27	970.2	42.9	141589	21	AAE21127 Human low adenosin
28	970.2	42.9	141589	21	AAE21152 Human low adenosin
29	970.2	42.9	141589	21	AAA35005 Human adenosine re
30	970.2	42.9	141589	21	AAA35030 Human adenosine re
31	970.2	42.9	146981	21	AAE21442 Human ELAM-1 poly
32	922.2	40.8	1696	15	AAO71015 Lym-1 gene exon X
33	856.8	37.9	2214	13	AAO23624 Murine lymphocyte
34	856.8	37.9	2214	13	AAO24988 Sequence encoding
35	856.8	37.9	2214	14	AAO43155 Murine lymphocyte
36	856.8	37.9	2214	14	AAO44244 MLHR DNA. Mus mus
37	856.8	37.9	2214	16	AAO92803 Mouse LHR CDNA. M
38	856.8	37.9	2214	16	AAT05870 Mouse LHR CDNA. M
39	856.8	37.9	2214	17	AAT30004 Mouse lymphocyte c
40	856.8	37.9	2214	20	AAV08322 Mouse lymphocyte h
41	848.8	36.7	2214	12	AAO12119 Sequence encoding
42	828.8	36.7	1496	11	AAO05542 Sequence encoding
43	817.8	36.2	2219	19	AAV19013 Mus musculus lymph
44	885.2	17.1	531	15	AAO71009 Lym-1 gene exon I
45	385.2	17.1	5666	14	AAO38840 Sequence of exons

ALIGNMENTS

RESULT	ID	AAV08321 standard; DNA; 2259 BP.	Human lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein; lymphocyte binding; endothelium; graft rejection; inflammation; therapy; arthritis; autoimmune disease; lymphoma metastasis; lymphocyte accumulation; human; ss.
AAV08321	XX		
AAV08321	XX		
AAV08321	XX		
02-FEB-1999 (first entry)	XX		
Human lymphocyte homing receptor coding sequence.	XX		
Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein; lymphocyte binding; endothelium; graft rejection; inflammation; therapy; arthritis; autoimmune disease; lymphoma metastasis; lymphocyte accumulation; human; ss.	XX		
Homo sapiens.	OS		
US5840844-A.	PN		
24-NOV-1998.	PD		
10-AUG-1995; 95US-0513278.	PF		
23-FEB-1989; 89US-0315015.	PR		
31-OCT-1991; 91US-0786149.	PR		
06-MAY-1993; 93US-0059029.	PR		
10-AUG-1995; 95US-0513278.	PR		
(GETH) GENENTECH INC.	PA		
(REGC) UNIV CALIFORNIA.	PA		
Lasky LA, Rosen SD, Singer MS, Stachel SE;	PI		
WPI; 1999-034122/03.	DR		

Db 1741 ttcttaactccagtggaagtaatgaggggtcctgctcaagttgaaagagcttccatttcgacgtg 1800
QY 1801 TAGCCCTGGCCGCTGTGGAATTGGACCATCTATTATTACGTGGCTTCAGGGCTCCGCCACTT 1860
Db 1801 tagccctggccgctgtggaattggacaatccatttaactgagcttcagggctcccccacctt 1860
QY 1861 CTTGAGCCACCTCTCTTTTTCAGTTGGTGTACTTCACACGCTGACATCATGAGTGGCA 1920
Db 1861 ctctgagccacctctcttcttcagttgctgcgaactccacacctagacatccaaagatgcga 1920
QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCCCTGCGCGGTTTTTATGTTTGGGGGTTTGTCTGT 1980
Db 1921 agcaaaagagagagagagaaatagccctgcgcggtttttagtttggtggggttttgctgt 1980
QY 1981 TTCCCTTTTATGAGACCATCTATTCTTTATATGTCATAGTTTCTTTTATACGATATTA 2040
Db 1981 ttccctttaaagagaccatctcattcttaataagtaagttcttcttcaacgatatla 2040
QY 2041 TTAGTAAAGAAACATCATCGAATGCTAGTGCAGAGTCACTCTTTGATGTCATATGG 2100
Db 2041 ttagtaagaagaacatcatcgaaatgctagctgcaagtcacatctcttgatgcatatg 2100
QY 2101 AAGAGTTAAAGAGGTGAGAAATTCCTTGATTTCACAAATGAATGCTCTCTTCCCTG 2160
Db 2101 aagagttaaagaggtgagaaatctcttgatcacaatgaaatgctctccttccctg 2160
QY 2161 CCCCCAGAACTTTTATCATCTTACCTAGATTCATATTTCTTTAAATTCATCTCAGGC 2220
Db 2161 ccccccagaactttatccacttaactagaattcacaatcttctaataatcattcaccagc 2220
QY 2221 CTCCCTCAACCCGAGGGGCGCGAGCACACTGGAATTC 2259
Db 2221 ctccctcaaccccgaggcgccagcacactggaattc 2259

RESULT 2

AA044243
ID AA044243 standard: DNA; 2259 BP.

XX AA044243;

DT 11-JAN-1994 (first entry)

XX HULHR DNA.

XX Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;

KM LHR; endothelium; lymphoid tissue; signal; domain; complement binding;

KM carbohydrate binding; epidermal growth factor-like; egf; intracellular;

KM transmembrane binding; cytoplasmic; ligand binding partner protein;

KM TMD; LBPP; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

XX CDS

XX sig_peptide

XX mat_peptide

XX US525538-A.

XX 06-JUL-1993.

XX 23-FEB-1989;

XX 23-FEB-1989;

XX 22-NOV-1989;

XX 16-DEC-1991;

XX (GEPH) GENENTECH INC.

XX

PI Capon DJ, Lasky LA;
XX MPI; 1993-226664/28.
DR P-PSDB; AAR38908.
XX
XX New lymphocyte homing receptor immunoglobulin fusion
PT polypeptide(s) - used to inhibit binding of lymphocytes in
PT therapeutic and diagnostic uses
XX
XX Disclosure; Fig 1; 44pp; English.
XX
XX The sequences given in AA044243-44 encode human and murine lymphocyte
CC cell surface glycoprotein (LHR) respectively. The proteins encoded
CC by these sequences mediate the binding of lymphocytes to the
CC endothelium of lymphoid tissue. LHR is a glycoprotein which contains
CC a signal domain, a carbohydrate binding domain, an epidermal growth
CC factor-like (egf) domain, at least one complement binding domain
CC repeat, a transmembrane binding domain (TMD) and a charged intra-
CC cellular or cytoplasmic domain. The murine and human amino acid
CC sequences show a high degree of overall homology (83%), however
CC degrees of homology between the various domains is variable. These
CC proteins may be fused to a ligand binding partner protein (LBPP) which
CC causes an increase in the half life of the LHR. The fusions may be
CC used therapeutically to compete with the normal binding of
CC lymphocytes to lymphoid tissue. They may be used in organ or graft
CC rejection and for the treatment of inflammation.

Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match 99.9%; Score 2255.8; DB 14; Length 2259;

Best Local Similarity 99.9%; Pred. No. 0; Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGCTGCTCTCCTACCTGACGACGACACTCCCTTGGCAAGAGCT 60
Db 1 gaattccagtgctgctgctctccctcacttcagcacagcacactccttggcaagagct 60
QY 61 GAGACCCCTTGTGCTAAAGTCAAGAGGCTCAATGGGCTGCAGAGAGACTAGAGAGACCA 120
Db 61 gagacccttgctgtaagtcagagagctcaatgggctgcagagagactagagagaccaa 120
QY 121 GCAAAGCCATGATTTTCCATGGAATGTCAGAGCCACCCAGAGGACTATGGAATCT 180
Db 121 gcaaaagccatgatatttccatggaatgtcagagccacccagagagactatggaatct 180
QY 181 TCAGTTGTGGGGGTGAGCAATGCTGTGTGATTCTCTGGCAGATTCAGAACCTACT 240
Db 181 tcagttgtgggggtgagcaatgctgtgtgattctctggcagatctcagaaacctact 240
QY 241 GCTGACCTTACCATTTATCTGAANAACCATGACCTGGCAAGGCTAGAGATTCTGCC 300
Db 241 gctgaccttaccatttatctganaaaccatgacctggcaaggctagagattctgcc 300
QY 301 GAGACATTAACAGATTAGTTCATCAAAAGAGGGGAATTTGATCTGAGAG 360
Db 301 gagacattaacagatttagttcatcaaaaagagggaatttgatctgagaga 360
QY 361 AGACTGTGCCCTTCAGTCTGTTCTTACTAGTAGAATCCGGAATAGAGAGAAATAT 420
Db 361 agactgtgcccttcagtctgttctactagtagaattccggaaatagagagaat 420
QY 421 GCACTGTGGTGGAGACCAAAATCTCTACAGAGAGAGCAAGAACTGGGAGATGCTG 480
Db 421 gcactgtgggtggagaccaaaatctctacagagagagcaagaaactgggagatgctg 480
QY 481 AGCCCAACAACAAGAGCAAGAGAGAGAGTGGGTGAGATCTTATCAAGAGAGAAAG 540
Db 481 agcccaacaacaagagcaagagagagagtggtgagatcttatacaagagagaaag 540
QY 541 ATGACAGCAATGAGAGATGAGGCTGCACAAATTAAGGAGGCTCTGTACACAG 600
Db 541 atgacagcaatgagagatgagagctgcacaaatttaaggagctctgttacacag 600

QY 601 CTTCCTCCAGCCCTGGTCAATGCAGTGGCCATGGAGAAATGTGAAATCATCATATATC 660
 Db 601 ctctctgcccagccctgtctcatgcaagtgccatggaagaatgtgtgaaatacatacaatc 660
 QY 661 ACACCTCAAACTGTGATGTGGGGTACTATATGGCCCCAGTGTCAAGCTTGTATTCAGTGTG 720
 Db 661 acacccctgcaactgtgagtgtggttactatggtcccccagtgccagctgtgattcaagtg 720
 QY 721 AGCCTTTGAGGGCCCCGAGCTGGGTACATGGAGCTACTACCCCTTTGGAACCTTCA 780
 Db 721 agcctttgagggccccagagctggtgaaacaatgacatgactcaaccccttggaaactca 780
 QY 781 GCTTTCAGCTCAGAGTGTGCTTCAGCTGTCTATAGGAACAACTTAATCTGAGTTGAAG 840
 Db 781 gcttcagctcacagtgcttccctcagctgctgaaggaaacaactaacctgagattggaag 840
 QY 841 AAACCCACCTGGAGCACTTTGGAAACTGGTCATCTCAGACCAACCTGTCAAGTATTC 900
 Db 841 aaacccacctgtagacatlttgaaactgtcaltcccaagaaacacctgtcaagtgaltc 900
 QY 901 AGTGTAGCCTCTATCAGACACGATTTGGGATCATGAACCTGTAGCCATCCCTGGCCA 960
 Db 901 agtgtagcctctatcagcaaccagatttgggtgaltcagatcgttagccatccccgtggcca 960
 QY 961 GCTTCAGCTTTACCTGTGATGTACCTTCATCTGCTCAGAAAGAACTGATTAATGGGA 1020
 Db 961 gcttcagcttacctgtcagatgtaccttcaatcgtcagagaagaaactggttaattggga 1020
 QY 1021 AGAAGAAACCCATTTGTGAATCATCTGGAATCTGGTCAATCTTACTCCAAATATGCAAA 1080
 Db 1021 agaaagaaacccatltgtgaltcatctggaatctgtgcaaatccctagccaataatgtc 1080
 QY 1081 AATTGGACAAGATTTCTCAATGATTAAGAGGGGATTAATAACCCCTTCATTCACAG 1140
 Db 1081 aattggacaaagattctcctaagatlaagaggtgattataaaccctctcaltcccaag 1140
 QY 1141 TGGCACTCATGTGTACTGATCTCTGGGTGGCATTTATCATTTGGCTGGCAAGAGAT 1200
 Db 1141 tggcactcatgtgtactgcatctctgggttggcatttatcatatggctggcaagagat 1200
 QY 1201 TAAAAAAGGCAAGAAATCCAGAGAGATGATGAATGACCCATATTAATGCCCTTGTTG 1260
 Db 1201 taaaaaaggcaagaataccaagagaatgaatgaatgaatgaatgaatgaatgaatgaatga 1260
 QY 1261 AAAGAAATTTCTTGAATCTAAAAATCATGAGATCCTTTAATCCTTCAGAGAAACGTT 1320
 Db 1261 aaagaaatctcttgaaataactaaaaatcatgagatccctttaaacccttccatgaag 1320
 QY 1321 TTGTGTGGTGGCACTCTACGTCAAAACATGAAGTGTCTTCCTTCAGTGCATCTGGGAG 1380
 Db 1321 ttgtgtgggtggcactctacgtcaaaacatgaagtgttcttccttcagtcacatctgg 1380
 QY 1381 ATTTCACCCGACCAAGATTCCTTCAGTGTGCATTTGGCCCTCATTTATCCCTCAACC 1440
 Db 1381 atttcacccgaccaaagttccttcagttccatcttcgcccctcatattatccctcaacc 1440
 QY 1441 CCCAGCCACAGAGTGTATATACAGTCAAGCTTTGTCTTTCTGAGAGAAACAAATTA 1500
 Db 1441 cccagccacagagtggttataaagctcagcttctgtcttctcgaagagaacaataaa 1500
 QY 1501 GACCATTAAGGAAAGATTCATGTGAAATATTAAGATGGCTGACTTTGCTCTTTTGGAC 1560
 Db 1501 gaccataaggaaagattcatgtgaaataaagaatgctgacttctccttcttctgac 1560
 QY 1561 TCTTGTTCAGTTCATTCAGTGTCTACTTGTATGACAGACACTTCTAAATGAAGTGC 1620
 Db 1561 tcttgttccagtctcaatcaatgaatgtctgtactgtatgaacaacacttcaatgaagtcgc 1620
 QY 1621 AAATTTGATACATATGATATGAGTCAAGTTCCTTGAGATCAATTTACAGTCTC 1680
 Db 1621 aaatttgatacatatgtgaatataatgagctcagcttcttctgacagatcaaatctcagctgc 1680

QY 1681 TTCTGATACGTGGAGTACACTCTTATAGAAAGTCAAAAAGTCTACGCTCCCTTC 1740
 Db 1681 ttctgtatactgttggaggtacacactctatagaagaagttcaaaagttcacagctctcttc 1740
 QY 1741 TTTCCTACTCCAGTGAAGTATGGGGTCTGCTCAAGTTGAAGAAGTCTATTTCACATG 1800
 Db 1741 ttctactaccagtgaaatgaatgggtctgctgctcaagttgaaagagttcctatttgacatg 1800
 QY 1801 TACGCTGGCCGCTCTGATGATTTGGACCATCTCTTATACGTGGCTTACAGGCTCCCACTT 1860
 Db 1801 tagccttcgcccgtctgtgaaatgaaatccatctttaaactggtcttaaggtccctccactt 1860
 QY 1861 CTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACCTAGCATCTCATGAGTGGCA 1920
 Db 1861 ctctcagccacctctcttcttcaagttggtgacttccacacctagcatctcatgagtgcca 1920
 QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCTGCGCGGTTTTTATGTTGGGGGTTTTGCTGT 1980
 Db 1921 agcaaaagagagagagaaatagacctgctgcggttltttagtttgggggttgcgt 1980
 QY 1981 TTCCCTTTATGAGACCCATTCCTATTTCTATAGTCAATGTTCTTTATACGATATTA 2040
 Db 1981 ttccctttatgagacccatctcttcttcaatcttcttcaatgaaatgttcttcttcaatgaa 2040
 QY 2041 TTAGTAAGAAACATCACTGAATGCTAGCTGACATGATCTTTGATGATCATATG 2100
 Db 2041 tttagtaagaatacatcactgaatgtcagctgcaagtgacaatcttcttgatgataag 2100
 QY 2101 AAGAGTTAAACAGTGGAGAAATTCCTTGATTCACATGAATGCTCTCTTCCCTG 2160
 Db 2101 aagagttaaaacaagtgagaatcttctgattcacaatgaatgtctctcttccctg 2160
 QY 2161 CCCCGAAGACTTTTATACACTTACCTAGATCTACATTTCTTAAATTCATCTCAGGC 2220
 Db 2161 ccccgagaacttcttccacttaacttaacttaacttaacttaacttaacttaacttaactta 2220
 QY 2221 CTCCTCAACCCACAGGGGCGCCAGCACACTGGAATTC 2259
 Db 2221 ctccctcaaccccaaggcgccagcaactggaattc 2259

RESULT 3
 AA092802
 ID AA092802 standard; cDNA: 2259 BP.
 XX AC
 XX AA092802;
 DT 01-DEC-1995 (first entry)
 DE XX
 DE Human LHR cDNA.
 KW Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;
 KW LHR; ligand binding partner; immunoglobulin; constant region;
 KW antibody engineering; immunomodulator; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 129..1247
 FT CDS
 FT sig_peptide
 FT mat_peptide
 FT 186..224
 FT 243..1244
 FT tag- b
 FT tag- c
 XX US5428130-A.
 PN 27-JUN-1995.
 XX
 XX 23-FEB-1989; 89US-0315015.
 XX 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.

```
PR 16-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
XX (GETH ) GENENTECH INC.
XX Capon DJ, Lasky LA;
XX WPI: 1995-240086/31.
XX P-PSDB; AAR76506.
XX
XX New hybrid ligand binding partner molecules - fused to immunoglobulin
XX constant region sequences to increase stability and in vivo plasma
XX half-life
XX
XX Disclosure: Fig.1a-1c; 40pp; English.
XX
XX A murine Mel 14 antigen cDNA clone was used to screen a lambda gt10
XX cDNA library derived from human peripheral blood lymphocyte mRNA
XX obtd. from primary cells. A cDNA clone encoding LHR was isolated.
XX
XX Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;
XX
Query Match          99.9%; Score 2255.8; DB 16; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
0;
QY 1 GAATTCAGTGTGCTGCTTCTTACCTGACGACAGACAGACACTCCCTTGGCAAGACCT 60
DB 1 gaattcagtgctgcttccctccacctgcagcacactcctcttggcaagacct 60
QY 61 GAAACCCCTTGTGCTAATCAAGAGGCTCATGGGCTGCAGAAAGCACTAGAGAGACCAA 120
DB 61 gaaaccccttgctgaatcgaagagctcatgggctgcagaaagcaactagagaccaa 120
QY 121 GCAAGGCAATGATTTTCATGGAATGTGACAGACCCAGAGGACTTATGGAACATCT 180
DB 121 gcaaggcaatgatTTTCATGGAATGTGACAGACCCAGAGGACTTATGGAACATCT 180
QY 181 TCAGATTGTGGGGGTGACAAATGCTCTGTTGTGATTTCTGGCCATCATGGAACCTACT 240
DB 181 tcaagtgtgggggtgacaatgctctgttgtgatTTCTGGCCATCATGGAACCTACT 240
QY 241 GCGGACTTACCATTTATTTGAAAAAACCCATGAACTGGCAAAGGCTTAGAAGATTCTGCC 300
DB 241 gctggacttacCATTTATTTGAAAAAACCCATGAACTGGCAAAGGCTTAGAAGATTCTGCC 300
QY 301 GAGACAAATTACAGATTTAGTTGCCATACAAAACAAGCGGAAATGAGATCTGGAGA 360
DB 301 gagacaattacagatTTAGTTGCCATACAAAACAAGCGGAAATGAGATCTGGAGA 360
QY 361 AGACTGTGCGCTTCAGTCTGTTCTTACTACTGATAGGAATCCGGAGATAGAGGAATAT 420
DB 361 agactgtgCGCTTCAGTCTGTTCTTACTACTGATAGGAATCCGGAGATAGAGGAATAT 420
QY 421 GGCAGTGGGTGGGGAACCAAAATCTCTCACTGAAGAAGAGAGAACTGGGGAGATGTG 480
DB 421 ggcagtgggtggggaaccaaATCTCTCACTGAAGAAGAGAGAACTGGGGAGATGTG 480
QY 481 AGCCCAACAAGAAAGAAAGAGAGAGACTGCTGAGATCTATATCAAGAAACAAG 540
DB 481 agcccaacaagaaagaaagagagagactgctgagatCTATATCAAGAAACAAG 540
QY 541 ATGCAGGCAAAATGAGAGATGACGCTGCAACAAACTAAAGGACCCCTCTGTTACAG 600
DB 541 atgcaggcaaaATGAGAGATGACGCTGCAACAAACTAAAGGACCCCTCTGTTACAG 600
QY 601 CTCTTGCCAGCCCTGTGTCATGAGAGTGGCCATGAGAAATGTGTAAGAAATCAATAATC 660
DB 601 ctcttgccagccCTGTGTCATGAGAGTGGCCATGAGAAATGTGTAAGAAATCAATAATC 660
QY 661 ACACCTGCAACTGTGATGGGTACTATGAGGCCCGCCAGTCAAGCTTGATTCAGGTG 720
DB 661 acacctgcaactGTGATGGGTACTATGAGGCCCGCCAGTCAAGCTTGATTCAGGTG 720
DB 661 acacctgcaactgtagtctggtgtactatggtgccccaggtgtccagctgtgtagtctggtg 720
QY 721 AGCCTTGGAGGCCCCAGAGCTGGGTACATGACTGTACTACCCCTTTGGAAACTTCA 780
DB 721 agccttggagggccccagagctggtgtaccatgtagactgtactaccctcttggaaacttca 780
QY 781 GCTTCAGCTCAGTGTGAGGCTTCCAGTGCCTGTGAAGAAACAACTTAACCTGGATTTGAG 840
DB 781 gcttcagctcagtgtagcttccagctgtctggaagaaacaaacttaacctgagtagtgaag 840
QY 841 AAACACCTGTGAGCAATTTGGAAGTGTATCTCCAGAACCAACCTGTCAACTGATTC 900
DB 841 aaacacctgtgagcaatTTGGAAGTGTATCTCCAGAACCAACCTGTCAACTGATTC 900
QY 901 AGTGTAGCCTTATATCAGACACACAGATTTGGGATATCATGAACTGATGCCATCCCTGGCCA 960
DB 901 agtgtagccttataTATCAGACACACAGATTTGGGATATCATGAACTGATGCCATCCCTGGCCA 960
QY 961 GCTTCAGCTTTTACCTGTGAGTACCTTCAATCTGCTCAGAAAGAACTGAGTAAATTGGGA 1020
DB 961 gcttcagctTTTACCTGTGAGTACCTTCAATCTGCTCAGAAAGAACTGAGTAAATTGGGA 1020
QY 961 gcttcagcttaccctctcagcagatcttggagatcagaaactgagcaatcccttgcca 1080
DB 961 gcttcagcttaccctctcagcagatcttggagatcagaaactgagcaatcccttgcca 1080
QY 1021 AGAAGAAACCATTTGTGAATCATCTGGAATCTGTCAAAATCTAGTCAATATGTCAA 1080
DB 1021 agaagaaacCATTTGTGAATCATCTGGAATCTGTCAAAATCTAGTCAATATGTCAA 1080
QY 1081 AATTGGACAAAAGTTTCTCAATGATTAAGAGGGTGAATTATACCCCTCTTCAATTCAG 1140
DB 1081 aattggacaaaagTTTCTCAATGATTAAGAGGGTGAATTATACCCCTCTTCAATTCAG 1140
QY 1141 TGGCAGTCAATGTACACGATCTCTGGGTTGGGATTTATCATTTGGCTGGCAAGGAGAT 1200
DB 1141 tggcagtcaatGTACACGATCTCTGGGTTGGGATTTATCATTTGGCTGGCAAGGAGAT 1200
QY 1201 TAAAAAAGGCAAGAAATCCAAAGAAAGTATGAATGACCCATTAATGCGCCCTTG 1260
DB 1201 taaaaaaggcaagaaATCCAAAGAAAGTATGAATGACCCATTAATGCGCCCTTG 1260
QY 1261 AAAGAAAATTTCTTGGAATTAATAATCATGAGATCCTTTAAATCTTCCATGAACGTT 1320
DB 1261 aaagaaaATTTCTTGGAATTAATAATCATGAGATCCTTTAAATCTTCCATGAACGTT 1320
QY 1321 TTGTGTGGTGGACCTCTCGTCAACATGAAGATGTGTTCTTCACTGATCTGGGAG 1380
DB 1321 ttgtgtgggtggacCTCTCGTCAACATGAAGATGTGTTCTTCACTGATCTGGGAG 1380
QY 1381 ATTTCTACCGGACCAACAGATTCCTTTCAGCTTCCATTTCCGCCCTCATATTATCCCTCAACC 1440
DB 1381 atttctaccggacCAACAGATTCCTTTCAGCTTCCATTTCCGCCCTCATATTATCCCTCAACC 1440
QY 1441 CCCAGCCCAACAGTGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAGAAACAATAA 1500
DB 1441 cccagcccaacagTGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAGAAACAATAA 1500
QY 1501 GACCATTAAGGAAAGATGATGTAATTAAGAAATGAAGGCTTGTGCTTTCTTGAC 1560
DB 1501 gaccatTAAGGAAAGATGATGTAATTAAGAAATGAAGGCTTGTGCTTTCTTGAC 1560
QY 1561 TCTTGTGTTTCAATTCAGTGTGCTGTACTTGATGACAGACACTTCTAAATGAAGTGC 1620
DB 1561 tcttgtgttTCAATTCAGTGTGCTGTACTTGATGACAGACACTTCTAAATGAAGTGC 1620
QY 1621 AAATTTATACATATGTAATATGGAATCAGTTTCTTGCAGATCAAAATTTACAGTGTGC 1680
DB 1621 aaatttatacatATGTAATATGGAATCAGTTTCTTGCAGATCAAAATTTACAGTGTGC 1680
QY 1681 TTTCTATACCTCAGTGAATGAGGCTCTGCTCAAGTTGAAAGAGTCAATTTGACAGT 1740
DB 1681 ttctatacctcagTGAATGAGGCTCTGCTCAAGTTGAAAGAGTCAATTTGACAGT 1740
QY 1741 TTTCTAATCTCAGTGAATGAGGCTCTGCTCAAGTTGAAAGAGTCAATTTGACAGT 1800
DB 1741 ttctatacctcagTGAATGAGGCTCTGCTCAAGTTGAAAGAGTCAATTTGACAGT 1800
```

```

QY 1801 TAGCTGCGCGTGTGATTTGACATCTATTTACTGGCTTCAGGCTCCACCTT 1860
DB 1801 tagctcgcgctgtgatgattgaccatctatttaactgcttcaggctcccccactt 1860
QY 1861 CTTACGACCCCTCTTTTTCAGTTGGCTGACTTCACACCTGACATGCATGAGTGCCA 1920
DB 1861 cttacgacccctcttttcaagtgtgctgacttccacactagcatctcatgagtgcca 1920
QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCTGCGCGCTTTTGTAGTTGGGGTTCGCTGT 1980
DB 1921 agcaaaagagagagagagaaatagctgcgcgctttttagtttgagggttctgctgt 1980
QY 1981 TTTCCTTTATGAGACCCATTCCTATTCTTATAGTCATGTTCTTTATCAGCATATTA 2040
DB 1981 ttctctttagagaccacttcttcttctttagtagtcaatgcttcttattacagatat 2040
QY 2041 TTAGTAAGAAACATCCTGAAATGCTAGCGCAAGGACATCTCTTGTGATGCAATGG 2100
DB 2041 ttagtaagaaacatcctgaaatgctagctgcaagtgacatctctttagtcatatg 2100
QY 2101 AAGAGTTAAACAGAGTGAGAAATTCCTGTGATTCACATGAAATGCTCTCTTCCGCTG 2160
DB 2101 aagagttaaacagagtgagaaatctctgtgattcaacaatgaaatgctctcttccctg 2160
QY 2161 CCCCCAGACTTTTATCCACTTACCTAGATTCTACATATTCCTTAAATTCATCTCAGGC 2220
DB 2161 cccccagacttttatacttacttacttacttacttacttacttacttacttacttactt 2220
QY 2221 CTGCTCAACCCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2259
DB 2221 ctgctcaacccgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 2259

```

RESULT 4

AAT05869
ID AAT05869 standard; cDNA; 2259 BP.

XX AAT05869;

XX 31-JAN-1996 (first entry)

DE Human LHR cDNA.

KW Lymphocyte cell surface glycoprotein; LHR; transmembrane receptor;
KW immunoglobulin; IgG; constant region; receptor-mediated disease;
KW vector; plasma-life; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 129..1247
FT sig_peptide 186..224
FT mat_peptide 243..1244
FT /tag= b
FT /tag= C
FT /product= LHR

XX US5455165-A.

XX 03-OCT-1995.

XX 23-FEB-1989; 89US-0315015.

XX 22-NOV-1989; 89US-0440635.

XX 23-FEB-1989; 89US-0315015.

XX 16-DEC-1991; 91US-0808122.

XX 08-DEC-1992; 92US-0986931.

XX 21-JAN-1994; 94US-0185669.

XX (GETH) GENENTECH INC.

PI Capon DJ, Lasky LA;
XX WPI; 1995-350776/45.
DR P-PSDB; AAR83050.
PT Expression vector encoding fusion protein to increase plasma life -
PT comprises receptor ligand binding site and Ig constant region, for
PT treatment of receptor mediated disease
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used
CC to screen an oligo-dT primed lambda gt10 cDNA library derived from
CC human peripheral blood lymphocyte mRNA obtd. from primary cells. A
CC 2.2 kb clone (sequence given in AAT05869) showing 83% DNA sequence
CC homology to the murine LHR gene (AAT05870) was isolated. The LHR genes
CC are used to construct LHR-196 hybrids used to target therapeutic
CC moieties to lymphoid tissue.
XX
SQ Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match 99.9%; Score 2255.8; DB 16; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 GATTTCACTGTCGTCGCTTCTCTACCTGACACACACACTCCCTTGGCAGGACT 60
DB 1 gaattcaactgtgctgcttctctacactgacacacacactcccttggcaggact 60
QY 61 GAGACCTTGTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAAAGACTGAGAGGCCAA 120
DB 61 gagaccttgtgctaaagtcagagagagagagagagagagagagagagagagagagag 120
QY 121 GCAAGCCATGATATTTCCATGGAATGTCAGAGCAGCCAGAGGACTTATGAAATCT 180
DB 121 gcaagccatgatatctccatggaatgtcagagcagccagagagagagagagagagag 180
QY 181 TCAAGTTGTGGGGGTGGAATGCTCTGTGATTTCTTCTGCGCATATGGAATCTACT 240
DB 181 tcaagttgtgggggtggaatgctctgtgatttcttctgacatcagagagagagagag 240
QY 241 GCTGACTTACCATTTATCTGAAAAACCCATGAATGCGCAAGGCTAGAGATTTGCC 300
DB 241 gctgacttacatttattctgaaaaacccatgaatgcgcaaggctagagatcttgcgc 300
QY 301 GAGACAATTACACAGATTAGTGGCATACAAAACAAGCGGAATTGATCTGAGAGA 360
DB 301 gagacaattacacagatttagtggcatacaaaacagcggaattgagatctgagaga 360
QY 361 AGACTCTGCCCTTCAGTGTCTTACTAGTATGATAGGATCCGGAATGAGGGAATAT 420
DB 361 agactctgccccttcagtgttcttactacagatgataagaaatccggaatgaggaat 420
QY 421 GGAGCTGGGTGGGAACCAAAATCTCTCACTGAAGAAGAGAGAACTGGGAGATGGTG 480
DB 421 ggagctgggtgggaaccaaactctctactgaagaagagagagagagagagagagag 480
QY 481 AGCCCAACAAACAAGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 agcccaacaaacaagaaagcaagagagagagagagagagagagagagagagagagag 540
QY 541 ATGAGAGCAATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 atgagagcaatgagagatgagagagagagagagagagagagagagagagagagagag 600
QY 601 CTCTTTCGACCCCTGTCATGACAGTGGCCATGAGAGATGTGAGAAATCATCAATATC 660
DB 601 ctctttcgacccctgtcatgacagtggccatgagagatgtgagaaatcatcaatattc 660
QY 661 ACACCTGCAACTGTGATGTGGGACTATGAGGCCAGAGTGCATGCTTGATTCAGTGG 720
DB 661 acactgcaactgtgatgtgggactatgaggccagagtgcattgcttgatcagtgctg 720

```

QY	721	AGCTTTGGAGGCCCCAGACCTGGGTACATGACGTGTACTACCCCTTTTGGAAACTTCA	780
Db	721	agcctcttggagggccccagagctcgtgtatcaatctgacctctatcaaccctcttggaaacttca	780
QY	781	GCTTCACCTCAACATGTGTGCTTACGTGCGCTGTGAAGCAACAACTTAACTGGGATTGAG	840
Db	781	gcttcagctcaacagctgtgccttcagctgtctctgaaggaaacaacttaactcgtgattgaag	840
QY	841	AAACCACCTGTGACCACTTTTGGAAAGTGTATCTTCAGAACCAACTGTCAAGTATTC	900
Db	841	aaaccacctgtgagcccatcttggaactcgttcacccacagaaaccaacctctgaatgatttc	900
QY	901	AGTGTGAGCCCTTATTCAGACCAAGATTTTGGGGATCATGAACTGTATGGCATCCCTGGGCA	960
Db	901	agtgvtgagccctcatcaacagacccagatcttggggatcaatgaaacgtatgacatccctggcca	960
QY	961	GCTTCACCTTTACCTGTGATGTATACCTTCACTGCTCAGAACGAAGTAAATTGGA	1020
Db	961	gcttcagcttactcctctgtcatcttcactcatcgtctcagaaggaaactgattatgtgga	1020
QY	1021	AGAGAAACCATTTTGTGATTCATCTGTGAATCTGTGCAAAATCCTAGTCCATATGTCAA	1080
Db	1021	agaaagaaacacatctgtgaaatcactcgtgaatccgtgcaaaatccatgacaaatagtcaaa	1080
QY	1081	AATTGGACAAAGTTTCTCATATGTTAAGAGAGGTATATATACCCCTTTCATTCAG	1140
Db	1081	aattggcaaaagttcttcaatigtatcaaggaggtgatataaccctcttcaatccag	1140
QY	1141	TGGCAGTCATATGTTACTGCACTTCTCTGTGGTGGCATTTATCATTTTGGCTGGCAGAGAT	1200
Db	1141	tggcagtcatactgtactcgtcatcttcctgggtctgtgcatttcaatctgtctggccaaggagt	1200
QY	1201	TAAAAAAAGGCAAGAAATCCACAGAGAAAGTATGATATACCATATTAATATGCGCCTGTG	1260
Db	1201	taaaaaaaggcaagaaatcccaagaagaatgaaagaaagaaatcaatcaatcaatccctctgtg	1260
QY	1261	AAAGAAAAATCTTGTGAACTACTAAAAATCATAGAGATCCTTTAATCCTTCATGAAACGT	1320
Db	1261	aaagaaatctcttgaataactaaatcatagatccctttaaactccttcagtaagagct	1320
QY	1321	TTTGTGTGTGGCACTCCCTGACGTCAANCAATGAAGTGTGTCTTCTTAAGTCATCTGGAG	1380
Db	1321	tttgtgtgtggcacctctctacgtcaaacatctgaagtgtgtctctcagtgacatctggagag	1380
QY	1381	ATTTCTATCCGACCAACAGATGTTCCCTTACAGTTCATTTCCCTCATATTATCCCTCAAC	1440
Db	1381	attctcaaccgacaagaagctccttcagcttcaatcttgcctcattatccctcaacc	1440
QY	1441	CCGAGCCCAAGGTGTTTATACAGCTCAAGCTTTTGTCTTTTCTGAGGAGAAACAATAA	1500
Db	1441	ccgagcccaaggtgtttatatacagcccaagcttcttctcttcttgagagaaacaataaa	1500
QY	1501	GACCATTAAGGGAAAAAGTTATGTGGAATAATAAGATGGCTCACTTCTCTTCTTGAC	1560
Db	1501	gaccataagggaaaagatctcatgtggaatataaagaatgctcgtaccttgcctctcttgag	1560
QY	1561	TCTTGTGTTTCAAGTTTCAATTCAGTGTGTACTGTATGATGACAGACACTTCTAATGAAGTC	1620
Db	1561	tcttgttctcagtttcaatctcagtgctgttactgtatgacagacactcttaaatgaagtc	1620
QY	1621	AAATTTGATACATATGTGAATATGACCTAGTTTCTTGACATCAAAATTTACAGTGTCTC	1680
Db	1621	aaatttgatacatatgtgaatatgacatcagttctcttgcaatcaaaattcacaagtctc	1680
QY	1681	TTTCTGTATCTGTGAGAGTCACTCTTATAGAAAGTCAAAAAGTCAAGCTCAAGCTTCTTC	1740
Db	1681	ttctgtatactgtgagggtacacatctataagaagtctcaaaaagctcctacgtctctcttc	1740
QY	1741	TTTCTAATCTCCAGTAAGTATAGGGTCTCTGTCTCAAGTTGAAAGTCTTATTTGACATG	1800
Db	1741	tttctaactccaatgaaatgaaatctgtcctgtccaagtctgaagaagtcctatcttgcaatg	1800

Qy	1801	TACCTCGCGCGTGTGAATTGACACCTTCCATTATTAACGGGTTAGAGCGTCCACACTT	1860
Db	1801	tagcttcgcgcgtctcgtgaattgagaccatccatttaacgcgtcttaaggcctcccaactt	1860
Qy	1861	CTTCAGCACCCTCTCTTTTCAGTTGGTGACATTCACACACAGACATGTCAATGAGTGCCA	1920
Db	1861	cttaagcacactctctcttcttcagltgctgcgacttccacaccagatactctatgagtgcca	1920
Qy	1921	AGCAAAAGAGAGAGAGAGAAAATAGCTCGCGGGTGTGTTTTAGTTGGGGGTGTTGCTGT	1980
Db	1921	agcaaaagagagagagagaaatagcctgcgcggttctttagtcttgagggtcttcgtct	1980
Qy	1981	TTCTCTTTATGAGAGCCCATTCCTCTATTTCTTATAGCAATGTTCTTTATACAGATATTA	2040
Db	1981	ttcctctttagagagcccatccatctcttaagtaagtaagttcttcttatacagatatata	2040
Qy	2041	TTTAGTAGAAAACATCTACTGMAATGCTAGCTGCACAGTGACATCTCTTGATGTGATATGG	2100
Db	2041	ttagtaagaaaacatacctgaatgtctagctgaagtgagcatctcttgatgcatatag	2100
Qy	2101	AAGAGTTAAACACAGTGTGGAGAAATTCTCTTGATTGACAAATGAAATGCTCTCTTCCCTG	2160
Db	2101	aagagttaaaaacagtgaggaaaattctcttgatctacaagaayactctctctccctg	2160
Qy	2161	CCCCAGAACCTTTATCTACCTATCTACGTAGATTCTACATATTCTTTAAATTTATCTCAGGC	2220
Db	2161	ccccagaaactttatctcaacttaactcagatctcaactatctctttaaattcaatctcagyc	2220
Qy	2221	CTGCCTCAACCCACAGGGGCGCGCCAGCACATGGAAATTC	2259
Db	2221	ctgcctcaacccacagggcgcgccagcacacatgaaatttc	2259

RESULT	5	
AT30003		
ID	AA30003	standard; DNA; 2259 BP.
XX		
AC	AA30003;	
XX		
DT	31-OCT-1996	(first entry)
XX		
DE	Human lymphocyte cell surface glycoprotein (HLHR) coding sequence	
XX		
KW	Immunoglobulin; transmembrane receptor; adhesion; targeting;	
KW	diagnosis; therapy; drug delivery; antiviral; neuromodulator;	
KW	immunomodulator; cell adhesion; graft rejection; inflammation;	
KW	metastasis; ss.	
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	129..1247
FT		/*lag= a
FT		/product= Lymphocyte cell surface glycoprotein.
FT	sig_peptide	129..242
FT		/*lag= b
FT	mat_peptide	243..1244
FT		/*lag= c
XX		
PN	US5514582-A.	
XX		
PD	07-MAY-1996.	
XX		
PE	23-FEB-1989;	89US-0315015.
XX		
PR	22-NOV-1989;	89US-0440625.
PR	23-FEB-1989;	89US-0315015.
PR	16-DEC-1991;	91US-0808122.
PR	08-DEC-1992;	92US-0986931.
PR	21-JAN-1994;	94US-0185670.
XX		
PA	(GETH) GENENTECH INC.	
XX		

PI Capon DJ, Lasky LA;
 XX
 DR WPI; 1996-238773/24.
 DR P-PSDB; AAR98106.

PI Nucleic acid encoding hybrid immunoglobulin comprising the ligand
 binding site of a receptor fused to Ig constant region - useful for
 PT diagnosis and treatment e.g. of inflammation

XX
 PS Example 2; Figure 1; 41pp; English.

CC A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP, enzymes, growth factors to particularly deliver
 CC LBP such as toxins, enzymes, and their targets; or therapeutically to deliver
 CC typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes.

XX Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match 99.9%; Score 2255.8; DB 17; Length 2259;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGCTTCTTCTACCTGACAGACACACTCCCTTGGCAAGACCT 60
 Db 1 gaattcagtgctgtgcttcttcttctcactgcagcacagcacactccttggcaagacct 60
 QY 61 GAGACCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Db 61 gagaaccttgcctaaagctcaagagctcgaatggtcgaagaactagaagaagccaa 120
 QY 121 GCAAGCCATGATATTTCCATGGAATGTGAGACACCCAGAGGACTTATGGAACATCT 180
 Db 121 gcaagccatgatatttccatggaatgtgcagacccagagggactatggaacacct 180
 QY 181 TCAAGTTGGGGGTGAGCAATGCTGTGTGATTTCTGCGACATCATGGAACCTACT 240
 Db 181 tcaagttgggggtgagcaatgctgtgtgatttcttgcgcacatcatggaacctact 240
 QY 241 GCTGACTTACCTATTTCTGAAAAACCATGAACTGGCAAGGGCTTAAAGTTCTGCC 300
 Db 241 gctgacttacctatttctgaaaaacccatgaactggcaagggtctaaagattctgc 300
 QY 301 GAGACAATTACACAGATTTAGTTGCCATCAAAACAGGCGGAAATTTGATTTGAGAG 360
 Db 301 gagacaattacacagatttagttgccatacaaaacaggcggaattggtatctcgaga 360
 QY 361 AGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 361 agactgtgcttgccttgccttgccttgccttgccttgccttgccttgccttgccttgc 420
 QY 421 GGACGTGGGTGGAACAACAATCTCTCAGTGAAGAACAGAGAACTGGGAGATGGTG 480
 Db 421 ggaactgggtggaaacaacaatctctcagtggaagaaacagagaaactgggagatgg 480
 QY 481 AGCCCAACAACAAGAAGAAGAGAGACTGCGTGAGATCTATATCAAGACAACAAG 540
 Db 481 agcccaacaacaagaagaagagagactgctgtgagatctatatcaagaagaacaag 540

QY 541 ATGACGCAANTGGAAGATGAGCGCTGCCAACAACCTAAAGGACGCCCTCTGTACACAG 600
 Db 541 atgacgcaaatggaagatgagcgctgccacaacactaaaggacgccctctgttacacag 600
 QY 601 CTCTTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 601 ctcttccagccctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 660
 QY 661 ACACCTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Db 661 acacctgcaactgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 720
 QY 721 AGCCTTTGGAGGCCCAAGAGCTGGTACCAATGAGTGTCTACCCCTTGGAACTTCA 780
 Db 721 agcctttggaggcccaagagctggtaccaatgagtgtctaccccttggaaacttca 780
 QY 781 GCTTACGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Db 781 gcttacgctacagtgtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 840
 QY 841 AAACAACCTGTGACCATTTGGAACCTGCTCATCTCCAGAACCAACCTGCTCAAGTATTC 900
 Db 841 aaacaacctgtgaccatttggaaacctgctcatctccagaaaccaacctgctcaagtatc 900
 QY 901 AGGTGAGGCTGTATGAGACCAATTTGGGATGATGATGATGATGATGATGATGATGATG 960
 Db 901 aggtgagcctgtatgagaccatTTGGGATGATGATGATGATGATGATGATGATGATG 960
 QY 961 GCTTACGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Db 961 gcttacgcttacctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1020
 QY 1021 AGAAGAAACCAATTTGTGATCATCTGGAATGCTGCTCAATTCATAGTCCAAATATGTC 1080
 Db 1021 agaagaaaccaatTTGTGATCATCTGGAATGCTGCTCAATTCATAGTCCAAATATGTC 1080
 QY 1081 AATTGGCAAAAGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
 Db 1081 aattggcaaaagtttcatgattgattgattgattgattgattgattgattgattgattgatt 1140
 QY 1141 TGGCAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Db 1141 tggcagtcattgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1200
 QY 1201 TAAAAAAGGCAAGAAATCCAAAGAAATGATGATGATGATGATGATGATGATGATGATG 1260
 Db 1201 taaaaaaggcaagaaatccaaagaaatgattgattgattgattgattgattgattgattgatt 1260
 QY 1261 AAAGAAATTTTGGATATCAATAAATCATGATGATGATGATGATGATGATGATGATGATG 1320
 Db 1261 aaagaaattttggatattcaataaattcatgattgattgattgattgattgattgattgattgatt 1320
 QY 1321 TTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 Db 1321 ttgtgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1380
 QY 1381 ATTTCACCCGACCAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 Db 1381 atttcacccgaccaacagtctgctgctgctgctgctgctgctgctgctgctgctgctgct 1440
 QY 1441 CCCAGCCCAAGGTTTATATACAGCTAGCTTTTGTCTTTTGTGAGAGAAACAATAA 1500
 Db 1441 ccagcccaaggtttatatacagctagcttttgtcttttgtgagagaaacaataa 1500
 QY 1501 GACCATAGGAAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 Db 1501 gaccataggaaggaagattgattgattgattgattgattgattgattgattgattgattgatt 1560
 QY 1561 TCTGTTTTCAGTTTCAATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 Db 1561 tctgttttcagtttcaattcagtgctgctgctgctgctgctgctgctgctgctgctgctgct 1620
 QY 1621 AAATTTATACATATGTAATATGAGACTAGTTTCTTGCAGATCAAAATTTCAAGTGTGCT 1680


```

QY 541 ATGCAGCAATATGAGACATGACGCTGCGCAAACTAAAGCAGCCCTGTATTACAG 600
   |||
Db 541 atgacggaatgagacgaigagcgctgcacaactaaagcgccctcgtttacag 600
QY 601 CTCTTGACGACCTCGTGCATGACGTGGCCATGGAAGATGTGTAAATCATTAATC 660
   |||
Db 601 ctcttcgcagccctcgttcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 660
QY 661 ACACCTCAATGTGATGTGGGCTACTATGGGCGCCAGTGCACCTGTGATGTAGTGTG 720
   |||
Db 661 acacctcaactgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 720
QY 721 AGCCTTGAAGGCCCGACAGCTGGGTACATGACATGACCTGACCTTGGAACTTCA 780
   |||
Db 721 agccttggagggcccgagagctgggtacatgacatgacatgacatgacatgacatgac 780
QY 781 GCTTCACCTCAGANTGTGCTTCAGCTGCTCTGTGAAGAACAACTTAAGTGGATTAAG 840
   |||
Db 781 gcttcacctcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 840
QY 841 AAACACCTGTGACACATTTTGAAGATGTGATCTCCAGAACCACTGTCAAGTGTTC 900
   |||
Db 841 aaacacactgtgacaccttggaaactgtgtacatccagaaacacactgtcaagtgtatc 900
QY 901 AGTGTAGCCTCTATACGACACCAAGATTGGGATCATGAACCTGAGCCATCCCTGGCCA 960
   |||
Db 901 agtgtagcctctatcagcaccagattggggtatcatgactgtagcaccctggcca 960
QY 961 GCTTCACCTTACTCTGACATGTACCTTCATGCTGCAGAGAGACAGATTAATGGGA 1020
   |||
Db 961 gcttcaccttactctgcacgtgacatccatccgctcagaagaagacgtatcatgtgga 1020
QY 1021 AGAAGAAACCATTTTGTGATCATCTGTGAATCTGTCAATCTAGTCATAATGTCAAA 1080
   |||
Db 1021 agaagaacacatttgtgaatcatctgtgaatctgtgaatctgtgaatctgtgaatct 1080
QY 1081 AATTGACAAATAATTTCTCAATGATTAAGAGGCTGATTTAACCCCTCTTATTCAG 1140
   |||
Db 1081 aattgacaaataatcttcaatgattaaagaggtgatttaaaccctcttattccag 1140
QY 1141 TGGCAGTCATGATGTACGATCTCTGTGGTGGCATTTTATCATTTGGCTGGCAAGGAT 1200
   |||
Db 1141 tggcagtcatgattgtacgattctctgtgggtggcatTTTTATCATTTGGCTGGCAAGGAT 1200
QY 1201 TAAAAAAGGCAAGAAATCCACAGAGATGATGACCCATTAATTCGCCCTTGTGTC 1260
   |||
Db 1201 taaaaaaggaagaatccaagaagatgatagaccatataatccgcttgggtg 1260
QY 1261 AAAGAAATTTCTTGAATACTTAAATCATGAGATTCCTTAAATCCTTCATGAAACGTT 1320
   |||
Db 1261 aaagaaatcttctggaataactaaatacatgagatcctttaaacttccatgaaacgtt 1320
QY 1321 TTGTGTGTGGGACCTCTACGTCACATGAAGTGTGTTCTTCTGAGTCATCTGGGAG 1380
   |||
Db 1321 ttgtgtgtgggacctctacgctcaactgaagatgtgttcttctcagtcacatcgtggaag 1380
QY 1381 AATTTCACCCGACCAACAGTTCCTTCAGCTTCATTTGSCCCTCATTTATCCCTCAAC 1440
   |||
Db 1381 atttctaccgaccaaagcttcttcaagcttccattgcccctcatattaccctcaacc 1440
QY 1441 CCAGGCCACAGGTTTATACAGTCACTTTTGTCTTTCTGAGGAAACAAATAA 1500
   |||
Db 1441 ccagggccacaggtgttatacagctcagcttcttcttcttcttcttcttcttcttct 1500
QY 1501 GACCATTAAGGAAGATTCATGTGGAATATTAAGATGCTGACTTGTGCTTTCTTGAC 1560
   |||
Db 1501 gaccataaggaagatcatgtgtgaataataaagatgtgacttcttcttcttcttcttct 1560
QY 1561 TCTTGTGTTTCACTTCAATTCAGTGTGATGATGACAGACACTTCTAAATGAAGTGC 1620
   |||
Db 1561 tcttgttctcagttcactcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 1620
QY 1621 AAATTTGATACATATGTGAATATGACATCAGTTTCTTGACAGATCAAAATTTACGTC 1680

```

```

Db 1621 aaattgatcatatgtatgatactgacacagtttcttctgacatacaattcagtcgctc 1680
QY 1681 TTCTGATACCTGTGAGAGTACACTCTTAAGAAAGTTCAAAAGTCTACGCTCTCTTTC 1740
   |||
Db 1681 ttctgatactgtgagaggtacactcttataagaagtccaanaagtcatacgtctctcttc 1740
QY 1741 TTCTTAACCTCCATGAAATATGGGCTCCTGCTCAAGTTGAAAGAGTCTTATTTGACATG 1800
   |||
Db 1741 ttcttaactcagtgaaataatgggtcctgctcagttcagttcagttcagttcagttcagtt 1800
QY 1801 TACCTTGCGGCTGTGAAATTTGACATCTCTTATTAAGTGTGCTTCAGGCTCCGACCTT 1860
   |||
Db 1801 tagcctgcgcgtctgtgaattgacacatccatttaactgactgactcagcctccacactt 1860
QY 1861 CTTCAGCACCTCTCTTTTTCAGTGTGCTGACTTCCACACGTACATCTCATGAGTGC 1920
   |||
Db 1861 cttcagcacactctcttcttctcagttgtgctgacttccacacctagcatctcatgagtg 1920
QY 1921 AGCAAAAGGAGAAAGAAATAGCCCTGCGGCTTTTATGTTGGGCTTTTGTGCTGT 1980
   |||
Db 1921 agcaaaaggaagaagaagaatagcctgcgcggttctttagtttgggttgggttgcgt 1980
QY 1981 TTCTTTTATGAGACCATCTCTTATTTCTTATAGTCAATGTTCTTTATCAGATATTTA 2040
   |||
Db 1981 ttctctttagagaccatctcctattcttctatagtcacatggttcttcttctacagatata 2040
QY 2041 TTATGTAAGAAACATCAGTGAAGTGTAGCTGCAAGTCAATCTCTTTGATGTATAG 2100
   |||
Db 2041 ttatgtaagaataacatcagtaaatgtagctgtcaggtgacatctcttcttcttctatcag 2100
QY 2101 AAGAGTTAAAGAGGAGGAGAAATTCCTGATTCAATGAAATGCTGCTCTTCCCTG 2160
   |||
Db 2101 aagagttaaagagagtgagaaatccctgtatccaatgaaatgctcctcttccctg 2160
QY 2161 CCCCGAAGCTTTTATTCACCTTACCTAGATTCTACATATTTCTTAAATTTGATCAGGC 2220
   |||
Db 2161 ccccgagaacttcttaccacttaccatgacttctacatattctttaaattcattcagc 2220
QY 2221 CTCCCTCAACCCGACGAGGCGCGCAGACATGGAATTC 2259
   |||
Db 2221 ctccctcaaccccgagggcgcgacagcacatgaaatc 2259

```

```

RESULT 7
AA043154
ID AA043154 standard; CDNA; 2259 BP.
XX
AC AA043154;
XX
DT 08-OCT-1993 (first entry)
XX
DE Human Lymphocyte Homing Receptor coding sequence.
XX
KW HuLHR; Lymphocyte binding inhibition; Lymphoma metastasis;
KW transplant rejection; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS -129..1247
FT FT /*tag= a
FT FT /product= HuLHR
FT sig_peptide 186..224
FT FT /*tag= b
XX
PM US216131-A.
XX
PD 01-JUN-1993.
XX
PF 23-FEB-1989; 89US-0315015.
XX
PR 23-FEB-1989; 89US-0315015.

```


PR 31-OCT-1991; 91US-0786149.
XX (GETH) GENENTECH INC.
XX Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;
PI WPI; 1993-188588/23.
XX P-PSDB; AAR37960.
DR
XX Human and murine lymphocyte homing receptors to treat graft
PT rejection and inflammation - comprise carbohydrate binding,
PT epidermal growth factor and complement binding domains
XX
PS Example 2; Fig 1; 32pp; English.
XX A human peripheral blood lymphocyte cDNA library in lambda gt10 was
CC screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone
CC (i.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was
CC isolated and sequenced. The ORF codes for 372 amino acids with a mol.
CC wt. of approximately 42,200. Comparison of the HuhR cDNA with the
CC previously determined murine LHR sequence (AA043155) showed 83%
CC homology.
XX
SQ Sequence 2259 BP; 635 A; 515 C; 490 G; 619 T; 0 other;

Query Match 99.8%; Score 2254.2; DB 14; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGGCTTCTCTACCTCAGCAGCAGACACTCCCTTGGCAAGACCT 60
DB 1 gaattcagtgctggcttctctaccctcagcagcacaccccttggcaggacct 60

QY 61 GAGACCTTGTGCTAAGTCAGAGGCTCAATGGCTGCAGAAAGACTAGAGAGCA 120
DB 61 gagaccttgtgctaaagtcgaagtgctcaatggctgcgaagaagactagaagagccaa 120

QY 121 GCAGAGCCATGATATTTCATGGAATGTACAGCACCCAGAGGACTTATGGACATCT 180
DB 121 gcaagaccatgatattttcatggaaatgtacagcacccagagacttatggaacatct 180

QY 181 TCAAGTGTGGGGGTGAGCAATGCTGTGTGATTTCTGGGCACATCATGGAACTTAC 240
DB 181 tcaagtgtgggggtgagcaatgctgtgtgatttctgggcacatcatggaaacttacc 240

QY 241 GCTGGAATTACATTTATCTGAAAAACCATGAACTGCAAAAGGCTAGAGAATCTGCC 300
DB 241 gctggacttacattatcttgaanaaaccatgaaactgcaaaaggctagaagatctgcc 300

QY 301 GAGACATTTACACAGATTATAGTTGCCATACAAAACAGGCGAAATTGAGTATCTGACA 360
DB 301 gagacaattacacagattatagttgccatcaaaacagcggaattgagatctggaaga 360

QY 361 AACACTGTGCTTCATGCTCTTCTTACTACTAGTAGTAATCCGGAATAGAGGAAATAT 420
DB 361 aagactgtgcttcgatgctcttcttactactagtagaataatccggaatagaggaat 420

QY 421 GGACGTGGGTGGGAACCAAAATCTCTCACTCAAGACAGAGAACTGGGGAGATGTG 480
DB 421 ggaactgggtgggaaccaaattctctcactgaagaagcaggaactctggggagatgtg 480

QY 481 AGCCCAACAACAAGAAACAAGAGAGACTGCGTGGAGATCTATATCAAGACAACAAG 540
DB 481 agcccaacaacaagaacaagagagactgctggagatcttatatacaagaagaacaag 540

QY 541 ATGCAAGCAAAATGGAAGCAATGACGCTGCCACAATAAAGCAGCCCTGTATACAG 600
DB 541 atgcagcaaaaatggaaagcaatgacgctgccacaataaagcagccctgtatcacag 600

QY 601 CTTCTTGCCAGCCCTGTGTCATGCAGTGGCCATGGAGAATGTGTGAATCATCAATATTC 660
DB 601 ctctcttgccagccctgtgctcatgctgagcagtgagagaatctgtagaatacatcaataatc 660

QY 661 AACCTGCAACTGTGATGTGGGGTACTATAGGCCCCAGATGTCAGCTTGTGATTCAGTGTG 720
DB 661 aacctgcaactgtgatgtggggactatagggcccccagatgtcagcttgtgattcagtggtg 720

QY 721 AGCCTTTGAGAGCCCGAGAGCTGGGTACATGAGACTGTACTCACCCCTTGGAAACTTCA 780
DB 721 agcctttgagagcccgagagctgggtacatgagactgtactcaccccttggaaacttca 780

QY 781 GCTTCAGCTCACAAGTGTGCTTACGCTGCTGTGAAGAACAACTTAACTGGATTGAG 840
DB 781 gcttcagctcacagtgcttaccctcagctgctgtgaagaaacaaacttaactacggaatgag 840

QY 841 AAACCACTGTGAGCACTTTGGAACGTGTCATCTCCAGAACCAACTGTCAAGTGTTC 900
DB 841 aaacctgtgagcactttggaaactgttcacatctccagaaccaaactgtcaagtgatc 900

QY 901 AGTGTAGCCTTATACAGCACAGATTTTGGGATCATGAACTGTAGCCATCCCTGGCCA 960
DB 901 agtgtagccttatacagcacagatTTTGGGATCATGAACTGTAGCCATCCCTGGCCA 960

QY 961 GCTTCAGCTTACCTTGCATGTGACCTTCATCTGCTCAGAGAACTGACTTAATTGGGA 1020
DB 961 gcttcagcttacctcctgcataccttcaatctcgtccaagaagaaactgaattggga 1020

QY 1021 AGAAGAAAACCATTTGTGATTCATCTGGAATCTGTGTCATCTTACTGCAATATGTCAAA 1080
DB 1021 agaagaaaacccatttgtgaatcctggaatctgtgtaaaactcctagccaatagtcaaa 1080

QY 1081 AATTGGACAAATTTCTCAATATTTAGAGAGGTGATTTAACCCCTTTTATTCAC 1140
DB 1081 aattggacaaaatTTCTCAATATTTAGAGAGGTGATTTAACCCCTTTTATTCAC 1140

QY 1141 TGGCAGTCATGTTACTGTGATTTCTGCGTTGGCATTTATCATTTGGCTTGCAAGAGAT 1200
DB 1141 tggcagtcatagttactgtgatttctcgttggcatTTTATCATTTGGCTTGCAAGAGAT 1200

QY 1201 TAAAAAAGCAAGAAATCCAAAGAAAGTGAATGATACCCATTTAAATGCCCTTGCTG 1260
DB 1201 taaaaaagcaagaaatccaaagaaagtgaatgatacccatatcaaatgccccttggtg 1260

QY 1261 AAAGAAATTTCTTGAATATTAATAATCATGAGATCCTTTAAATCCCTCATGAAAGTT 1320
DB 1261 aaagaaatTTCTTGAATATTAATAATCATGAGATCCTTTAAATCCCTCATGAAAGTT 1320

QY 1321 TTGTGTGTGGACACTTCCTACGTCGTCAAAACATGAAGTGTTCCTTCAGTGCATGGGAG 1380
DB 1321 ttgtgtgtggacactTCCTACGTCGTCAAAACATGAAGTGTTCCTTCAGTGCATGGGAG 1380

QY 1381 ATTTCTACCCGACCAACAGTTCCTTCACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1440
DB 1381 atttctacccgaccaaagttccttcacgcttcacatcttcgcccctatcttaccctaac 1440

QY 1441 CCCAGCCACAGAGTGTATATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAATAA 1500
DB 1441 cccagcccaagagtttatatacagctcagagcttcttcttcttcgggaggaacaaataa 1500

QY 1501 GACCAATPAAGGGAAGAAATTCATGTAATTAAGATGCTGACTTGTCTTGTGAC 1560
DB 1501 gaccataaggaagaaatTCATGTAATTAAGATGCTGACTTGTCTTGTGAC 1560

QY 1561 TCTTGTGTTTCAGTTTCATTTCAATGCTGTGATGAGACAGACACTTAAATGAAGTGC 1620
DB 1561 tcttgtgttTCAGTTTCATTTCAATGCTGTGATGAGACAGACACTTAAATGAAGTGC 1620

QY 1621 AAATTTGATACATATGTGAATATGACATGTTTCTTGAGAGATCAAAATTTACGTCGTC 1680
DB 1621 aaatttgatacatatgtgaatATGACATGTTTCTTGAGAGATCAAAATTTACGTCGTC 1680

QY 1681 TTCTGTATACCTGTGAGAGTACACTCTTATAGAAAGTTCAAAAAGTCTACGCTTCTCTTC 1740
DB 1681 ttctgtatacctgtgagagTACACTCTTATAGAAAGTTCAAAAAGTCTACGCTTCTCTTC 1740

QY	1741	TTTTCTAATCCAGAGAAAGTAAATGGGGTCGCGTCACAGTTGAAAGAGTCCATATTGGCACTG	1800		
Db	1741	tttctcaactcaagtgaagtaatggyggccctggccaagtgtgaagatctccatttgcacatg	1800		
QY	1801	TAGCCTGCGCGCTGTGTGAATTTGAGACATCCATTATTTAACTGAGGCTTCAGGCTCCACACTT	1860		
Db	1801	tagctctgcgctgtgtgaattgagccatctctatttaactgcgtctcaagctctcccaactt	1860		
QY	1861	CTTTCAGCACCTCTCTTTTTCAGTTGGCTGACCTTCCACACCTAGCATCTCATGAGTGGCA	1920		
Db	1861	cttcagccacctctctcttcttcagltgctggaacttccacacccatagatctcactgaagtgcca	1920		
QY	1921	AGCAAAAGAGAGAAGAGAGAAATAGCCTGCGCGGCTTTTATGTTGGGGGCTTTTGCTGT	1980		
Db	1921	agcaaaagagagaagagagaataagctctgcgcggttlltagtttgggggttlttgctgt	1980		
QY	1981	TTCTCTTTATATAGACCCATTCCTCAATTCTTTATAGTCATGTTTCTTTTATACAGATATTA	2040		
Db	1981	tctccttlatagagccatctccattctctatatagttaaaagtttctcttatacagataltta	2040		
QY	2041	TTAGTAAGAAACATCATCTGAAATGCGAGCTGCAATGATGATCATCTCTTTGATGTCAATAG	2100		
Db	2041	ttagtaagaaacacatctacttgaatgtctagctgcaagtgcacatctcttgaigtacatag	2100		
QY	2101	AAGAGTTAAACAGACGTGGAGAAATTCCTTGATTCACATGAATAAGTCTCTCCCTG	2160		
Db	2101	aagagttaaacacagltgagaaatctcttgatcacaaatgaatgctctctcttccctg	2160		
QY	2161	CCCCCAGAACCTTTATTCACACTTACTAGATTTGACATATTCCTTTAAATTCATCTCAGGC	2220		
Db	2161	ccccccagaaactttatctacttacccttagatctcaacatcttcttaaaattcatctcagcg	2220		
QY	2221	CTGCCTCAACCCACGCGGGCGGCAGACACATGGAATTC	2259		
Db	2221	ctgcctcaacccacagggcgccgacacatcgaattc	2259		
RESULT 8					
AAQ12118	AAQ12118 standard; DNA; 2259 BP.				
AAQ12118:	(first entry)				
XX	09-SEP-1991				
DE	Sequence encoding human lymphocyte cell surface glycoprotein (LHR).				
KW	Ligand binding partner; lbp; stable plasma protein; spp; antiviral;				
KW	immunomodulatory; neuromodulatory; receptor mediated abnormality; ds.				
XX	Homo sapiens.				
OS	Key	Location/Qualifiers			
XX	Key	129..1247			
XX	CDS	/*tag= a			
XX	sig_peptide	186..224			
XX	mat_peptide	/*tag= b			
XX		243..1244			
XX		/*tag= c			
XX	MO9108298-A.				
XX	13-JUN-1991.				
XX	21-NOV-1990;	90MO-US06849.			
XX	22-NOV-1989;	89US-0444625.			
XX	(GETH) GENENTECH INC.				
XX	Capon DJ, Lasky LA;				
XX	PI				
XX	WI; 1991-193202/26.				
XX	IR				

DR	P-PSDB; AAR12469.
XX	
PT	New hybrid immunoglobulin(s) - for use as diagnostic reagents for
PT	lygand binding molecules and to treat organ and graft rejection
PT	and inflammation.
XX	
PS	Disclosure; Fig 1; 67pp; English.
XX	
CC	The gene product may be used as a ligand binding partner in combina-
CC	tion with a stable plasma protein eg. IgG1-IgG4, IgA, IgE, IgD or IgM.
CC	The fusion product is joined by N- or C-terminal groups, preferably
CC	the N-terminal of the Fc region of the spp is linked to the C-terminal
CC	of lbp. They may be used to provide antiviral, immunomodulatory
CC	and neurochemical treatment as well as in treatment of receptor
CC	mediated abnormalities.
XX	
SO	Sequence 2259 BP; 634 A; 516 C; 487 G; 618 T; 4 other;

Query Match	99.7%	Score 2251.8;	DB 12;	Length 2259;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 2253; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	1	GAATTCAGAGTCGTGGCTTCTCACCCTGACGACGACGACACACTCCCTTTGGCAAGGACCT	60
Db	1	gaattccagtctgcctcgtctccaccctccymmaagccacacccctcttggcaaggaact	60
QY	61	GAGACCCCTTGTGTAAATCAAGAGGCTCAATGGGCTCGAGAAAGTATAGAGAGACCAA	120
Db	61	gagaccctctgtctaagtaagtaagagtgctcaatggtctgcagaagaacttagaagaagccaa	120
QY	121	GCAAAACCATGATATTTCCATGGAAATGTCAAGCACCCAGAGGGACTTATGGAACATCT	180
Db	121	gcaaaagccatgataattccatgaaatgcagaagacccacagaggaacttatgaaacatct	180
QY	181	TCAAGTTGGGGGTGACAAATGCTGCTGTGTGGATTTCCCTGGCAATCATGTGAACCTACT	240
Db	181	tcaagtctgagggggtgagcaaatgctgctgtgttgatctctgtgcaatcatcaggaacctact	240
QY	241	GCTGGACTTACCATTTATTTCTGAAAAACCCATGAGTGGCAAAAGGGCTAGAAATTTCTGCC	300
Db	241	gctggacttacatattatcttgaaaaaaccaatgaactgctgaaagagctagaagattctccc	300
QY	301	GAGACAAATTACACAGATTTAGTTGCCATTACAAAACAAGCGCAAAATTGAGTATCTGGAGA	360
Db	301	gagacaattaccacaagatttagcttgcatacaaaacaagcggaaatltgatacttcyaga	360
QY	361	AAACTCTGCGCTTCAGTGGTCTTACTACTGATGATGGAATCCGGAAGATAGGAGCAATAT	420
Db	361	aagactctgcccctcagtcgtctctactactcgtatagaaatccggaatagaagaaatat	420
QY	421	GGAGCTGGGTGGGAAACAACAATCTCTCACTGGAAGAAGACAGAACTGGGAGATGGTG	480
Db	421	ggaagctgggtgggaaccaaacaactctctcaactgaagaagcaggaactcgggagtggtg	480
QY	481	AGCCCAACAACAAGAAAGAAACAGGAGACTGGGTGGAATCTATATCAAGAGAAACAAG	540
Db	481	agcccaacaacaagaagaacaagaggagcmcgtygagatcctataccaagaagaacaag	540
QY	541	ATGCAAGCAAAATGGAACATGACGCGCTCCCAACAACTTAAAGCAGCCCTGTGTTACACAG	600
Db	541	atgcagagcaaatggaacgatgacgctctgcacaaactaaagcagccctctgltacacag	600
QY	601	CTTCTTGGCCAGCCCTGTCATATGACAGTGGCCATGAGAAATGTTAGAAATTCATTAATC	660
Db	601	cttcttgcagccctgctcatcagctggtccatggaatgctgtagaatactcaataatc	660
QY	661	ACAACCTGCAACTGTATGTTGGGGTACTATGTTGGGCCCATATGACACTTGTGATTCAAGTGTG	720
Db	661	acaactgcaactgtatgtgtgggtactatggtgcccagctgtcagctctgtatctaaagtgtg	720
QY	721	AGCCTTTGGAGGCCCAAGAGCTGGGTATCAATGAGACTGACTACACCCCTTTGAAACTTCA	780

D	721	agccttvgagagccccaagcagctggtgtaccaaigtgactgtactcaacccttvggaaacttca	780
O	781	gcttcagctcACAGTgtgTCCCTTACGCTGTGTGAAGAAACAATTTAACTGGAGTTGAG	840
D	781	gcttcagctcacaagctgagcttcaagctgtctctcgaaggaacaaacttaactggtatgag	840
O	841	AAACCACTGTGGACATTTTGGAAACTGTCATCTTCAGAACCAACCTGTCAAGTATTC	900
D	841	aaacacactgtgagccatttggaactgtgtcattccacgaacaaacctgaagtgatlc	900
O	901	AGTGMAGCCCTATTCAGACACGAAATTTGGGGATCATGTAACGTGTGCCATCCCTCGGCA	960
D	901	agtgtagccctctacagccacagatcttgggatactgaacgtgacatccctcgggca	960
O	961	GCTTCAGCTTACCTCGATGTACCTTCATCGTCACAAAGAACTGATTAATTGGGA	1020
D	961	gcttcagcttaccctctgactgtacttcaatctgctccgaagaagactgagttaattggga	1020
O	1021	AGAAAGAAACCAATTTGTGAATCATCTGGAATCTGTCAATCTTAGTCAATATGTCAA	1080
D	1021	agaagaaaacatttgygatactcctgagatctgtgcaaatccctatgccaatagtcaaa	1080
O	1081	AATTGGACAAAAGTTTCTCATATATTAAGGAGGTCATTATACCCCTCTTTCATTCCAG	1140
D	1081	aattggacaaaagtttctcaatgattaaaggaggtgattataccccctcttaccag	1140
O	1141	TGGCAGTCATGTACTACGATTCCTGCGGGTGGCATTTATCTTGGCGGCAAGAGAT	1200
D	1141	tggcagtcatagtgttaactcgtcactcttcgggttggcattatacttgcgtcggaaggat	1200
O	1201	TAAAAAAGGCAAGAAATCCAAAGAGAATGATGATGCCATATTAAATCGCCCTTGGTG	1260
D	1201	taaaaaaggcaagaanaatcccaagagatgaatgaaagcccatataaatgccttgggtg	1260
O	1261	AAAGAAATTTCTGGGAATACTAAAAATCATGAGATCCTTTAAATCCTTCCATGAACGT	1320
D	1261	aaagaaatttcttggaaatactaaataactatgagatcctttaaactcttccactgaacgtt	1320
O	1321	TTTGGTGTGGACACCTCTACGTCAAAACATGAAGTGTCTCTTACAGTCATCGGGAAG	1380
D	1321	tttggtgtggtgacacctctcactcgtcacaacatgaagtggttcttcaagtgcattcgggaag	1380
O	1381	ATTTCTACCCGACCAACAGTTCTCTTACGCTTCATTTGCGCCCTCATTTATCCGTCAAC	1440
D	1381	atttctacccgacaacagactctctcagcttcatgacttgccttaccctatattaccctcaac	1440
O	1441	CCGACGCCACAGGTGTTTATACAGCTCACGTTTGTCTTCTGAGAGAAACAATAA	1500
D	1441	ccgagcccaagtggttatacagcccaagcttcttgccttcttgaaggagaaacaaataa	1500
O	1501	GACATTAAGGGAAAGGTTTATGTGAAATATAAGTGGCTGACTTCTCTTCTTGAC	1560
D	1501	gacataaaggaaagagcttcaatgvgaaatacaagaatgvgacttgccttctcttgac	1560
O	1561	TCTGTTTTTCAGTTTCAATTCAGTGTGTACTGTATGAGACGACATTTTAAATGAAGTG	1620
D	1561	tctgttttcaagttcaatctcagtgctgtactgtatgaagaagcactcttaatagaagtg	1620
O	1621	AAATTTGATACATATGTGAATATGACCTAGTTTCTTGACATCAAAATTTACGCTGC	1680
D	1621	aaatttgatacatatgtgaaatacagactgttcttctgcagatcaaatcttcaacgtgtc	1680
O	1681	TTTGCTATACGTGGAGCTGTACACTTTATAGAAAGTCAAAAAGTCATCGCTCTCTTG	1740
D	1681	ttctgtatacgtgtaggtactactcttataagaagttcaaaaagctcagctctcttc	1740
O	1741	TTTTTAATCAGTGAAGTATGATGGGTCTCTGCTCAAGTTGAAGAAGTCTTATTTGCACTG	1800
D	1741	ttcttaactcaagtggaagtaatggtgctgtctcaagtgaaaggtctctatttgcagtg	1800
O	1801	TAGCCTCGCGCTGTGTGAATTTGACACATCCCTATTTAACTGGCTTAGCGCTCCCACTT	1860
D	1801	ttagcttcgctctcgttgaatcttgacaactctttaaactgagcttcaaggtctcccaactt	1860

Qy	1861	CTTCAGCCACCTCTCTTTTTCAGTTGCTGACCTTCACACCTGACATCTGCANAGNTGCCA	1920
Db	1861	cttcagccacctctcttcttccagttcgctgacttccaccacccagacgtcatalgagtcgca	1920
Qy	1921	AGCAAAAGAGACAAAGAGACAAATTAACCTCGCGGGTTTTTTAGTTGGGGTTTTGCTGT	1980
Db	1921	agcaaaaggagagagagagaaatagccgcggtcttcttagcttgggggttttgcgcgt	1980
Qy	1981	TTTCCTTTTATGAGACCCATTCTTAATTTCTTTATAGTCAATGTTCTTTTATCAGATATTA	2040
Db	1981	tttcctttatgagccatccattctcttatagtaagtaagttcttcttatacagatatla	2040
Qy	2041	TTTAGTAGAAACACATCTCAATAGTACTAGTGAATGACATCTCTTTGATGATCATATGG	2100
Db	2041	tttagtaagaaacacacacctcgtgaaatgctgacgtcgaatgacatctcttgaigtcatatvg	2100
Qy	2101	AAGAGTTTAAACAGAGTGGAGAATATCTCTTGATTCACAAAGAAATGCTCTCCCTTCCCTG	2160
Db	2101	aagagttcaaacaggtgtagaaatctcctgattcaacaaatgaatgctctcttccctg	2160
Qy	2221	CTCCCTCAACCCCGCGGGCGCCGACACACACTGGAATTC	2259
Db	2221	ctccctcaaccccgcgggcgccgacagcaactggaattc	2259
RESULT 9			
AAQ23623			
ID	AAQ23623 standard, DNA; 2260 BP.		
AC	AAQ23623:		
XX			
DT	01-SEP-1992 (first entry)		
XX			
DE	Human lymphocyte homing receptor gene.		
XX			
KW	HulHR; LHR; binding; endothelium; immunogens; graft; organ; ss;		
KW	rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.		
XX			
OS	Homo sapiens.		
XX			
FT			
XX			
PN	US5098833-A.		
XX			
PD	24-MAR-1992.		
XX			
PF	23-FEB-1989; 89US-0315015.		
XX			
PR	23-FEB-1989; 89US-0315015.		
XX			
PA	(REGC) UNIV OF CALIFORNIA.		
XX			
PI	Laaky LA, Rosen SD, Stachel SE, Slinger MS, Yednock TA;		
XX			
DR	WPI: 1992-123385/15.		
XX			
XX	P-PsDB: AAR22802.		
XX			
PT	New DNA encoding at least one domain of lymphocyte homing		
XX			
PT	receptor - useful for treating graft rejection, inflammation,		
XX			
XX			
PS	Claim 3; Fig 1; 32pp; English.		
XX			
CC	The DNA sequence was obtd. by screening an oligo dt primed lambda		
CC	gt10 cDNA library derived from human peripheral blood lymphocyte		
CC	mRNA obtd. from primary cells, with a 2.2 kb EcoRI insert of the		

CC murine Me1 14 antigen cDNA clone. 12 positive plaques were isolated
CC and those with the largest EcoRI insert were sequenced. The 2.2 kb
CC clone encodes an open reading frame of 372 amino acids. The human
CC LHR is 83 percent homologous with the murine LHR sequence and LHR
CC contains regions encoding a carbohydrate binding domain, an Egr-1-like
CC domain, a complement binding domain and a transmembrane domain.
CC Cells transformed by the hLHR DNA are used to produce LHR (which
CC mediates binding of lymphocytes to the endothelium of lymphoid
CC tissue). LHR or its variants are useful as reagents for assaying
CC LHR or anti-LHR antibodies, to purify the antibodies, as immunogens,
CC and therapeutically to compete with normal binding of lymphocytes
CC (to prevent graft/organ rejection) to treat inflammation (such as
CC rheumatoid arthritis or other autoimmune diseases); for control of
CC lymphocyte metastasis, and to treat conditions associated with
CC accumulation of lymphocytes). Derivs. and variants of LHR may be
CC produced having modified properties, e.g. increased activity, longer
CC plasma half-life, reduced side effects and better aq. solubility.
CC See also AA023624 and AA023464.

XX Sequence 2260 BP: 636 A; 518 C; 487 G; 619 T; 0 other;

Query Match 99.2% Score 2241.6; DB 13; Length 2260;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2244; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGCTCCCTCACCCTGCAGCAGCAGACTCCCTTGGCAGAGACT 60
Db 1 gaattcagtgctgtgcttccctcactgcagcagcagcactcttggcagaagacct 60
QY 61 GAGACCTTGGCTAATCTCAGAGAGGCTCATGGCTCAGAGAGACTAGAGAGACAA 120
Db 61 gagaccttggctaaagctcaagagctcaatggtcagagaagacaggaagaccaa 120
QY 121 GAAAGCCATGATATTTCCATGGAATGTGAGAGACCCAGAGGAGATTGTGAACATC 180
Db 121 gcaagccatgatattcttcctgaatgtcagagcaccagagagactatggaatact 180
QY 181 TCAAGTTGTGGGGTGAGCAATGCTGTGTGATTTCTGGCAGATCATGAACTACT 240
Db 181 tcaagttgtgggtgagcaatgctgtgtgatttccctgacatcatggaactact 240
QY 241 GCTGACTTACATTTATCTGAAAAACCCATGAACGTGGCAAGGCTAGAAATTTGCC 300
Db 241 gctgacttaccattctcgaataaacccatgaaacgagaaaggtcagaagtttgc 300
QY 301 GAGACAATTAACAGATTTAGTGCATACAAACAAAGGCGAAATTTGATATCGAGAG 360
Db 301 gagacaattacacagattagtgccatcaaaacaaagcggaaattgatactcggaga 360
QY 361 AGACTGTGCTTCACTGCTTACTACTGATAGAAATCCGAGATAGAGAAATAT 420
Db 361 agactgtgcttcactgcttactactgataagaaacgaaagtagaagagata 420
QY 421 GCACGTGGGTGGGAACCAATCTCTACAGAGAGACAGAACTGGGAGATGGTG 480
Db 421 gcaagtgggtgggaaccaaattctctacgaaagacagagactcggagatgg 480
QY 481 AGCCCAACAAAGAAAGAAAGAGAGACTGCGTGAGATCTATATCAAGAGAAACAAG 540
Db 481 agcccaacaaagaaagaaagacagactcgtgagatctatcaagagaacaag 540
QY 541 ATGCAAGGCAAAATGGAAGTGAAGCTGCGCACAACATAAGGACCCCTTTACACAG 600
Db 541 atgcaggcaaaatggaaagtgaagctcgcacaaataaagcacccttltcacag 600
QY 601 CTTCTTGCCAGCCCTGCTCATGCTGAGGAGATGAGAAATGATCAATCAATATC 660
Db 601 ctctcttgccagccctgtcatgctgagagcagatgagaaatcatcaataatc 660
QY 661 ACACCTGCACTGTGATGTGGGGTACTATGGGCCCACTGTCACTGTGATTCAGTGTG 720
Db 661 acaactgcaactgtgactgtggttactatggtgcccagtgcaagcttgtgattcag 720

QY 721 AGCCTTTGAGAGCCCGACAGCTGGGTACCAATGACATGTACTCAACCCCTTTGAAATCTCA 780
Db 721 agcctttgagagcccgacagctgggtaccaaataagactgtactcaaccccttggaaactca 780
QY 781 GCTTCAGCTCAGAGTGTGCTTCAGGCTGCTGAGGAAACAACTTACTGGATTTGAAG 840
Db 781 gcttcagctcagagtggtcttcagagctcgtcgaagaaacaaacttaactggtgaag 840
QY 841 AAACACCTTGGAGACATTTTGAAGTGTGATCTGCAGAACCAACCTGTCAAGTATTC 900
Db 841 aaacaccttggagacatttggaaactgtcatctccagaaacacctcaagatc 900
QY 901 AGGTGAGCCTTATACAGACCCAGATTTGGGGATCAATGAATGTAGCCATCCCTGGCCA 960
Db 901 aggtgagccttatacagaccagatttgggatactagactgtagccatccctggcca 960
QY 961 GCTTCAGCTTACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 gcttcagcttacctctgtcatgtacttcaatctgcacagaaagaaactgtaattgga 1020
QY 1021 AGAAGAAAACCATTTGTGATCATCTGAAATCTGATCAATCTGATCCATATGTCAAA 1080
Db 1021 agaagaaaaccatTTGTGATCATCTGAAATCTGATCAATCTGATCCATATGTCAAA 1080
QY 1081 AATTGACAAAAGTTTCTGATGATTAAGGAGAGGATTAATTAACCCCTTTATCTCAG 1140
Db 1081 aattgacaaaagtttctgatatgaatgaagagagatataaacccttctacacag 1140
QY 1141 TGGCAGTCAATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 tggcagtcaatgctgactgacttctctggttggcattatacttggctggcaagagat 1200
QY 1201 TAAAAAAGGCAAGAAATCAAGAGAGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 taaaaaaggcaagaaatcaagagatgataagatgataagatgataagatgataagat 1260
QY 1261 AAAGAAAATTTTGAATATCTGAAATATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 aaagaaaatTTTGAATATCTGAAATATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 TTGTGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1321 ttgtgtgtgggctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1380
QY 1381 ATTCTACCCGACCAAGCTTCTTCACTTCCATTTGCCCTCATTTATCCCTCAAC 1440
Db 1381 attctacccgaccaaagcttcttcaacttccatcttccgcccctcatltaaccctcaac 1440
QY 1441 CCCAGCCACAGGTGTATACAGCTCAGCTTTTGTCTTTTGAGAGAGAAACAAATTA 1500
Db 1441 ccagccacaggtgtatacagctcagcttcttgccttctcgtgagagaaacaaataa 1500
QY 1501 GACCAATAGGGAAGAGATTCATGTGGAATTAAGATGCTGACTTGTCTTCTTGAC 1560
Db 1501 gaccaatagggaagagattcatgtggaatataaagatgctgacttgccttcttgac 1560
QY 1561 TCTTGTATTCAGTTCAATTCAGTGTGCTGATGATGATGATGATGATGATGATGATG 1620
Db 1561 tcttgtatTCAGTTCAATTCAGTGTGCTGATGATGATGATGATGATGATGATGATG 1620
QY 1621 AAATTTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 aaatttgataatgataatgataatgataatgataatgataatgataatgataatgata 1680
QY 1681 TTCTGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db 1681 ttctgatactggtgagatgataatgataatgataatgataatgataatgataatgata 1740
QY 1741 TTCTTAACCTCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 ttcttaacctcagtgatgataatgataatgataatgataatgataatgataatgataatg 1800

OY	1801	TACCTTCGGCGTCTGTCGAATTGGACATCCCTATTAACTGGCTTAGCGCTCCCACTT	1860
Db	1801	tagcttcgcgcgtctgtyhaatltyggaccatctatlttaactcygtcttaaggccctccaccctt	1860
OY	1861	CTTAGCACACCTCTCTTTTTCAGTTTGGCTGAACTTCCACACACAGCATCTCATGTAGTGCA	1920
Db	1861	cttagcacacctctcttlttcaglttgcgtgcacttccacccagatctctatctatgtygcga	1920
OY	1921	AGCAAAAGGAGAGAGAGAGAAATAGCCTGCGCGGCTTTTAACTTGGGGCTTTTGCTGT	1980
Db	1921	agcnaaagagagaaagagaaatagcgcgcgcgtcttltttaglttgggggttlttgcgt	1980
OY	1981	TTTCCTTTATGAGAGACCATTCCTATTCTTTCTTATAGTCAATGTTCTTTTATACAGATATTA	2040
Db	1981	ttctctttaaagagaccatcttccatltctctatctatagtcgaatglttcttctaatacagatatla	2040
OY	2041	TTATGTAAGAAAACATCATCTGAAATGCTAGCTGCAAGTGACATCTTTGATGTATATGG	2100
Db	2041	ttagtaagaaaaacatctcgtaaatgctagctgcaagtgcacatctctttagtcatatg	2100
OY	2101	AAGGTTAAAAACAGTGTGNAAAATTCCTTGATTTCCAAATGGAATGCTCTCTTCCCTG	2160
Db	2101	aagagttaaaacagtygagaaaaatctcttgatctcaagaagaaatgctctcttctccctg	2160
OY	2161	CCCCAGACATTTTATTCACATTTACTAGATTTCTACATATTTCTTAAATTCATCTCAGGC	2220
Db	2161	ccccagaaactttatctcacttaactcctaggtctctacatctctttaaattcatctatctcagyc	2220
OY	2221	CTCCCTCAACCCACAGGGGCGGCACGA	2248
Db	2221	cttccctcaacccacaggggscgcacga	2248

RESULT	10
AAQ24987	
ID	AAQ24987 standard; DNA; 2262 BP.
XX	
AC	AAQ24987;
XX	
DT	22-NOV-1992 (first entry)
XX	
DE	Sequence encoding human lymphocyte cell surface glycoprotein
DE	(HLAHR).
XX	
XX	Lymphocyte cell surface glycoprotein; ligand binding protein;
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	CDS
FT	129..185
FT	/*tag- a
FT	186..242
FT	/*tag- b
FT	mat_peptide
FT	143..1247
FT	/*tag- c
XX	
PN	US5116964-A.
XX	
PD	26-MAY-1992.
XX	
PF	22-NOV-1989; 89US-0440625.
XX	
PR	23-FEB-1989; 89US-0315015.
PR	22-NOV-1989; 89US-0440625.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Capon DJ, Laaky LA;
XX	
DR	WPI: 1992-199589/24.
DR	P-PSDB; MAR24026.
XX	
PT	Nucleic acid encoding polypeptide fusions - comprising ligand

PR binding partner protein and immunoglobulin chain, for use in
PT diagnosis and therapy
XX
XX
XX · Disclosure: Fig 1-1 - 1-3; 43pp; English.
PS
XX LHR mediates the binding of lymphocytes to the endothelium of
CC lymphoid tissue. Full length cDNA clones and DNA encoding the human
CC and the murine LHR (HULHR and MLHR, respectively) have been
CC identified and isolated (see AAQ24967 and AAQ24968). LHR is a
CC glycoprotein which contains the following protein domains: a signal
CC sequence, a carbohydrate binding domain, and epidermal growth
CC factor-like (egf) domain, at least one and preferably two complement
CC binding domain repeat, a transmembrane binding domain (TM), and a
CC charged intracellular or cytoplasmic domain. LHR is used as the
CC ligand-binding partner in fusion polypeptides with an immunoglobulin,
CC for use in diagnosis and therapy.

S0 Sequence 2262 BP; 635 A; 518 C; 488 G; 621 T; 0 other;
XX

Query Match	99.2%;	Score 2241.2;	DB 13;	Length 2262;
Best Local Similarity	99.7%;	Prod. No. 0;		
Matches 2256;	Conservative 1;	Mismatches 3;	Indels 3;	Gaps 1;
OY	1	GAATTCCAGTGTGCGGGCTTCCTCACTCGACACAGACACTCCCTTTGGCAAGACCT	60	
Db	1	gaattccagtgctgcggcttcctcacctgcagcacagacatcccttgggaagagacct	60	
OY	61	GAGACCTTTGTTCTCTAAGTCACAGAGCCTCAATGGCTGCAGAAAGACTAGAGAAAGACCA	120	
Db	61	gagacccttgcgtcaagtcgaagagctcaatggctgcagaagaactctgagaagaacca	120	
OY	121	GCAAGCCATGATATTTCCATGTGAATGTCAAGACACCAGAGGGACTTATGGAACATCT	180	
Db	121	gcaaaagccatgatttccatigaaatgtcagagaccacagagggaacttatgaaacatct	180	
OY	181	TCAGTTGTGGGGGTGAGACATGCTCTGTGTGTGATTTCCTGGCACATCATGGAACCTTCT	240	
Db	181	tcaagtgtgggggtgagaaatgctctgtgtgtgatttcctgtgcacatcatgaaacctact	240	
OY	241	GCTGGACTTACCATTTCTGAAAAACCCATGAACTGGCAAAAGGCTGAAGATTCTGCC	300	
Db	241	gctggacttacatattctctgaaaaaccatgaaactggcaaaaggtctagaatcttcgccc	300	
OY	301	GAGACAATTACACAAATTAGTTAGTGGCATTACAAAACAAGGGGAATTAGTATTCGGAGA	360	
Db	301	gacacaattacacagatcttagtctgcacaaacaaagcggaatactgagatctcggaga	360	
OY	361	AGACTCTGCCCCCTTCAGTGTGTTTCTACTACTGAGTATGGAATCCGAAAGATAGAGCAAAAT	420	
Db	361	agactctgccttcacgtctgtctctactactctgatatcggaatctgagagaaatcat	420	
OY	421	GGACGTGGGTGGGAACAACAATCTCTCACTGGAAGAAGACAGAACTGGGAGATGGTG	480	
Db	421	ggacgttgggtgggaaccaaacaatctctcaactcgaagaagcagaagactcgggagtggtg	480	
OY	481	AGCCCCAACACAGAAGAAACAAGAGAGACTGCGTGGAGTCTATTTCAGAGAAACAAG	540	
Db	481	agcccaacaacaagaagaaagaagagagactggtgtgagatctatatacaagaanaacaag	540	
OY	541	ATGCAGGCAAAATGGAAAGCATGACGCCCTGCCACAAACTAAAGCAGCCCTCTGTTACAG	600	
Db	541	atgcaggaacaatlgagaacgatgagcctgcacaaactaaagacagccctctgttacacag	600	
OY	601	CTTCTTGGCAGCCCGGTGCATGACATGTGGCCATGGAATGTGAAATTCATCATATTC	660	
Db	601	cttcttgcagcccggtgtcatgtagtggccatlgagaatgtgtcagaatactcaataatc	660	
OY	661	ACACTGCAACTGTATGTGGGTACTATAGGCCCCCAATGTCACGTTTGATTCAGTGTG	720	
Db	661	aaacctgcaactgtgtagtgggtactctatggccccagctgcagactgtgattcaggtgtg	720	
OY	721	AGCCTTTGGAGCCCAACAGCTGGGTGTACATGAGACTGTACTCACCCCTTTGGAAACTTCA	780	

PT Cloning of cDNA encoding cell surface antigen - useful for isolation
PT of diagnostic and therapeutic proteins

PS Example 14; Column 71-74; 79pp; English.

XX 2 cDNA clones encoding Leu8 determinants (AAR91442 and AAR91443) were
XX isolated from a human T-cell library using a novel immunoselection
CC cloning method. The longer insert (AAR14723) contained 2,350
CC residues, while the shorter lacked 436 internal residues but was
CC otherwise identical. Dot blot hybridisation of a fragmented
CC human T cell genome showed a pattern consistent with a single copy
CC gene. A major transcript of 2.4 kb was present in peripheral
CC blood mononuclear cells (PBMC), tonsillar B cells, and several
CC lymphocytic cell lines, and a minor transcript of 2.0 kb in PBMC,
CC Jurkat and HSB-2 leukaemic T-cell lines. Leu8 antigens can be
CC obtd. for diagnostic and therapeutic use.

SQ Sequence 2350 BP; 679 A; 520 C; 490 G; 661 T; 0 other;

Query Match 94.2%; Score 2127.8; DB 17; Length 2350;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2179; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

OY 44 CCTTTGGCAGAGACCTGAGACCTGCTGCTAAGAGGCTCAATGGGCTGCAGAAAG 103
DB 4 cctttggcaaggacctggaaccttgcgaagtcgaagaggtcctcaatggctgcagaag 63
OY 104 AACTAGAGAGAGACCAAGCAAAAGCCATGATATTTCATGGAAATGTCAGAGACCCAGAG 163
DB 64 aactagaagaagcgaagaagaagcatalgtatctcagtaagaaatgacagacccagaag 123
OY 164 GGCATTATGAGACATCTTCAAGTTGTGGGGGTGACAAATGCTGTTGATTTCTGGC 223
DB 124 ggcattatggaacatcttcaagttgtggggtgacaaatgctgttgcatttccctggc 183
OY 224 ACATCATGGAACCTACTGCTGGAGCTTACCATTTCTGAAAAACCATGAACTGGGAAAG 283
DB 184 acatcatggaacacttcaagttgtggggtgacaaatgctgttgcatttccctggc 243
OY 284 GGGTAGAATTTCTGCCGAGACAAATTACAGATTAGTTGCCATCAAAACAAAGCGGA 343
DB 244 gggtagaagatctgcgcgaagaacataacagattagttgccatacaaaacaaagcgga 303
OY 344 AATTGATATCTGGAGAGACTCTGCCCTTCACTGCTTACTACTGATAGGAATCCG 403
DB 304 aattgatattctggagaagactctgccttccagtcgttcttactactgataagaatccg 363
OY 404 GAAGATAGAGAAATTTGACGCTGGGTGGGAACCAAAATCTCTACCTGAGAAAGCAGA 463
DB 364 gaagatagaagaatactgacgctgggtgggaaccaaatactctcactgaagaagcaga 423
OY 464 GAACTGGGAGATGTGAGCCCAACAAGAAAGAAAGAGAGAGACTGGCTGAGATCTA 523
DB 424 gaactgggagatgtgagcccaacaagaagaagaagagactggctgagagatctca 483
OY 524 TATCAAGAGAAACAAAGATGACGCAAAATGGAAGATGACGCTGCCACAAATTAAGC 583
DB 484 tatcaagagaaacaagaatgacgcaaaatggaaatgacgctgccacaataaagc 543
OY 584 AGCCCTCTGTACACAGCTTTTGGCCAGCCCTGGTGTATGACAGTGGCCATGAGAAATGTGT 643
DB 544 agccctctgttacacagcttttggccagccctgggtgtatgacagtggccatgagaaatgtgt 603
OY 644 AGAATATCAATTAATACACAGCTCAACTGTGATGTGGGTACTATAGGGCCCCAGTGTCA 703
DB 604 agaataatcaataatataacacagctcaactgtgatgtgggtactatagggcccccagtgta 663
OY 704 GCTTGTGATTAAGTGTGACCTTTTGGAGGCCCCAGAGCTGGGTACCATGAGACTGTACTCA 763
DB 664 gcttgtgattaaagtgtgaccttttggagggcccccagagctgggtaccatgagactgtactca 723
OY 764 CCCCTTTGGAACCTTACGCTTACAGCTCACAGTGTGCTTACAGTGTCTGAAGAAACAAA 823

DB 724 cttcttgggaacttcagcttcagcttcagcagtgcttccttcagcttcagctgaagaaacaa 783
OY 824 CTTTAACATGATGGAAGAAACACACTGTGTGACCATTTTGAAGCTGATCTCCAGAAC 883
DB 784 ctttaacatgatggaagaaacacactgtgtgaccttcagcttcagctgaagaaacaa 843
OY 884 AACCTGCAAGTATTCAGTGTAGGCTTATACAGACCAAGATTTGGGGATCATGAACTG 943
DB 844 aacctgcaagtattcagtgtagcctctcagaacagatttggggaatcagtaacag 903
OY 944 TAACCATCCCTCCAGCTTCACTTACCTGTGATGATGATGATGATGATGATGATGATG 1003
DB 904 tagcatccctccagcttcagcttcagcttcagcttcagcttcagcttcagcttcag 963
OY 1004 AACTGATTAATTTGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGTCAAATCC 1063
DB 964 aactgatataatttgggaagaaaccaaatttgtgaatcatctggaaatctgtcacaatcc 1023
OY 1064 TAATCCAAATTTGCAAAATTTGGCAAAATTTCTCAATGATTAAGAGGCTGATTAATA 1123
DB 1024 tagtcaaatatgtcaaaaatltgacaaaagttctcaatgataaggaaggtgatatlaa 1083
OY 1124 CCCCTCTTCAATTCAGTGTGACGCTGATGATGATGATGATGATGATGATGATGATGAT 1183
DB 1084 cccctcttcaatccagctgagctgagctgagctgagctgagctgagctgagctgagct 1143
OY 1184 TTGCTGTGCAAGAGATTAAAGAAAGCAAAATCCAGAGAGATGATGATGATGATGATG 1243
DB 1144 ttgctgtgcaagagatttaaaaaaagcaaaatccaaagagatgataagaaatgaaatgaa 1203
OY 1244 TTTAAATGCGCTTGTGGAAGAAATTTCTTGAATTAATTAATTAATTAATTAATTAAT 1303
DB 1204 ttaaatgcgcttgtggaagaaatcttgaatataataataatcagatcctttaa 1263
OY 1304 TCCCTTCATGAAGAGTTTGT 1362
DB 1264 tcccttcataagaaagtttgt 1323
OY 1363 TTCAAGTGCATCTGTGGAAGATTTTACCCGACCAAGATTTCTTCACTTGTGCCCC 1422
DB 1324 ttcaagtgcattctggaagatttctacatgacaaagcttcttccatcttccatcttgc 1383
OY 1423 CTGATTTATCTCCCAACCCCAAGCCCAAGAGGTTTATACAGCTGACCTTTTGTCTTT 1482
DB 1384 ctgattatctcccaaccccaagcccaagagtgattataagctcagcttcttgcctt 1443
OY 1483 CTGAGGAGAAACAAATTAAGACCAT -AAGGGAAGAGATTCTGTTGGAATTAAGATGCGT 1541
DB 1444 ctgaggaagaacaacaagaacccaagaagaaagatccatgagaaatcaaaagaatggct 1503
OY 1542 GACTTGTCTTCTTCTGACTCTTGTGTTTCAATTCAATTCAGTGTGATGATGATGATG 1601
DB 1504 gacttgtcttcttctgactcttgttcttcaatcaatcaatcaatcaatcaatcaatca 1563
OY 1602 ACACTTTAAATGAAGTCAAAATTTGATACATATGATATGAGACTCAGTTTCTTGA 1661
DB 1564 acactttaaatgaagtcaaaatttgatcatatgataatgagactcagtttcttgcga 1623
OY 1662 GATCAAAATTTACAGT 1721
DB 1624 gatcaaaatttacagtggt 1683
OY 1722 AAGTCTACGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1781
DB 1684 aagcttaccgctctcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1743
OY 1782 AAGAGTCTTATTTGGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1841
DB 1744 aagagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1803
OY 1842 CTTCAGGCGTCCGACCTTCTTCAAGCAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1901

Db	1804	cttca-aggctccccaaccttcttcagccacactctcttcttcagttgctgtaacttccacaac	1862
Qy	1902	TAGCATCTCATGAGTGGCCAGCAAAAAGAGAGAAGAGAAATAGCTGCGGCTTTT	1961
Db	1863	tagcatctcatgagtgccaagcaaaagagagagaagaatagcctgcgtgtgttttt	1922
Qy	1962	AGTTGGGGGGTTTTGGCTGCTTCCCTTTATGAGACCATTCTTAATTCTTAATGTCATGT	2021
Db	1923	agttggggggttttgcctgcgttctcttcttatgagcccatctctatcttatagtaagtg	1982
Qy	2022	TTCCTTTATCAGATATTATTAGTAAAGAAACATCAGTAATGTAGCTGCAAGTACA	2081
Db	1983	ttctctttatcaagatattatctagaaagaacaactcgtgaatgctgcagtgaca	2042
Qy	2082	TCTCTTGATGTCATATGAAAGAGTTAAAAACAGAGTGGAAGAAATCTTGATTTCAACAATGA	2141
Db	2043	ttctcttgatgctatgataagagaagataaaaaagtgagagaattccttgattcaaatga	2102
Qy	2142	AATGCTCTCCTTTTCCCTGGCCCCAGAACCTTTTATGC-ACTTACCTAGATTCTACATATT	2200
Db	2103	aatgctctctcttccctgcgccacagacctttatcgcattactagattctacatatt	2162
Qy	2201	CTTAAATTCATCTCAAGGCTCCGCCAACCCAC	2235
Db	2163	cttcaaatctcatctcagcctctcttcccaacccac	2197

RESULT	12
AAA50596	
ID	AAA50596 standard; cDNA; 2350 BP.

DT 19-DEC-2000 (first entry)
 YY

Human T-cell specific Leu8 antigen cDNA

KW leu8: cell surface antigen; human; immunoselection; panning;
 KW immunodiagnosis; diagnosis; immunotherapy; gene therapy;
 KW immune disorder; infection; asthma; immune-complex disease;
 KW amyloidosis; multiple sclerosis; inflammation; antinflammatory
 KW ss

OS Homo sapiens.

FH	Key	Location/Qualifiers
----	-----	---------------------

/*tag=

PN US6111093-A

PD 29-AUG-2000

PF 28-OCT-1998; 98US-0181612.

PR 01-DEC-1992

PR 13-JUL-1989

PR 13-JUL-1990;
yy

PA (GEHO) GEN HOSPITAL CORP.
XY

PI Stamenkovic I, Seed B;
XY

DR WPI; 2000-586382/55.
DR D-PDR; 2000-586382/55.

XX
XX
XX

PT	useful for i
PT	in foot ion

PT diseases -
xy

PS Example 14; Column 69-72; 75pp; English

The present sequence is that of a cDNA clone encoding a T-cell specific Leu8 antigen (see AAY96138). It is 1 of 2 clones (see also AAY50622) isolated from a human T-cell library by the method of the invention. The method, designed to isolate cell surface antigen (CSA) nucleic acids, is based upon transient expression of a CSA in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to (penning on) an antibody-coated substrate such as a culture dish. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, diseases, and disorders in animals, including humans. These disorders include asthma, immune-complex disease, amyloidosis, parasitic diseases or multiple sclerosis. The ability to interfere with the binding of Leu8-T-cells to antigen presenting cells, or the ability to cause such binding to occur on surfaces other than lymphocyte cells, can be useful in diagnostics and therapy. The level of activated Leu8-T-cells relative to resting Leu8+ cells could serve as a measure of immune response to a particular antigen. Modification of the specificity of the extracellular domain of Leu8, which mediates adhesion to specific endothelial cells of lymph nodes, could serve to regulate the homing potential of resting T cells. Soluble forms of Leu8 could act as antiinflammatory agents by reducing lymphocyte migration.

Sequence 2350 BP; 679 A; 520 C; 490 G; 661 T; 0 other;

Query Match	94.2%;	Score 2127.8;	DB 21;	Length 2350;
Best Local Similarity	99.3%;	Pred. No. 0;		
Matches 2179; Conservative	0;	Mismatches 12;	Indels 4;	Gaps 4;

QY	44	CCCTTTGGCAAGACTCTGAGACCTTGTGCTAGTCAAGAGGCTCAATGGCTGACGAAG	10
Db	4	cccttgggcaagagaccttgaagaccttgcgttaagtaagaagagctcaatggtgtctgaag	63
QY	104	AAC TAGAAGAGGACCAACCAAGACATGATATTTCCATGTGAATATGCAGACCAACAG	16
Db	64	aactagagaagagccaagccaagccaagcagatattcca tggaaatgltcagagacccagag	122
QY	164	GGACTTATGGAAACATCTTCAA GTTGTGGGGGTGGACAAATGCTGTGTTGATTCCTGGC	22
Db	124	ggactata tggaaacatcttcaagttctg tgggggtggacaatgctgtgtgatttcctgyc	18
QY	224	ACATCATGGAACTACGTCGTGGACATTACCTATTTCTGAAAAAACCATGAACTGGCAAG	28
Db	184	acataca tggaaacgcgccttgc tggactaaccata tcttgaaaaaaccatggaactgccaag	24
QY	284	GGCTTAGAAGATTCTGCCGAGACAATTACACAGTTTAA GTTGGCATACAAACAAGGGGGA	34
Db	244	ggctagaagattcttgcgcgagacaattacacaga tttagttgccatacaaaaagaagcgga	30
QY	344	AATTGATATCTGGAGAAGAC TCTGCCCTTCACTCGTTCCTACTGATAGGAATCCG	40
Db	304	aattgatatcttgcgagaagactctgccttccttcag tcttctactactgattagaatccg	36
QY	404	GAAAGTATAGSAGGATATGAGACGTGGGTGGGAACCAACAATCTCTCACTGAAGAAGCA	46
Db	364	gaagataaggaaata tggacgtcgttgggaacacaacaatcttcaacttgaagaagcaga	42
QY	464	GAACTGGGGCAATGTGAGGCCAACCAAGAAAGAAAGGAGACGTGGGAGATCTA	52
Db	424	gaacttggggaaatg tggagcccaacaacaagaagaacagagagactctgc tggagactcta	48
QY	524	TATCAAGAGAAACAAAGATGCAAGGCAAAATGGAACATGACCTTGCCACAACCTAAAGGC	58
Db	484	tatcaagaagaacaagaatg tgcagtgcaaat tggagaaga tgaagccttcgccaacaactaaagtc	54
QY	584	AGCCCTCTGTTACACAGCTTCTTGGCCAGCCCTGGTCATGACAGTGGCCATGAGAAATGTG	64
Db	544	agccctctgttaacaagactcttgcacagccctgtgcata tggagtgatgacatagaataatctat	60

QY	644	AGAAATCATCAATTAATATACACCTCGCAACTGTATATGTGGGGTACTATGGGCCCACTGTCA	703
Db	604	agaaatcataatataatataccctcgcaactgtatgtggyggtactatggycccaagtgtca	663
QY	704	GCTTGTGATTACAGTGTAGAGCCTTTGGAGGGCCAGAGCGTGGGTACCAATGAACTGATCA	763
Db	664	gtctgtgattcaagtgtagagcctcttgagggcccaagcgctgggtaccaaigagctgactca	723
QY	764	CCCCCTTGGAAACTTCAGCTTCAGCTTCACAGTGTGGCTTCACCTCCTCGAAGAAACAA	823
Db	724	ctctcttggaactcaactcaagctcgaactcaagaagtgctcttcagctgtcctctgaagaaacaa	783
QY	824	CTTAAGTGGGATTGACAGAAACACACTGTGGACCATTTTGGAACCTGTCATCTCCAGAAC	883
Db	784	cttaactgaggtatgaagaaaccacactgagaccatttggaaactgycatctccagaacc	843
QY	884	AACCTGTCAAGTGAATTACGTGTAGGCTCTATCAGACACAGATTTGGGATCATGAACTG	943
Db	844	aacctgtcaagtgatltcaagttagacctctatcaagacagaatttgggatacatgaaactg	903
QY	944	TAGACATCCCTGGCCAGCTTCAGCTTTAACTTCGTGATCTACCTTCATCTGCTGCAAGG	1003
Db	904	tagcaatccctgycagctcgaactcgaactctgcacgtacatctccatccatctgcgaagg	963
QY	1004	AACGTAGTTAATTGGGAGAGAAACCAATTGTGATCATCTGGAAATCTGGTCAATCC	1063
Db	964	aactgagttaatttgggagagaaacaacttgtgatacatcttggaatctgtaacatcc	1023
QY	1064	TAGTCCAAATATGTCAAAAAATTGACACAAAAGTTTCTCAATGATTAAGAGGGGATTAATA	1123
Db	1024	tagtccaatatlgtcaaaaatttgacaagaagttctcaatgataagaggygtatataa	1083
QY	1124	CCCCCTCTCATTCACAGTGGCAGTCATGGTACTGCATTCCTGGGTGGGCAATTATCAT	1183
Db	1084	ccccctctcatctccagctgagctcagctcagttactcgtactctctgtgttggaaattatcat	1143
QY	1184	TTTGCTGTGGCAAGGAGATTAAAAAAAGCAAGAAATCCAGAGAAATATGAAATGAGCCCTA	1243
Db	1144	tttgctgtgcaagagagattaaaaaagcaagaataccaaagaaatagatgagacccta	1203
QY	1244	TTAAATGCCCCCTGGTGAAAAGAAATTCCTGGATACTAAATCATGAGATCCTTTAAA	1303
Db	1204	ttaaatgccttggtgaaagaaatcttggatactaaatacatgagatccctttaa	1263
QY	1304	TCCCTTCATGAAGACGTTTGTGTGGTGGCACCCTCCTAGCTCAAAATGAAGTGTG-TTCC	1362
Db	1264	tcctcttcataagaaagtttctgtgtgtagaacctccacagctcaaaatgaagtggttcc	1323
QY	1363	TTTCAGTGCATCTGGGAAGATTCTTACCCGACCAACAGTTCCTTCAGCTTCATTTCCGCC	1422
Db	1324	ttctagtgcatctggaagatcttctacttgacccaacaagttccctcgaacttccatctgccc	1383
QY	1423	CTCATTTATCCCTTCACCCGACCCACAGAGTGTATTACAGCTCAGCTTTTGTCTTTT	1482
Db	1384	ctcatctatccctcaaacccccagcccaagaagtgttatacagctcagcttttgccttt	1443
QY	1483	CTGAGGAGAAACAAATTAAGCCAT-TAAGGAAAGATTATGTGGAATTAAGATGGCT	1541
Db	1444	ctgagagaaacaanaataagaccaataaaggaaagatltcaatgtgaaataataaagtgct	1503
QY	1542	GACTTTCCTCTTCCTTCAGACTCTGTTTTCAGATTCAATTCAGTGCCTGATCTTGATGAGAG	1601
Db	1504	gacttgcctcttcttgaaactcgtgttcaagtttcaatccaagtgcgtgaacttgatgaag	1563
QY	1602	ACACTTCTAATGAAGTCAAAATTTGATACATATGTGAATATGAGCTCAAGTTTCTTGCA	1661
Db	1564	acaacttctaataatgaagcaaatgtgatacataatgaaatgaaatgagctcagtttcttgc	1623
QY	1662	GATCAAAATTTACAGTGTCTTCTGTATACTGTGGAGGTACACTTTATATGAAGATTCAA	1721
Db	1624	gatacaaatccaagctgcgtcttcgtatactgtggaagtaacactctataagaagaagttcaa	1683

Oy	1722	AAGTCTACGCTCTCCTTTTCATTCTCAACTCAGTGAAAGTAGTAATGGGGTCCGTGCACAGTTGA	1781
Dd	1684	aagttctacgctctccttcttcttaactccagtgaaatgaatgggtgcctgcctcaagtcca	1743
Oy	1782	AAGAATCTCATTTTCACATGTAAGCGTCGCGCTCGTAATAATTGGACATGCCATATTAACTGG	1841
Dd	1744	aagaatctcatcttcagacgttagcctcgccgcgtcgtaatttgagaccatacttaacctga	1803
Oy	1842	CTTCAGGGCCCTCCACACCCTTTCTTCAGCCACACTCTCTTTTCAAGTTGGCTGACTTCCACACC	1901
Dd	1804	cctca-gcctcccacaactctctcaagcacactctcttcttcagttgctgacttccaacac	1862
Oy	1902	TAGCATCTCATGAGTGGCCAAAGCAAAGAGAGAGAGAAAATAGCCTGCGCGGTTTTTT	1961
Dd	1863	tagcatctcatgagtgccaaagcaaaagagagagaaaatagaccctgcgtgttltl	1922
Oy	1962	AGTTGGGGGGTTTTGGCGTTTCCTTTTATGAGACCCATCCATTTCTTATATGTCAAATGT	2021
Dd	1923	agttgggggggtttggcgttcttcccttaabagaccatctccatctctaagtcacatcgt	1982
Oy	2022	TTCTTTTATCACGATATTATTATTAGTAAGAAAACAATCACTGAATAATGCTAGCTGCAAGTGACA	2081
Dd	1983	tctcttatccgatatattatgtaaagaanaacacacactgaabaatgtacgtcgcaagtcgaca	2042
Oy	2082	TCCTCTTGATGTCATATGAGGAAGTTAAAAACAGTGGAGAAATTCCTTGATTCCACAATGA	2141
Dd	2043	tctcttgatgatcataagaaagattaacaacagtcgagagaatctccttgattccaatga	2102
Oy	2142	AATGCTCTTCCTTTCCCTGGCCCCGACAGACTTTTATCC-ACCTACTAAGATTCTACATATT	2200
Dd	2103	aatgctcttcccttccccctgcgcccaagaccttlatccgacttaccatgattctacatat	2162
Oy	2201	CTTTAAATTTTCATCTCAAGGCGTCGCCCTCAACCCCAC	2255
Dd	2163	cfttaaatctcatccagcgtccctcccaaccac	2197
RESULT 13			
AAQ21184			
ID	AAQ21184	standard; DNA; 2350 BP.	
XX	XX		
AC	AAQ21184;		
XX	XX		
Df	21-MAY-1992 (first entry)		
XX	XX		
DE	Encodes T lymphocyte-specific Leu8 Antigen major form.		
XX	XX		
KW	Rapid immunoselection cloning technique; cell surface antigen;		
KM	homing receptor; antigen-presenting cells; ss.		
OS	Homo sapiens.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	CDS	50..1207	
FT		/+tag- a	
XX	PN	WO9201049-A.	
XX	PD	23-JAN-1992.	
XX	PF	15-JUL-1990; 90MO-USO4986.	
XX	PR	13-JUL-1990; 90US-0553759.	
PA	(GEHO-) GEN HOSPITAL CORP.		
PI	Seed B, Aruffo A, Amiot M;		
DR	WPl. 1992-056864/07.		
DR	P-PSDB; AAR20815.		
PT	Immu C53 cell surface antigen and DNA encoding it - for		
PT	neuro-cellary and diagnosis of haematopoietic neoplasms, etc.		

XX Example 14; Page 106; 160pp; English.

PS Two cDNA clones encoding Leu8 determinants were isolated from a
CC human T cell library using the rapid immunoselection cloning method
CC (see e.g. AAO21164 for description of method). The shorter insert
CC (see AAO22500) lacks 436 internal residues (i.e. nucleotides 1079 to
CC 1514 of the longer insert). RNA blot hybridisation
CC revealed a major transcript of 2.4kb in peripheral blood
CC mononuclear cells, tonsillar B cells and the Jurkat and HSB-2
CC leukemic T cell lines. A minor transcript of 2.0kb was present in
CC peripheral blood mononuclear cells and the Jurkat and HSB-2
CC leukemic T cell lines. The protein encoded by the larger insert
CC is closely related to the murine Mel-14 homing receptor.

SO Sequence 2350 BP; 679 A; 519 C; 490 G; 662 T; 0 other;

Query Match 94.1%; Score 2126.2; DB 13; Length 2350;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2178; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

QY 44 CCTTTGGCAGAGACCTCGAACCCCTGTGCTAGTCAAGGCTCAATGGGCTGCAGAG 103
DB 4 cctttggcaagacctgagacctctgtgctaagtcaagagctcaatggctgcagaa 63
QY 104 AACTAGAGAGACCAAGCAAGCCATGATATTTCCATGGAAATGTACAGACCCAGAG 163
DB 64 aactagagagagccaaagccatgatatcttcattggaatgtcagagccagag 123
QY 164 GACCTTATGAGACATCTTCAAGTTGTGGGGTGGAGCAATGCTCTGTTGATTTCCTGGC 223
DB 124 gacctaatagaaatctcaagtggtggggtggagcaatgctctgttgatttcttcg 183
QY 224 ACATCATGAGACCTACTGCTGAGCTTACCATTTATCTGAAAAACCCATGAACTGCAGAA 283
DB 184 acatcatgagacctactgctgagcttaccatcttctgaaaaaccatgaactgcgaa 243
QY 284 GGCTAGAAATTTCTGCCGAGACAAATTACACAGATTAGTTGCCATCAAAACAGCGGA 343
DB 244 ggctagaagaattctgcgcgagcaatcaacagattagttgcatacaaaagcgga 303
QY 344 AATTGATTTCTGAGAGACACTCTGCCCTTCAAGCTCTTACTACTGATAGGAATCCG 403
DB 304 aattgattctcggaaagactctgccttcaagtcgtcttactactgtaggaatccg 363
QY 404 GAAGATAGAGAGAAATATGAGCGTGGTGGAGCAACAATCTCTACAGTGAAGAGACAA 463
DB 364 gaagataagagaaataatgacgtgggtggagcaacaatctctcaactgaaagacga 423
QY 464 GAATGGGAGATGATGAGCCCAACAAAGAAAGAAAGAGAGACTGGGTGAGATCTA 523
DB 424 gaactggagatgtgtgagcccaacaagaagaacaaagagactggtgagatctca 483
QY 524 TATCAAGAGAAACAAAGATGACAGCAATGGAAGATGACGCTTCCACAACTAAAGGC 583
DB 484 tatcaagagaaacaagaatgacagcaaatggaatgacgccttcacaaactaaaggc 543
QY 584 ACCCGCTGTGTACAGAGCTTCTTGGCAGCCCTGTCATGCAATGGCGCATGGAGATGTGT 643
DB 544 acccgctgtgtacagagcttcttgcagccctgtcatcagtggtgcattggaatgtgt 603
QY 644 AGAAATCATTAATATCATCACCTGCACATGATGTGGGGTACTATGGGCCCCAGATGCA 703
DB 604 agaatacatcataatattacactgcaactgtgagtgtgggtactcttggccccagtgca 663
QY 704 GCTTTGATTCAGTGTGAGCTTTGGAGGCCCCAGAGCTGGGTACCATGAGACTGATCTCA 763
DB 664 gtcttgatctcagtggtgagccttggagccccagagctgtgtacatcagtgactgtac 723
QY 764 CCCCCTTGGAAACTTCACATTCAGCTACAGTGTGCTTACAGCTGCTGAAGAGAAACAA 823
DB 724 cttcttggaaacttcacatctcagctacagtggtgcttctcagctgtcttgaaggaacaa 783

QY 824 CTTAACTGGGATTGAAGAAACCACTGTGACCATTTGGAAACTGCTATCTCCAGAAC 883
DB 784 cttaactgggattgaaagaacccaccctgtgaccatttgaactgtcatctccagaaac 843
QY 884 AACCTGCAAGTATTCAGTGTGAGCGCTCTATCAGACACAGATTGGGGATCATGAACTG 943
DB 844 aacctgcaagtattcagtggtgagcgtctcatcagacacagattgggatacagaactg 903
QY 944 TAGCATCCCTGGCCAGCTTACGCTTACCTGTCATGCTTACCTGCTGAGAAAG 1003
DB 904 tagcatccctggccagcttcaagcttcaactctgattgacttcatctgctcagaag 963
QY 1004 AACTGATTAATTTGGGAAAGAAACCAATTTGTGATATATCTGAATCTGCTAAATCC 1063
DB 964 aactgattaatgtggaagaagaacacatcttgatcatctcgaatctggtcacaatcc 1023
QY 1064 TAGTCCATATGTCAAAATTTGACAAAAGTTTCTCAATGATTAAGAGAGGATTTATTA 1123
DB 1024 tagtccaatatgtcaaaatttgacaaaagtttccaatgattaaaggagtgattataa 1083
QY 1124 CCCCCTTCAATTCAGTGTGACATGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
DB 1084 cccccttcaattcagtggtgacatgctatgctatctcctggttggacttatacat 1143
QY 1184 TTGGCGTGGCAGAGAGATTAAAGGCAAGAAATCCAAAGAAATATGATGACCCATA 1243
DB 1144 ttggcgtggcagagagattaaaggcagaagaatccaaagaaatgaaatgaaatgaccata 1203
QY 1244 TTAATGCGCCTTGTGTAAGAAATTTCTGGAATCTTAAATATCATGATGATGATGATG 1303
DB 1204 ttaatgcgcccttgtgtaagaataatcttggaaatcttcaaaatcatatgagatccttaa 1263
QY 1304 TCCCTTCATGAAGACGTTTGTGTGTGTCGACCTCTTACGTCAAAACATGAGTGTG- 1362
DB 1264 tcccttcatagaacglttgtgtgtgtgacccctcctcagctcaaaacatgaatgtgttcc 1323
QY 1363 TTACAGGATCTGGGAGAGATTCTACCGGACCAACAGTCTCTCAAGTTCATTTCCGCC 1422
DB 1324 ttacagatcctcgggaagattcttaccggaacaaagttcctcagcttccatttgcgcc 1383
QY 1423 CTCATTTATCCCTCAACCCCGACGCGACAGGTGTTATACAGCTCAGCTTTTGTCTTT 1482
DB 1384 ctcatattccctcaaccccgacaggtgttataagctcagcttcttcttctt 1443
QY 1483 CTGAGAGAAACAAATTAAGACCAT- AAGGAAAGGATTCAATGGAATATTAAGATGGCT 1541
DB 1444 ctgagagaaacaataaagacataaaggaagatcatcgttggaatataaagatgct 1503
QY 1542 GACTTGTCTTCTTGTGACTCTGTTTCACTTCAATTCAGTGTGCTGACTGATGACAG 1601
DB 1504 gacttgtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1563
QY 1602 ACACCTTCAATTAAGTGAAGTGAATTAATGATGATGATGATGATGATGATGATGATGATG 1661
DB 1564 acaacttcaaatgaagtgcaaatattgataacatgataatgataatgataatgataatgata 1623
QY 1662 GATCAAAATTTACAGTCTGTTCTGATATCTGTGAGGATACACTTTATAGAAAGTTCAA 1721
DB 1624 gatcaaaatltacagctgtcttcttcttcttcttcttcttcttcttcttcttcttctt 1683
QY 1722 AAGTCTAGCTCTCTCTTCTTCTTCACTCAAGTGAATGAGGAGTCTGCTCAAGTTGA 1781
DB 1684 aagctctagctctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1743
QY 1782 AAGAGTCTATTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1841
DB 1744 aagagtctatttgacatgtagctgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1803
QY 1842 CTTAGAGCTCTCCACCTCTTCTTCAAGCCACTCTCTTTTCAAGTTGGTGTGATCCACACC 1901
DB 1804 ctta- gcttcccaacttctcagccaactcttcttcttcttcttcttcttcttcttcttct 1862


```

OY 884 AACCTGCAAGTATTCAGTGTGAGCCTCTATCAGCACAGATTGGGATCATGAACG 943
    |||||
Db 844 aacctgcaagatgattcagtgtagcctctatcagcacagattgggagtcagtacg 903
OY 944 TAGCCATGCCCTGGCAGCTTCAGCTTTACCTCTGCATGTACTTCATCTGTCAGAGG 1003
    |||||
Db 904 tagccatccctggcagcttcagcttacctctgcatagtaacctcctcgcacgaag 963
OY 1004 AACTGATTAATGGGAGAGAAACCAATTTGTGATCATCTGGAATCTGGCAATCC 1063
    |||||
Db 964 aactgattaatgggagaaagaaacatttgtaatactcgtgaatcgtgccaatcc 1023
OY 1064 TAGTCCATATGTCAAAATTTGGCAAAAATTTCTCAATGATTAAGAGGGTATTATAA 1123
    |||||
Db 1024 tagtccaatatgtcaaaaattgcaaaaagttctcaatgataaagagagtgattataa 1083
OY 1124 CCCCCTCTTCATTCAGTGGCAGTCATGGTTACTGCATTCCTCGGGTTGGCATTTATCAT 1183
    |||||
Db 1084 cccctctcatctcagtgagtgcatgttactgtcatctcgtggttgcatlcat 1143
OY 1184 TTGGCTGCGAAGAGATTTAAAAAAGCAAGAAATCCAGAGAAATGATGATCAACCAT 1243
    |||||
Db 1144 ttggtctgcaagagagataaaaaagcaagaataccaaagagatgatacccata 1203
OY 1244 TTTAAATCGCCCTTGTGAAAGAAAATTTGGAATCTTAAATCAATGATCTTTAA 1303
    |||||
Db 1204 ttaaatcgcccttgtagaagaataatcttggaatacctaataatcagatcccttaaa 1263
OY 1304 TCCCTTCATGAAACGTTTGTGTGTGGCAGCTCCTACGTCAAACATGAGAGTGC -TTCC 1362
    |||||
Db 1264 tcccttcatagaacgtttgtgtgtgagccctcctcagccaacatgagtggttcc 1323
OY 1363 TTACAGTGCATCTGGGAGAGATTTCTACCCAGCAAGTTCCTTACACTTTCATTTGGCC 1422
    |||||
Db 1324 ttcaagtgcactcgggagaaattcttacctgacacagttccttcaacttccatcttgc 1383
OY 1423 CTCATTTATCCCTCAACCCCGCCAGCCAGAGTGTATACAGTCTGCTTTTGTCTTT 1482
    |||||
Db 1384 ctcattatccctcaacccccccagccacagtggttatacagctcgtcttctgtctt 1443
OY 1483 CTGAGAGAGAAACAAATAGACCAT -AAGGAAAGATTCATGTGAATATAAGATGCT 1541
    |||||
Db 1444 ctgagagagaaacaataagaacataaaggaagatcatctcgagataataagatgct 1503
OY 1542 GACTTTGCTTTCTTGTGACTCTTGTGTTTCAAGTTCAAGTGTGCTTGTATGACAG 1601
    |||||
Db 1504 gactttgctcttcttgactctgttcaagttcaatcagtgctgtaacttgatgacag 1563
OY 1602 ACAGTCTTAATGAAGTGAATTTGATCATATGATGATATGAGTCAAGTCTTCTTGA 1661
    |||||
Db 1564 acacttctaagaagtgcaaatltgatacatatgataagtaagtaagtaagtaagta 1623
OY 1662 GATCAAAATTTCAAGTGTCTGTATGAGTGTGAGAGTCACTTTATAGAAATTTCAAA 1721
    |||||
Db 1624 gatcaaatctcaagctgtcttctgtatactgtgagagtaacctctataagaagttcaa 1683
OY 1722 AAGTCTACGCTCTCTTCTTTTCTAATCTCAGTGAAGTAAATGGGCTGCTCAATTTGA 1781
    |||||
Db 1684 aagtcacagctctcttcttcttaactcaatcagtgagtaatggggtccgctcaagtg 1743
OY 1782 AAGAGTCTAATTTGCACTGTAGCTCGCGTGTGTAATTTGACATTCCTATTTAACTGG 1841
    |||||
Db 1744 aagagtgctcatttgacgtgtagcctcgctgtaagtgaatgtgacacatctatctaactg 1803
OY 1842 CTTCAGGCTCTCCCACTTCTTCAGCCACCTCTCTTTTCAAGTGTGCTGATTCACAC 1901
    |||||
Db 1804 ctcca-gctcccccactcttcaagccactctcttcttcaagtgctgacttccacacc 1862
OY 1902 TTGCATTCATATGATGTCAGCAAGAAAGAGAGAGAGAAATAGGCTTCGGGCTTTT 1961
    |||||
Db 1863 tagcatctcatgtagtgccaagcaaaagagagagaaatagaccgtcgctgctgttct 1922

```

```

OY 1962 AGTTGGGGGTTTGGCTGCTTCCCTTTATGAGACCCATTCATTTCTTATAGTCAATGT 2021
    |||||
Db 1923 agttggggggtttgctgttcttcttcttcttcttcttcttcttcttcttcttcttctt 1982
OY 2022 TTCTTTTATCAGATATTTATTAGTAAAGAAACATGCTGAATGTAGCTGCAAGTGA 2081
    |||||
Db 1983 ttctttatcagatattttagtaagaaacatacactgaatgaatgctgagtgagaca 2042
OY 2082 TCTCTTGAATGATATGAGAGTAAACAGGTGAGAAATTCCTTGATTCACAAATGA 2141
    |||||
Db 2043 tctctttagatgataatgagagagtaaaaacagtgagaaatctcttgatccaatga 2102
OY 2142 AATGCTCTCTCTTCCCTGCCCGCCAGACTTTTATCC -ACTTACCTGATTTCTACATAT 2200
    |||||
Db 2103 aatgctctcttctccctgccccagaccttctatccgacttaactagatcttcaatatt 2162
OY 2201 CTTTAAATTCATGTCAGGCTCTCCTCAACCCAC 2235
    |||||
Db 2163 cttaaatctcatctcagcctccccaacccac 2197

```

RESULT 15

AAV81217
ID AAV81217 standard; cDNA: 2350 BP.

XX AAV81217;
XX

DT 10-MAY-1999 (first entry)
XX

DE Human Leu8 antigen cDNA.
XX

KW Leu8; cell surface antigen; human; T lymphocyte; cDNA library;
XX

OS Homo sapiens.
XX

XX Key Location/Qualifiers
FH 50.1207
FT CDS /*tag= a
XX

PN US5849898-A.
XX

PD 15-DEC-1998.
XX

PF 07-JUN-1995; 95US-0485447.
XX

XX 01-DEC-1992; 92US-0983647.
PR

PR 25-FEB-1988; 88US-0160416.
PR

PR 13-JUL-1989; 89US-0379076.
PR

PR 23-MAR-1990; 90US-0498809.
PR

PR 13-JUL-1990; 90US-0553759.
PR

PR 07-JUN-1995; 95US-0485447.
XX

XX (GEHO). GEN HOSPITAL CORP.
PA

XX Allen J, Amiot M, Aruffo A, Camerini D, Laufer L;
PI

XX Oquendo C, Seed B, Simmons D, Stamenkovic I, Stengelin S;
PI

XX WPT: 1999-069813/06.
DR

XX P-PSDB: AAW86199.
XX

XX cDNA encoding human CD40 antigen - useful for cloning cDNA encoding
PT cell surface antigens, constructing cDNA libraries, expression
PT vectors for expression in eukaryotic cells or their fragments
XX

XX Example 14; Column 67-70; 79pp; English.
PS

XX This nucleotide sequence comprises human Leu8 cDNA. The cDNA was
CC isolated from a human T lymphocyte cDNA library using a novel
CC method for cloning cDNAs from mammalian expression libraries. The
CC method is based on transient expression of an antigen in eukaryotic
CC cells and physical selection of cells expressing the antigen by
CC adhesion to an antibody-coated substrate. The method is useful for
CC

Sequence 2350 BP; 679 A; 521 C; 489 G; 661 T; 0 other;

4

```
OY 1962 AGTTGGGGGTTTTCGTGTTTCTTTAAGAGACCCATTCCPATTTCTTAAGTCAATGT 2021
    |||
Db 1923 agttggggggttttgcgttttcccttattagagcccatcttcttattatagtaagtcagt 1982
    |||
OY 2022 TTTCTTTATCAGATATTTATTAAGTAAACATCATCTGAATGCTAGCTGCAAGTGACA 2081
    |||
Db 1983 ttctttatcacgatatattagtaagaaacatcactgaatgctagctgcaagtgaca 2042
    |||
OY 2082 TTTCTTTGATGTCATATGAGAGAGTTAAACAGTGGAGAAATTCCTTGATTCACATGA 2141
    |||
Db 2043 tctccttgatgacataagaaagatlaaacaagtgagagaaatcccttgattcacaaatga 2102
    |||
OY 2142 AATGCTTCCTTTCCCTGCCCCCAGAACCTTTATTC-ACCTACCTAGATTCATATTT 2200
    |||
Db 2103 aatgctctcccttccctgccccccagaccttlatccgacttaactaagattctacataat 2162
    |||
OY 2201 CTTTAATTTCAATCAGGCTTCCCTCAACCCGAC 2235
    |||
Db 2163 cttaaatlcatlcaagctccctcaacccac 2197
    |||
```

Search completed: October 13, 2001, 01:44:50
Job time: 6945 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:57:46 ; Search time 80.31 Seconds
(without alignments)
5325.038 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259
Sequence: 1 GAATTCACAGTGTGCTGCTT.....CCGCCACACACTGGATTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, NA: *
1: /cgnl_7/ptodata/1/lna/5A.COMB.seq: *
2: /cgnl_7/ptodata/1/lna/5B.COMB.seq: *
3: /cgnl_7/ptodata/1/lna/6A.COMB.seq: *
4: /cgnl_7/ptodata/1/lna/6B.COMB.seq: *
5: /cgnl_7/ptodata/1/lna/PCURS.COMB.seq: *
6: /cgnl_7/ptodata/1/lna/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2259	100.0	2259	2	US-08-513-278-1 Sequence 1, Appl1
2	2087.6	92.4	2330	1	US-08-481-803-1 Sequence 1, Appl1
3	2087.6	92.4	2330	1	US-08-215-366A-1 Sequence 1, Appl1
4	2087.6	92.4	2330	1	US-08-340-539A-1 Sequence 1, Appl1
5	2087.6	92.4	2330	2	US-08-461-592B-1 Sequence 1, Appl1
6	1469.2	65.0	1829	6	5514582-1 Patent No. 5514582
7	922.2	40.8	1696	1	US-08-340-539A-11 Sequence 11, Appl1
8	922.2	40.8	1696	2	US-08-461-592B-11 Sequence 11, Appl1
9	856.8	37.9	2214	2	US-08-513-278-3 Sequence 3, Appl1
10	856.8	37.9	2214	6	5514582-3 Patent No. 5514582
11	385.2	17.1	531	1	US-08-340-539A-5 Sequence 5, Appl1
12	385.2	17.1	531	2	US-08-461-592B-5 Sequence 5, Appl1
13	310	13.7	1833	2	US-08-365-470-2 Sequence 2, Appl1
14	310	13.7	3834	3	US-09-209-668-18 Sequence 18, Appl1
15	310	13.7	3854	1	US-08-365-470-1 Sequence 1, Appl1
16	310	13.7	3858	2	US-08-344-155C-98 Sequence 98, Appl1
17	310	13.7	3863	6	5217870-1 Patent No. 5217870
18	294.8	13.1	3142	1	US-08-110-158-3 Sequence 3, Appl1
19	294.8	13.1	3144	5	PCW-US91-05059-1 Sequence 1, Appl1
20	240.2	10.6	2989	6	5378464-1 Patent No. 5378464
21	223.4	9.9	1592	2	US-08-252-493C-1 Sequence 1, Appl1
22	223.4	9.9	1592	3	US-09-276-197-1 Sequence 1, Appl1
23	189.4	8.4	451	1	US-08-340-539A-8 Sequence 8, Appl1
24	189.4	8.4	451	2	US-08-461-592B-8 Sequence 8, Appl1
25	183.8	8.1	712	1	US-08-340-539A-7 Sequence 7, Appl1
26	183.8	8.1	712	2	US-08-461-592B-7 Sequence 7, Appl1
27	131.2	5.8	544	1	US-08-340-539A-9 Sequence 9, Appl1

28	131.2	5.8	544	2	US-08-461-592B-9	Sequence 9, Appl1
29	107.2	4.7	832	1	US-08-340-539A-6	Sequence 6, Appl1
30	107.2	4.7	832	2	US-08-461-592B-6	Sequence 6, Appl1
31	96.4	4.3	1192	1	US-08-340-539A-3	Sequence 3, Appl1
32	96.4	4.3	1192	2	US-08-461-592B-3	Sequence 3, Appl1
33	84.2	3.7	363	1	US-08-340-539A-4	Sequence 4, Appl1
34	84.2	3.7	363	2	US-08-461-592B-4	Sequence 4, Appl1
35	57.6	2.5	7218	1	US-08-232-463-14	Sequence 14, Appl1
36	47.4	2.1	7218	1	US-08-232-463-14	Sequence 14, Appl1
37	37	1.6	1430	1	US-08-276-452A-25	Sequence 25, Appl1
38	37	1.6	1430	2	US-08-798-744-25	Sequence 25, Appl1
39	37	1.6	5852	1	US-07-867-106-2	Sequence 2, Appl1
40	35.8	1.6	1179	2	US-08-465-794-4	Sequence 4, Appl1
41	35.8	1.6	1179	3	US-09-049-813-4	Sequence 4, Appl1
42	33.6	1.5	1700	2	US-08-897-340-4	Sequence 4, Appl1
43	33.6	1.5	1700	3	US-09-252-329-4	Sequence 4, Appl1
44	33	1.5	543	4	US-09-117-257-18	Sequence 18, Appl1
45	33	1.5	543	4	US-08-945-476-18	Sequence 18, Appl1

ALIGNMENTS

RESULT 1
US-08-513-278-1
Sequence 1, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNICK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 565D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

[illegible]

```

: RESULT 2
: US-08-481-803-1
: Sequence 1, Application US/08481803
: Patent No. 5679346
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F. and Olivier G. Sperlini
: TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL
: TITLE OF INVENTION: SURFACE PROTEIN
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/481,803
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/215,366
: FILING DATE: 21-MAR-1994
: APPLICATION NUMBER: US 07/720,602
: FILING DATE: 25-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/313,109
: FILING DATE: 21-FEB-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: James F. Haley, Jr.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: CG-101 CON
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 53..1210
: US-08-481-803-1

```

Very Match	92.48;	Score 2087.6;	DB 1;	Length 2330;
At Local Similarity	98.58;	Pred. No. 0;		

Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

OY	44	CCCTTGGCAAGACCGTGACACCCTGTGCTAGTCACAAGGCTCAAATGGGCTGGCAGAG	103
Db	7	CCTTTGGCCAAGACCGTGAAACCCCTGTGTGTAAGTCAABAAGGCTCAAATGGGCTGGCAGAG	66
OY	104	AACTAGAAGAAGGACCAAGCAAAAGCCCATGATATTCTTCATGGAAATGTCAAGGCCACCAGAG	163
Db	67	AAC TAGAAGAAGGACCAAGCAAAAGCCCATGATATTCTTCATGGAAATGTCAAGGCCACCAGAG	126
OY	164	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAATGCTCTGTTGTGATTTCTTGCC	223
Db	127	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAATGCTCTGTTGTGATTTCTTGCC	186
OY	224	ACATCATGGAACCACTACGTCGAGACTTACCATTTATCTGAAAAAACCCATACTGGCAAG	283
Db	187	ACATCATGGAACCACTACGTCGAGACTTACCATTTATCTGAAAAAACCCATACTGGCAAG	246
OY	284	GGCTAGAAAGATTCTGCCGAGACAATTACACAGATTTAGTTGCATACAAAACMAAGCCGA	343
Db	247	GGCTAGAAAGATTCTGCCGAGACAATTACACAGATTTAGTTGCATACAAAACMAAGCCGA	306
OY	344	AATTGAGTATCTGGANAAGACTCTGCCCTTCACTGCTCTCTTACTACTGATAGGAATCCG	403
Db	307	AATTGAGTATCTGGANAAGACTCTGCCCTTCACTGCTCTCTTACTACTGATAGGAATCCG	366
OY	404	GAAGATAGAGAGAAATATGAGACGTGGGTGGGAACCAACAATCTCACAGAAAGCAGA	463
Db	367	GAAGATAGAGAGAAATATGAGACGTGGGTGGGAACCAACAATCTCACAGAAAGCAGA	426
OY	464	GAAC TGGGAGATGCTGAGCCCCAACAPACANAGANCAANGAGACTGCTGGAGATCTA	523
Db	427	GAAC TGGGAGATGCTGAGCCCCAACAPACANAGANCAANGAGACTGCTGGAGATCTA	486
OY	524	TATCAGAGAAACAAAGATGACGAGCAAAATGGAAAGATGAGCGCTGCGCAAACTAAAGC	583
Db	487	TATCAGAGAAACAAAGATGACGAGCAAAATGGAAAGATGAGCGCTGCGCAAACTAAAGC	546
OY	584	AGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGTGCTANTGCACTGGCCATGAGAAATGTGT	643
Db	547	AGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGTGCTANTGCACTGGCCATGAGAAATGTGT	606
OY	644	AGAAATCATTAATATACACACCTGCAAACTGTATGTGGGGTACTATNGGGCCCCACTGTCA	703
Db	607	AGAAATCATTAATATTAATACCTGCAAACTGTATGTGGGGTACTATNGGGCCCCACTGTCA	666
OY	704	GCTTGTATTCAGTGTGAGGCTTTGGAGGGCCCCAGAGCTGGGGTACCATGAGACTGTACTCA	763
Db	667	GTTTGTGATTCAGTGTGAGGCTTTGGAGGGCCCCAGAGCTGGGGTACCATGAGACTGTACTCA	726
OY	764	CCCCTTTGGAAACTTCAGCTTCAAGCTCACAGTGTGCTTCAAGCTGCTGTGAAGGAACAA	823
Db	727	CCCCTTTGGAAACTTCACCTTCAACCTCACAGTGTGCTTCAAGCTGCTGTGAAGGAACAA	786
OY	824	CTTAACGTGGGATTGGAACAAACACACTGTGGACACTTTGGAAACTGTCATCTCCAGAAC	883
Db	787	CTTAACGTGGGATTGGAACAAACACACTGTGACACTTTGGAAACTGTCATCTCCAGAAC	846
OY	884	AACCTGTCAAGTAGTTCAGTGTAGGCTCTATTCAGACCAAGATTTGGGAGATCAGAACTG	943
Db	847	AACCTGTCAAGTAGTTCAGTGTAGGCTCTATTCAGACCAAGATTTGGGAGATCAGAACTG	906
OY	944	TAGCAATCCCTGGCAGCTTCAGCTTACCTGATGATACCTTCATCTGCTGAGAG	1003
Db	907	TAGCAATCCCTGGCAGCTTCAGCTTACCTGATGATACCTTCATCTGCTGAGAG	966
OY	1004	AACGAGATTAAATGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGGTCAAAATCC	1063
Db	967	AACGAGATTAAATGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGGTCAAAATCC	1026
OY	1064	TAGTCCAAATATGTCCAAAAATTTGGACAAAAGTTTCTCAATGATTAAGAGGGGTGATTATA	1123
Db	1027	TAGTCCAAATATGTCCAAAAATTTGGACAAAAGTTTCTCAATGATTAAGAGGGGTGATTATA	1086

Oy	1064 TAGGCCAATATGTCAAAAATTGGACAAAAGTTTCTCAATGATTAAAGCAGCGGTATTATAA 1123
Dd	1027 TAGTCCCATATGTCTAAAAATTGGACAAAAGTTTCTCAATGATTAAAGCAGCGGTATTATAA 1086

QY 1124 CCCCCTCTCAATTCAGTGGAGTCATGCTTCTGCTGGTTGGCATTTATCAT 1183
|||||
Db 1087 CCCCCCTTCATTCAGAGGAGTCATGCTTCTGCTGGTTGGCATTTATCAT 1146
|||||
QY 1184 TTGGCTGGCAGAGATTAATAAAGGAGCAAAATCCAGAGAGTATGAATGACCAT 1243
|||||
Db 1147 TTGGCTGGCAGAGATTAATAAAGGAGCAAAATCCAGAGAGTATGAATGACCAT 1206
|||||
QY 1244 TTAATGCCCCCTGGTGAAGAAATTCCTGATTAATAAATCATGAGATCCCTTAAA 1303
|||||
Db 1207 TTAATGCCCCCTGGTGAAGAAATTCCTGATTAATAAATCATGAGATCCCTTAAA 1266
|||||
QY 1304 TCCCTTCATGAACGTTTGTGTGTGGCAGCTCTTACGTCAACATGAAGTGTG-TTCC 1362
|||||
Db 1267 TCCCTTCATGAACGTTTGTGTGTGGCAGCTCTTACGTCAACATGAAGTGTGTCC 1326
|||||
QY 1363 TTGAGTCATCTGGAGAGATTTCTACCCGACCAACACTTCTTCACTTTCATTTGCCCC 1422
|||||
Db 1327 TTGAGTCATCTGGAGAGATTTCTACCTGACCAACAGTTCTTCACTTTCACCC 1386
|||||
QY 1423 CTCATTTATCCCTCAACCCCGACAGGTTTATACAGCTCAGCTTTTGTCTTTT 1482
|||||
Db 1387 CTCATTTATCCCTCAACCCCGACAGGTTTATACAGCTCAGCTTTTGTCTTTT 1446
|||||
QY 1483 CTGAGGAGAAACAATTAAGACAT-AAGGAGAAAGATTCATGTGGAATTAAGATGGCT 1541
|||||
Db 1447 CTGAGGAGAAACAATTAAGACATTAAGGAGAAAGATTCATGTGGAATTAAGATGGCT 1506
|||||
QY 1542 GACTTTCCTCTTCTGACCTCTGTTTTCATTAAGTCAATGAGTCACTTCTTATGACAG 1601
|||||
Db 1507 GACTTTCCTCTTCTGACCTCTGTTTTCATTAAGTCAATGAGTCACTTCTTATGACAG 1566
|||||
QY 1602 ACACCTTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCA 1661
|||||
Db 1567 ACACCTTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCA 1626
|||||
QY 1662 GATCAAAATTCAGCTGTCTCTCTGTACTGTGAGGATACCTCTTAAGAAAGTTTCAA 1721
|||||
Db 1627 GATCAAAATTCAGCTGTCTCTCTGTACTGTGAGGATACCTCTTAAGAAAGTTTCAA 1680
|||||
QY 1722 AAGTCTACGCT 1781
|||||
Db 1681 AAGTCTACGCT 1740
|||||
QY 1782 AAGAGTCTAATTTGACACTGTAGCCCTGCGCTGTGAATTTGACACTTCTAATTTAAGTGG 1841
|||||
Db 1741 AAGAGTCTAATTTGACACTGTAGCCCTGCGCTGTGAATTTGACACTTCTAATTTAAGTGG 1800
|||||
QY 1842 CTTGAGGCTCCCGACCTCTTTCAGCACCTCTTTTTCAGTTGGCTGACTTCCACACC 1901
|||||
Db 1801 CTTGCA-GCCTCCCGACCTCTTTCAGCACCTCTTTTTCAGTTGGCTGACTTCCACACC 1859
|||||
QY 1902 TAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1961
|||||
Db 1860 TAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1919
|||||
QY 1962 AGTTTGGGGGTTTGTCTGTTCTTTTATGAGACCATCTTATTTCTAATGATCAATGT 2021
|||||
Db 1920 AGTTTGGGGGTTTGTCTGTTCTTTTATGAGACCATCTTATTTCTAATGATCAATGT 1979
|||||
QY 2022 TTCTTTTATCAGATATTTATTTATGAGAAACATCATGAAATGCTAGCTGCAAGTACA 2081
|||||
Db 1980 TTCTTTTATCAGATATTTATTTATGAGAAACATCATGAAATGCTAGCTGCAAGTACA 2039
|||||
QY 2082 TCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2141
|||||
Db 2040 TCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099
|||||
QY 2142 AATGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2201
|||||
Db 2100 AATGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2159
|||||
QY 2202 TTTAAATTTTCATCTCAGGCTCTCCCTCAACCCAC 2235
|||||

Db 2160 TTTAAATTTTCATCTCAGGCTCTCCCTCAACCCAC 2193
|||||
RESULT 3
US-08-215-366A-1
; Sequence 1, Application US/08215366A
; Patent No. 576775
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F. and Olivier G. Sperlnt
; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCTYE-ASSOCIATED
; NUMBER OF INVENTIONS: 1
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITE & CASE
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215.366A
; FILING DATE: 21-MAR-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/720,602
; FILING DATE: 25-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Neils T. Lippert
; REGISTRATION NUMBER: 25,888
; REFERENCE/DOCKET NUMBER: 1110684-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8582
; TELEFAX: (212) 354-8113
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 53..1210
; US-08-215-366A-1
Query Match 92.48; Score 2087.6; DB 1; Length 2330;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;
QY 44 CCGTTGGCAGAGACCTGAGACCCCTGTGCTAAGTCAAGAGCTCATGAGGCTGACGAAG 103
|||||
Db 7 CCGTTGGCAGAGACCTGAGACCCCTGTGCTAAGTCAAGAGCTCATGAGGCTGACGAAG 66
|||||
QY 104 AACTAGAGAGAGCAGCAAGCAAGCATATTTCCATGAAATGTCAGACACCCAGAG 163
|||||
Db 67 AACTAGAGAGAGCAGCAAGCAAGCATATTTCCATGAAATGTCAGACACCCAGAG 126
|||||
QY 164 GGAATTATGGAACATCTTCAAGTTGTGGGGGTGAGACAATGCTGTGTGATTTCTGTGC 223
|||||
Db 127 GGAATTATGGAACATCTTCAAGTTGTGGGGGTGAGACAATGCTGTGTGATTTCTGTGC 186
|||||

TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,539A
FILING DATE: 16-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-104 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 53..1207
US-08-340-539A-1

Query Match 92.4%; Score 2087.6; DB 1; Length 2330;
Best Local Similarity 98.5%; Pted. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

QY 44 CCCTTGGCAAGGACCTGAGACCCCTTGTGCTAGTCAAGAGGCTCAATGGGCTGCAGAG 103
|||
Db 7 CCTTGGGCAAGGACCTGAGACCCCTTGTGCTAGTCAAGAGGCTCAATGGGCTGCAGAG 66

QY 104 AACTAGGAAGGACCAAGCAAGCCATGATATTTCATGGAATGTCAAGACACCCAGAG 163
|||
Db 67 AACTAGGAAGGACCAAGCAAGCCATGATATTTCATGGAATGTCAAGACACCCAGAG 126

QY 164 GCATTATGGAACATCTCAAGTTGTGGGGGGGAGCAATGCTCTGTGATTTCTGCGC 223
|||
Db 127 GGCTTATGGAACATCTCAAGTTGTGGGGGGGAGCAATGCTCTGTGATTTCTGCGC 186

QY 224 ACATCATGGAACCTACTGCTGACATTCATTAATCTGAAAAACCATCAATCTGGCAAG 283
|||
Db 187 ACATCATGGAACCGACTGCTGACATTCATTAATCTGAAAAACCATCAATCTGGCAAG 246

QY 284 GGCTAGAAATTTCTGCCGAGACAATTACAGAGATTAGTTGCCATPACAAAGCGGA 343
|||
Db 247 GGCTAGAAATTTCTGCCGAGACAATTACAGAGATTAGTTGCCATPACAAAGCGGA 306

QY 344 AATTGATATCTGGAAGACATCTGCCCCCTTCAAGTCTTACTACTGATGGAATCGC 403
|||
Db 307 AATTGATATCTGGAAGACATCTGCCCCCTTCAAGTCTTACTACTGATGGAATCGC 366

QY 404 GAGATAGAGAGATATGAGCGTGGGTGGGAGCAACAATCTCTCACTGAAGAAGCAGA 463
|||
Db 367 GAGATAGAGAGATATGAGCGTGGGTGGGAGCAACAATCTCTCACTGAAGAAGCAGA 426

QY 464 GAACGGGAGATGTGAGCCCAACACAGAGAACAGAGAGACTGCTGAGATCTA 523
|||
Db 427 GAACGGGAGATGTGAGCCCAACACAGAGAACAGAGAGACTGCTGAGATCTA 486

QY 524 TATCAAGAGAAACAAAGATGACAGCAAAATGAGACGACCTGGCACAATAAGGC 583
|||
Db 487 TATCAAGAGAAACAAAGATGACAGCAAAATGAGACGACCTGGCACAATAAGGC 546

QY 584 AGCCCTGTGTACACAGCTTCTTGCCAGCCCTGCTCATGCACTGAGGCAATGTGT 643
|||
Db 547 AGCCCTGTGTACACAGCTTCTTGCCAGCCCTGCTCATGCACTGAGGCAATGTGT 606

QY 644 AGAATCATCAATATACACACCTGCACTGTATGAGGGGTACTATGGCCCCCACTGCA 703
|||
Db 607 AGAATCATCAATATATACACCTGCACTGTATGAGGGGTACTATGGCCCCCACTGCA 666

QY 704 GCTTGTATTCAGTGTGAGCCTTTGGAGGCCCCAGAGCTGGGTACATAGACTGTACTCA 763
|||
Db 667 GTTGTATTCAGTGTGAGCCTTTGGAGGCCCCAGAGCTGGGTACATAGACTGTACTCA 726

QY 764 CCCCTTGGAACTTACGCTTACGCTCACAGTGTGCTTACGCTCTCGAAGAACAA 823
|||
Db 727 CCCCTTGGAACTTACGCTTACGCTCACAGTGTGCTTACGCTCTCGAAGAACAA 786

QY 824 CTTAACGTGGATTAAGAAACACCGTGGACCATTTTGGAACTGTATCTCCAGAAC 883
|||
Db 787 CTTAACGTGGATTAAGAAACACCGTGGACCATTTTGGAACTGTATCTCCAGAAC 846

QY 884 AACCTGTCAAGTATTCAGTGTGAGCCTCTATACAGCACCAGATTGGGGATCATGAATG 943
|||
Db 847 AACCTGTCAAGTATTCAGTGTGAGCCTCTATACAGCACCAGATTGGGGATCATGAATG 906

QY 944 TAGCCATCCCTGGCCAGCTTACGCTTACCTGTGCAATGACCTTCACTCTCAGAAAG 1003
|||
Db 907 TAGCCATCCCTGGCCAGCTTACGCTTACCTGTGCAATGACCTTCACTCTCAGAAAG 966

QY 1004 AACTGAGTTAATTGGGAAGAAACCATTTGGAATCATCTGGAATCTGCTAAATCC 1063
|||
Db 967 AACTGAGTTAATTGGGAAGAAACCATTTGGAATCATCTGGAATCTGCTAAATCC 1026

QY 1064 TAGTCCATATGTCTCAAAAATTGGACAAAAGTTCTCAATGATTAAGAGGATTAATA 1123
|||
Db 1027 TAGTCCATATGTCTCAAAAATTGGACAAAAGTTCTCAATGATTAAGAGGATTAATA 1086

QY 1124 CCCCCTTCAATTCAGAGGCAATGATGATGATGATGATGATGATGATGATGATGAT 1183
|||
Db 1087 CCCCCTTCAATTCAGAGGCAATGATGATGATGATGATGATGATGATGATGATGAT 1146

QY 1184 TTGCTGGCAAGGAGATTAAGAAAGGCAAGAAATCCAAAGAGATTAAGATGCCATA 1243
|||
Db 1147 TTGCTGGCAAGGAGATTAAGAAAGGCAAGAAATCCAAAGAGATTAAGATGCCATA 1206

QY 1244 TTAATGCCCCCTTGGTGAAGAAAATTTTGGAAATCTAAATCATGAGATCCTTTAA 1303
|||
Db 1207 TTAATGCCCCCTTGGTGAAGAAAATTTTGGAAATCTAAATCATGAGATCCTTTAA 1266

QY 1304 TCTTCCATGAAGAGTTTGTGTGGTGGCACTCTACGTCAAAACATGAGAGTGTG -TTCC 1362
|||
Db 1267 TCTTCCATGAAGAGTTTGTGTGGTGGCACTCTACGTCAAAACATGAGAGTGTGTTCC 1326

QY 1363 TTCAAGTGCATGGAAGATTTCTACCCGACCAAGATGCTTCACTGATTCATTTGGCC 1422
|||
Db 1327 TTCAAGTGCATGGAAGATTTCTACCCGACCAAGATGCTTCACTGATTCATTTGGCC 1386

QY 1423 CTCAATTAATCCCTAACCCCCAGCCACAGGTGTTATACAGCTCAGCTTTTGTCTTT 1482
|||
Db 1387 CTCAATTAATCCCTAACCCCCAGCCACAGGTGTTATACAGCTCAGCTTTTGTCTTT 1446

QY 1483 CTGAGGAGAAACAAATAAGACCAT -AAGGGAAGAGTTCAATGGAATTAAGAGGCT 1541
|||
Db 1447 CTGAGGAGAAACAAATAAGACCATTAAGGGAAGAGATTCATGAGGATTAAGAGGCT 1506

QY 1542 GACTTGTCTCTTCTTCACTCTGTTTCAATTCAGTTCAATTCAGTGTACTGATGACAG 1601
|||

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

DB	Query Match	Best Local Similarity	Matches 2161, Conservative	92.44; 98.53; 0;	Score 2087.6; Pred. No. 0;	DB 2;	Length 2330;
0Y	44	CCCTTGGCAAGAGACCTGAGACCCCTGTGCTAAGTCGAAGAGCCGCAATGGCTGCGACAGAG	103				
Db	7	CTTGTGGGCAAGAGACCTGAGACCCCTGTGCTAAGTCGAAGAGCCGCAATGGCTGCGACAGAG	66				
0Y	104	AAC7AGAAGAGACCAACCAAGCCATGATATTTCCATGGAATGTCAGAGACACCCAGAG	163				
Db	67	AAC7AGAAGAGACCAACCAAGCCATGATATTTCCATGGAATGTCAGAGACACCCAGAG	126				
0Y	164	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGACAAATGCTGTGTTGATTTCTGCGC	223				
Db	127	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGACAAATGCTGTGTTGATTTCTGCGC	188				
0Y	224	ACATATATGGAACCTTACTCTGTGACTTACCATTTATTCGAAAAACCCATGAACTGGCAAG	283				
Db	187	ACATATATGGAACCTTACTCTGTGACTTACCATTTATTCGAAAAACCCATGAACTGGCAAG	246				
0Y	284	GGCTGGAAGATTCTGCGGAGACATTTACAGATTTTGGTCCATACAAAAACAAGCGGGA	343				
Db	247	GGCTGGAAGATTCTGCGGAGACATTTACAGATTTTGGTCCATACAAAAACAAGCGGGA	306				
0Y	344	AATTGAGTATCTGGAAGAGACTTGCCCTTCAGTCGTTCTTACTACTGATAGGAATCCG	403				
Db	307	AATTGAGTATCTGGAAGAGACTTGCCCTTCAGTCGTTCTTACTACTGATAGGAATCCG	366				
0Y	404	GAGATAGAGAGATATGAGCGTGGGTGGGAACCAACAATCTCTCACTGAGAGACAGA	463				
Db	367	GAGATAGAGAGATATGAGCGTGGGTGGGAACCAACAATCTCTCACTGAGAGACAGA	426				
0Y	464	GAACTGGGGAATGTGTGAGGCCCAACACAAACAAAGAGAGACCTGGCGGAGATCTA	523				
Db	427	GAACTGGGGAATGTGTGAGGCCCAACACAAACAAAGAGAGACCTGGCGGAGATCTA	486				
0Y	524	TATCAAGAGAAACAAGATGACAGCAAAATGGAAGATGAGCCCTGCACAAACTAAAGGC	583				
Db	487	TATCAAGAGAAACAAGATGACAGCAAAATGGAAGATGAGCCCTGCACAAACTAAAGGC	546				
0Y	584	AGCCCTCTGTACACAGCTTCTTGCCACAGCCCTGTGTCATGCAATGCGCATGAGAAATGTGT	643				
Db	547	AGCCCTCTGTACACAGCTTCTTGCCACAGCCCTGTGTCATGCAATGCGCATGAGAAATGTGT	606				

OY	1201	TAAGAAAGGCAAGAAATCCAGAGAAGATGATGCCATATTAAATGGCCTTGCTG	1260
OY	1131	tggcagcattcgttactcgtcaattccctcgggattgagcaattcaattcggctggaaggaat	1130
OY	1141	TTGGAGATCATGGTTTACATGACATTCCTCTGGGGTGGCAATTTATCATTTGGCTGGCAAGAGAT	1200
OY	1071	aattggaacaaagatcttccatgaattgaaggagtgatataaacccctctcattccag	1130
OY	1081	AATTGGACAAAAGTTTCTCAATATTAAGGAGGGTATTTATAACCCCTCTTCATTTCCAG	1140
OY	1011	agaagaacaacatttggaaatcatctggaatcatctggaatctggtcaaatctctgacataatgtaaa	1070
OY	1021	AGAAGAAACCATTTTGTGAATCATCTGGAATCTGTCAATCTGATGCCAATATGTCAA	1080
OY	991	AGTGTGAGCCTTATATGACACAGATTTGGGATCATATGAACGTGTAGCCATGCCCTGGCA	960
OY	891	agttgagcctctatacagcaccagatcttgggatactgaactgtagcattcccttggca	950
OY	961	GCTTCACCTTACCTCTGCATGTATACCTTCATCTGATCGCAACAAGACTGATTAATTGGA	1020
OY	951	gcttcagccttaacctctgcatgtaacctcaatctgctcgaagaagacbtgaattatggga	1010
OY	841	AAACCACTGTGACCAATTTGGAACGTGTATCTTCAGAACCAACTGTCAATGATTC	900
OY	841	aaacacactgtgacaaatttgaaactgttcaatctccagaaacaaacctc-----	890
OY	721	AGCCTTGGAGGGCCCGAGACTGGGTATGCATGACATGATCTCAACCCCTTGGAAACTTCA	780
OY	721	agccttggagggcccgagcttgggtatgcattgacatgtaactaccctcttgaaacttca	780
OY	781	GCTTCACCTACAGTGTGCTTACGCTTACGCTGCTGTAAGACAACAATTAAGTGGATTGAG	840
OY	781	gcttcagcctcaacgtgtgcttcaagctgtctcgaagaacaacttaactggtatggag	840
OY	661	ACACCTGCACACTGTGATGTGGGTACTATGAGGCCCACTGTCACTGTGTATCAGTGTG	720
OY	661	acaacttgcactgtgatgtgtgtgttaactatggcccagtgtaactgtgatcagttg	720
OY	601	AGCCTTGGAGGGCCCGAGACTGGGTATGCATGACATGATCTCAACCCCTTGGAAACTTCA	780
OY	601	agccttggagggcccgagcttgggtatgcattgacatgtaactaccctcttgaaacttca	780
OY	601	CTTCTTGCCAGCCCTGTGTCATGCAGTGGCCATGAGCAATGTATCAAAATTCATCAATATC	660
OY	601	ctctctgcagcccttgttcaatgagcattgaggaatgtgtgaaataatcaataatc	660
OY	541	ATGCAGCAAAATGGAAAGATGAGACGCTGCGCACAAATTAAGGACAGCCCTGTTTCAAG	600
OY	541	atgcagcgaatggaaagatgagacgctgcgcacaacaacuaaggagccctctgttacaag	600
OY	481	AGCCCAACACAGAAATAACAAGAGAGACTGCTGGAGTCTATATCAAGAGAAACAAG	540
OY	481	agcccaacaacaagaagaacaagaagactcgttggagaacctatacgaagaaacaag	540
OY	421	GGACGTGGGTGGGAACCAACAAATCTCTCACTGAAGAACAGAGAATGGGAGATGGTG	480
OY	421	ggacgtgggtgggaacccaacaaatctctcaatgaagaacagagaacttgggaagtgtg	480
OY	361	AGACTCTGCCCTTACGATGTTTCTTACTACTGATAGGAATCCGGAAGATAGAGAGAAAT	420
OY	361	agactctgccccttaagtcglttctactactggaatggaaatccggaagataggagaatat	420
OY	301	gagacaatcacaagatattagtttgcaataaacaagaacggaatatagtatctcggaga	360
OY	301	GAGCAATTTACACAGATTTAGTTGGCATATCAAAACAAGCGGCAATTTAGTATCTGAGA	360
OY	241	GCTGGACTTACCATTTATTTGAAAAAACCCATGAACCTGGCAAAAGGCTAGAGATTTCTGC	300
OY	241	gctggacttaccattatctcgaaaaacccaatgacctgcgaagaagctagaagaattctgc	300
OY	181	TCAAGTTGTGGGGGTGACAAATGCTGCTGTTGTGATTTCCCTGGCACATCATGAACTACT	240
OY	181	tcaagtgtgggggtgacaaatgctcctgttgttgaatttctctggacatacgaataactact	240
OY	121	gcaaaagcaatattctccatggaaaatgtaagaagcaccagaaggaacttaatggaacactc	180
OY	121	GCAAAAGCATGATTTTTCATTTGGAAATGTCAAGACACCAAGGGGACTTATGAACTACT	180

```

Db 1131 taataaagcgagaataatccaagaagatctgaatgaccataataacgcgcccttgctg 1250
Qy 1261 AAGAGAAATTTCTTGAAATTAATAAATCATGAGATCTTTAAATCTTCCATGAAGACGT 1320
Db 1251 aagaagaattctctggaatctaata----- 1274
Qy 1331 TTGTGTGTGGACCTCTCTAGTCGAACATGAAGTGTCTTCTTCAGTGCATCTGGGAG 1380
Db 1275 ----- 1274
Qy 1381 ATTTCTACCGACCAAGATTCCCTTCAGCTTCATTTGCGCCCTCATTTATCCCTCAAC 1440
Db 1275 ----- 1274
Qy 1441 CCCAGCCACAGTGTATTATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAAATTA 1500
Db 1275 -----agtggtataaagcctcagctcttctgctcttcgagagaaacaataa 1324
Qy 1501 GACCATTAAGGAAAGATTCATGTCGAATTAAGAATGCGCTGACTTGTCTTTCTTGAC 1560
Db 1325 gaccataaggaagaagatcatctgagataataagaatgcctgacttgctctctctgac 1384
Qy 1561 TCTGTATTTCAGTTTCAATTCACTGAGTGTACTTGATGACAGACACTTCTTAATGAAGGC 1620
Db 1385 tctgttttcaagttcaattcaatcagctgctgactctgagaaagacactctaaatgaagtc 1444
Qy 1621 AAATTTGATACATATATGGAATATGAGACTGATTTTCTTGCATCATCAAAATTTACGTCGC 1680
Db 1445 aaattgatatacatctggaatataagagactcagcttctctcgagatacaaatctcaagtc 1504
Qy 1681 TTCTGTATCTGTGAGGATCACTCTTATTAAGAAAGTTCAAAAAGTCTACGCTCTCTTC 1740
Db 1505 tctctgatactgtgagagctacactctctataagaagttcaaaaagctctacgctctcttc 1564
Qy 1741 TTTCTACTCGACGTAAGTAATGAGGCTCTGCTCAAGTTGAAGAGTCTATTTGCACTG 1800
Db 1565 ttcttaactccaagtgaagtaatgaggtcctgctcaagttgaaagagtcctatttgctg 1624
Qy 1801 TAGCGTCGCGCTGTGAATTTGAGACCATCCATTATTAAGTGGCTTC 1846
Db 1625 tagctgcgcgtcgtgtaattgagacatcctatttaactgcttca 1670

RESULT 7
US-08-340-539A-11
: Sequence 11, Application US/08340539A
: Patent No. 5808025
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F.
: APPLICANT: Kansas, Geoffrey S.
: TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
: TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/340,539A
: FILING DATE: 16-NOV-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/008,459
: FILING DATE: 25-JAN-1993

```

ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-104 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-340-539A-11

Query Match 40.8%; Score 922.2; DB 1; Length 1696;
Best Local Similarity 97.8%; Pred. No. 3.2e-261;
Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;

1227 AGTATGATGACCATATTAATGCGCCCTGGTGAAGAAATTTGGATATACTAAAA 1286
1287 TCATGAGATCCTTTAAATCCTTCATGAACGTTTGTGTGGACCTCTAGCTCAA 1346
368 TCATGAGATCCTTTAAATCCTTCATGAACGTTTGTGTGGACCTCTAGCTCAA 427
1347 ACATGAGATG-TCCTTATGAGCATCTGGAGAAATTTTACCCGACCAAGTCTT 1405
428 ACATGAGATGTTCTTCTTATGAGCATCTGGAGAAATTTTACCCGACCAAGTCTT 487
1406 CAGCTTCATTTGCGCCCTCATTTATCCCTCAACCCCGACGAGTGTATACAG 1465
488 CAGCTTCATTTGCGCCCTCATTTATCCCTCAACCCCGACGAGTGTATACAG 547
1466 TCAGCTTTTGTCTTTTGGAGAGAAACAATTAAGACAT -AAGGAAAGATTCATGT 1524
548 TCAGCTTTTGTCTTTTGGAGAGAAACAATTAAGACATTAAGGAAAGATTCATGT 607
1525 GGAATATTAAGATGCTGCTGCTTTGCTTTGACTCTTTTGAAGTTCATTAATCAGT 1584
608 GGAATATTAAGATGCTGCTGCTTTGCTTTGACTCTTTTGAAGTTCATTAATCAGT 667
1585 GCTGATCTTGATGACAGACACTTCTAAATGAAGTGAATTTGATCATATGTGAATATG 1644
668 GCTGATCTTGATGACAGACACTTCTAAATGAAGTGAATTTGATCATATGTGAATATG 727
1645 GACTGATTTCTTGAGATCAAAATTTGCTGCTGCTTTGACTCTTTTGAAGTTCATTAATCAGT 1704
728 GACTGATTTCTTGAGATCAAAATTTGCTGCTGCTTTGACTCTTTTGAAGTTCATTAATCAGT 786
1705 CTTATAGAAAGTTCAAAAAGTCTAGCTCTCTTTCTTTCTTAAGCCAGTGAAGTAAAGG 1764
787 CT-----ATGAAGTGAAGTCTAGCTCTCTTTCTTTCTTAAGCCAGTGAAGTAAAGG 841
1765 GCTCTGCTCAAGTTGAAGAGTCTTATTTGACTGAGCCCTGCGCTGTGAATTTGA 1824
842 GCTCTGCTCAAGTTGAAGAGTCTTATTTGACTGAGCCCTGCGCTGTGAATTTGA 901
1825 CCATCTTATTAAGTGGCTTACGCGCTCCCACTTTCTTACGCCACCTCTCTTTTTCAGT 1884
902 CCATCTTATTAAGTGGCTTACGCGCTCCCACTTTCTTACGCCACCTCTCTTTTTCAGT 960
1885 TGGCTGACTTCACACATGATCATGATGAGCCAGCAAGAGAGAGAGAGAGAAAT 1944
961 TGGCTGACTTCACACATGATCATGATGAGCCAGCAAGAGAGAGAGAGAGAAAT 1020
1945 AGCTGCGCGGTTTTTATGTTTGGGGGTTTTGCTGTTCTTTTATGAGACCAATTCCTA 2004
1021 AGCTGCGCGGTTTTTATGTTTGGGGGTTTTGCTGTTCTTTTATGAGACCAATTCCTA 1080

2005 TTCTTATAGTCAATGTTCTTTTATACAGATATTTAGTAAGAAACATCAGTAAAT 2064
1081 TTCTTATAGTCAATGTTCTTTTATACAGATATTTAGTAAGAAACATCAGTAAAT 1140
2065 GCTAGCTGACAGTCAATCTTTGATGATGAGAGTAAACAGTGGAGAAAT 2124
1141 GCTAGCTGACAGTCAATCTTTGATGATGAGAGTAAACAGTGGAGAAAT 1200
2125 TCCTTATTCACAGTAAATGCTCTCTTTCCCTGCGCCCGAGAACTTTTATCCACTTAC 2184
1201 TCCTTATTCACAGTAAATGCTCTCTTTCCCTGCGCCCGAGAACTTTTATCCACTTAC 1260
2185 CTAGATTCACATATTTCTTAATTTACATCAGGCTTCCCTCAACCCAC 2235
1261 CTAGATTCACATATTTCTTAATTTACATCAGGCTTCCCTCAACCCAC 1311

RESULT 8

US-08-461-592B-11
Sequence 11, Application US/08461592B

PATENT NO. 5834425
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,592B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,539
FILING DATE: 16-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CG-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-461-592B-11

Query Match 40.8%; Score 922.2; DB 2; Length 1696;
Best Local Similarity 97.8%; Pred. No. 3.2e-261;
Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;

OY	392	GATGGAAATCCGGAGATAGAGAGATATGACGTGGGTGGGAACCAAAATCTCTCAC	451
Db	369	GATTGGAAATCAGAAAAATTTGGAAAAATGTGGACATAGGGTGGGAAACCAAAATCTCTCAC	428
OY	452	TGAAGAAGCAGAGAACTGGGGAGATGGTAGCCCAACCAACAGAAAGAAAGAGAGACTG	511
Db	429	TAAAGAAGCAGAGAACTGGGGGTCTCTGGGAGCCCAACAAAGATCTCAAGAGAGACTG	488
OY	512	CGTGAATCTATATCTCAAGAAACAAAGATCGACGCAATGGAAGATGACGCTTCGCA	571
Db	489	TGTGGAATCTATATCTCAAGAAAGGAACAGAGACTCTGGAAAAAGAAAGATGACGCTTCGCA	548
OY	572	CAAACTAAAGCGAGCCCTGTGTTACACAGCTCTCTGGACGCGCTGGTCAATGACACTGCCA	631
Db	549	CAAAAGAAAGCGAGCTCTGTCTGTCACAGACCTCTTGCCAGCAGAGGCTTGTCAATGGCGG	608
OY	632	TGGAAGATGTGTAGAAATATCATCAATTAATCACAGCTGCACACTGTGATGTGGGGTACTATAGG	691
Db	609	TGGAGATGTGTGGAACCAATCATCAACATCACAGCTGTGATGTGATTCAGGATTAATAGG	668
OY	692	GCCCCAGTGTCACTGTGATTCACATGTGAGCTTTGGAGGCCCGCAGAGCTGGGTACAT	751
Db	669	GCCCCAGTGTCAATTAATGTGTCTCAATGTGAGCTTTGGAGGCCCGCTGAGTTGGTACAT	728
OY	752	GGACTTACTCACCCCTTTGGAACCTTCAAGCTTCAGCTCAGCTCAGTGTGCTTCAGCTGC	811
Db	729	GGACTTCATCCACCCCTTGGGAACCTTCAAGCTTCAGCTTCACATCCAGTGTGCTTCACAGCTTC	788
OY	812	TGAAGAAACAACTTAACGGGATTTGAAGAACCACTGTGGACATTTTGAACCTGGTC	871
Db	789	TGAGGAAAGAGAGCTACTTTGGGATGCAAGAACCACTGTGGACATTTTGAACCTGGTC	848
OY	872	ATTCAGAACCAACTGTCAAGTATCAAGTTCAGTGTGAGCCCTCTATAGCACCAAGATTGGG	931
Db	849	ATTCAGAGCCAAATCTGCCAAGTGTGTCCAGTGTGAGCCCTTGGAGGCCCTGAGATTGGG	908
OY	932	GATCATGAAGCTGTACCAATGCCCTGGCCAGCTTCAGTTTACTCTGCATGTACTCTCAT	991
Db	909	TACATGAGCTGTCACTCACCCCTTGGAAAACTTCAGCTTCACAGTTCACAGTGTCTTCAA	968
OY	992	CTGCTCAGAAAGATAGTAAATTTGGAAAGAAAGAACCATTTGGATCTATCTGSAAT	1051
Db	969	CTGTTCTGAGGGAAGAGAGTACTTGGAGCTGCAGAAACACAGTGTGAGACTCTGGAA	1028
OY	1052	CTGGCAATCTCTAGTCAATATGTCAAAATTTGACAAAGATTCTCATGATTTAAGA	1111
Db	1029	CTGGTCATCTCCAGAGCCATGTCCCAAGAGACAAACAAAGATTTCTCAAGATCAAGA	1088
OY	1112	GGGTATATTAACCCCTCTTCATTCAGAGGAGATGATGTACTGATCTCTGGSTT	1171
Db	1089	AGGTACATCAACCCCTCTTCATCTCTGTAGCCGTCAATGTGACACCGATTTCTGGGGCT	1148
OY	1172	GGCATTTTCATTTGGCTGCGCAAGAGATTTAAAAAAGCAAGAAATCCAGAGAGATAT	1231
Db	1149	GGCATTTTCATTTGGCTGCGCAAGAGGCGTTAAAAAAGCAAGAAATCTCAAGAAAGAT	1208
OY	1232	GAATACCCATTAATTAATTCGCCCTTGTGTAAGAAAAATTTCTTG-----GAATACATAA	1284
Db	1209	GGATGATCCATACGATTTCACTCTTTGTAAAGAAAGCCATGAAAGTGTAAAGACAAA	1268
OY	1285	AATCATGAGATCTTTAATCTCTTCATGAAAGCTTTTGTGTGTGGACACTCTTACATGTC	1344
Db	1269	CATTGGAAAAATACGTCAAGTCTCTCCCGTAGAGATTTTACAGCGAGGATCTCCACATTT	1328
OY	1345	AAACATGAAGAGTTCCTTCAGTGTGATGTGGAGATTTTCTACCCGACCAAGTTCTCT	1404
Db	1329	AGAGATCATGTTTGTG---TCAACGATCTTGGAAAGATTTTCTATACCAACAGCTCTCT	1386
OY	1405	TCAGCTTCATTTGCCCTCATTTATCTCTCAACCCCCACGACCAAGTGTATTACAG	1464
Db	1387	CTTAATTTTCCCTCTGCTCAATTCATCCATTAACCTATACCATTAATGTGTCTATACAG	1446
OY	1465	CTCAGCTTTTGTCTTTCTGAGAGAAAAACAATTAAGACCTAAGGAAAGATTCATGTT	1524

Db	1447	AGTACTATTATTATCATCTTTTTCGTGTGAGAGAC-----AAGCAAAAGCTTACTGT	1497
Qy	1525	GGAAATATAAATATGGCTGACTTTGCTCTTTCTTGACTTTGTTTTCAGTTCAATTCAGT	1584
Db	1498	AGAAATATAAACAGCGGCTTTTACTCTTCCCAACTCTGTGTTCCCTAGTCAATTCAGC	1557
Qy	1585	GCTGTACTTGATGACACACTCTTAATGAATGAATTTGATACATATGAAATATG	1644
Db	1558	ACAGAGAGTATGCCAACAAC-----AATGAAATATGATCCATGAGTAAATTTGGA	1607
Qy	1645	GATCCAGTTTCTTGACAGAT	1664
Db	1608	AATCTAGACTCTTGCCGAT	1627

RESULT 10
 5514582-3
 Patent No. 5514582
 APPLICANT: CARON, DANIEL J.; LASKY, LAURENCE A.
 TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
 IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 43
 CURRENT APPLICATION NUMBER:
 APPLICATION NUMBER: US/08/185,670
 FILING DATE: 21-JAN-1994
 Prior APPLICATION DATA:
 APPLICATION NUMBER: 986,931
 FILING DATE: 08-DEC-1992
 APPLICATION NUMBER: 808,122
 FILING DATE: 16-DEC-1991
 APPLICATION NUMBER: 440,625
 FILING DATE: 22-NOV-1989
 APPLICATION NUMBER: 315,015
 FILING DATE: 19-FEB-1989
 SEQ ID NO:3
 LENGTH: 2214
 5514582-3

Query Match	37.9%	Score 856.8	DB 6	Length 2214
Best Local Similarity	73.4%	Pred. 6	2e-242	
Matches 1160	Conservative	0	Mismatches 39	Indels 28
			Gaps	
QY	92	GGGCTCAGACAACTAGAGAAAGGACCAAGCAAGCATGATATTTCCATGGAAATGCA	151	
Db	69	ggcctcagagagacttcgacgagagagaccagcaagcagtggttccctggaagatgta	128	
QY	152	GAGCACCCAGAGGAGACTTATGGAACTCTTCAAGTTGGGGGTGGACATGCTGTGTG	211	
Db	129	gggtactactctggggtcggaggaacactctgaagctgtggtctgacactctctgtg	188	
QY	212	TGATTTCTCGGACATCATCGGAACCGTACGTCGAGCTTACCATTTTCGTGAAAAACCAT	271	
Db	189	tgaattccctcatcacaccatggaactccaactggttgacttaaccattcttgcgaagaagccat	248	
QY	272	GAACTGGCAAGGGCTAGAAAGATTCTGCCGAGACAAATTACAGATTTATGTTGCCATACA	331	
Db	249	gaacttgggaanaatctgataagaattcttcgaagaaataatcacagttttagtcgcataca	308	
QY	332	AAACGAGGGGGAATTTGATCTGTSAGAAAGACTGTGCCCTTCACTGTTCTTACTACTG	391	
Db	309	aaacaaagagagaatttgatgattatagagaataacatctgcgaagaagcccttactactg	368	
QY	392	GATTAAGAAATCCGAGAGATAGAGAAATTTGGACGTGGGTGGGAACCAACAATCTCTCAC	451	
Db	369	gatagaatcagaaataattgysaanaatgtgacatgggttggaaaccaaaaactctcac	428	
QY	452	TGAAGAACACAGAAACTGGGGAGATGCTGGACCCAAACAACAAGAAACAAGAGGACTG	511	
Db	429	taaaagaacgaagaactctgggtgctgtgggagcccaaaaacaagaagtcgaagagagactg	488	
QY	512	CGTGAGATCTATATCAAGAAACAAAGATGCGAGCAAGTAATGTGAACGATACAGGCTCTCA	571	

|||||
Db 489 tggggagatcatatcatcaaggaggagacgagactctgggaatatgagacgatgaagcgtctca 548
QY 572 CAAACTAAAGGACGCGCTGTTACACAGCTTCTTGGCAGCGCTGTGATGACAGTGGCCA 631
|||||
Db 549 caaagaaaggagcgtctctgtctacacagcctcttgcagcagggctcttgcaatgagcg 608
QY 632 TGGAGAAATGCTGAGAAATCATCATATATACACCTGCACTGTGATGTGGGTCTATGG 691
|||||
Db 609 tggagaatggtggaaactatcaacaatcacagtcgcatctgtatgacaggtatctacg 668
QY 692 GCGCCAGTGTGACCTTGTGATTCAGTGTGAGCCCTTGGAGCGCCCAAGCGGGGTATACAT 751
|||||
Db 669 gccccagtgccagatagtgtgtccagtgtagcgttggagggcccttgagtggtaccat 728
QY 752 GGACTGTACTCACCCCTTGGAAACTTCAGCTTCAGCTCAGCTCAGTGTGCTTCAGCTGCTC 811
|||||
Db 729 ggaactcatccccccttggaaacttcagctccagctccagtgtagcttcaactgttc 788
QY 812 TGAAGGACAACTTAATCTGAGATTTGAAGAACACCTGTGGACCATTTGGAACTGTGTC 871
|||||
Db 789 tggaggaaagagactacttggagctgcagaaacacagtgtagacatctgaaactgttc 848
QY 872 ATCTCAGAACCAACCTGTCAAGTATTCAGTGTGAGCTCTATACAGCACAGATTGGG 931
|||||
Db 849 atctccagagccaaactgtccaaagtgtccagtgtagccttggagggcccttgagtggtg 908
QY 932 GATCATGAACTGATGACCATCCCTGGCCAGCTTCAGCTTACCTGTGATGATTCATTCAT 991
|||||
Db 909 taccatgtagctacatccccccttggaaacttcagctccagtgtagccttgcagtggttc 968
QY 992 CTGCTCAGAAAGAACGTGATTAATTTGGGAGAAAGAAACCATTTGTGATCATCTGCAAT 1051
|||||
Db 969 ctgtctgaggagagagagctacttggagctgcagaaacacagtgtagcattgagaa 1028
QY 1052 CTGTGCAAACTCTAGTGCATATGTCAAAATTTGACAAAAGTTTTCATGATTAAGA 1111
|||||
Db 1029 ctgtgtcatctccagagcaaatctgcagaaagacaaacagagttctccaagatcaaga 1088
QY 1112 GGGTATTAATACCCCTCTTCATTCAGTGCAGTGCATGATTCATTCCTGTGCTT 1171
|||||
Db 1089 aggtgactaaaccccccttctctctctctctctctctctctctctctctctctctct 1148
QY 1172 GGATTTATTCATTTGGCTGGCAGGAGATTAATAAAGGCAAGAAATCCCAAGAGATAT 1231
|||||
Db 1149 ggcattctcaatttgcctggcagagcggttaaaaaagagaaatctcaaaagaaagat 1208
QY 1232 GAATGACCCATTAATTCGCGCTTGGTGAAGAAATTTCTTG-----GAATACTAAA 1284
|||||
Db 1209 ggaatgacatcaatgacttcccttctgtgaaagaaagccatgaagtgtcaaaagcaaa 1268
QY 1285 AATCATGAGATCTTAAATCTTCAATGAAAGCTTTTGTGGTGGACCTCTCTACGTC 1344
|||||
Db 1269 catgtgaaataatcaatcaagtcctccgtgaaagatttacaacgagcctctccacatc 1328
QY 1345 AAACATGAAGATGCTGCTTCCTTCACTGATCTGGGAAGATTTCACCGACCAAGTTCT 1404
|||||
Db 1329 agagaaatgagctgttgc--tcaacgaatctggaagatcttcatatgcaaaagcctc 1386
QY 1405 TCAGCTTCATTCGCGCCCTCATTTATCCCTCAACCCCGCCACAGGCTTTTATACAG 1464
|||||
Db 1387 cctaattcccctccgtcatcatcatccatcaaccatcccaataatgtgtgtctatacag 1446
QY 1465 CTCAGCTTTTGTCTTTCTGAGGAGAAACAAATAGACCATAGAGGAAGATTCATGT 1524
|||||
Db 1447 agtagaattatcatcatcttctcgtgaggaac-----aagcaaaagtcttactgt 1497
QY 1525 GGAATTAAGAGATGGCTGACTTGGCTTCTTGTGACTCTTGTGCTTCAAGTTCAATTCAGT 1584
|||||
Db 1498 agaatataaagaaagctgtcttactcttctccaaactctgttctccagttcaattcagc 1557
QY 1585 GCGTACTTGTATGACAGACACTTCTAAATGAGTGCANATTTGATACATATGGAATATG 1644
|||||

Db 1558 acagaagctaatgcgaacac-----agtgaataatatgtcatgtgaatttga 1607
QY 1645 GACTCAGTGTCTTGTGACAGAT 1664
|||||
Db 1608 aactcagactctcttgcgcat 1627

RESULT 11
US-08-340-539A-5
; Sequence 5, Application US/08340539A
; Patent No. 5808025
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULANEUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539A
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gunnison, Jane
; REGISTRATION NUMBER: 38,479
; REFERENCE/DOCKET NUMBER: CG-104 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-340-539A-5

Query Match 17.1%; Score 385.2; DB 1; Length 531;
Best Local Similarity 99.2%; Pred. No. 1.2e-103;
Matches 387; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 453 GAAGAACGACGAGAACTGGGAGATGTGAGCCCAACAAGAGACAGAGAGACTGC 512
| | | | |
Db 312 GAAGAACGACGAGAACTGGGAGATGTGAGCCCAACAAGAGAGAGAGACTGC 371
| | | | |
QY 513 GTGAGATCTATATCAAGAGAAAGATGAGCAATGGAACGATGACGCTGCCAC 572
| | | | |
Db 372 GTGAGATCTATATCAAGAGAAAGATGAGCAATGGAACGATGACGCTGCCAC 431
| | | | |
QY 573 AAAGTAAGGACGACCTCTGTTACACAGCT 602
| | | | |
Db 432 AAAGTAAGGACGACCTCTGTTACACAGCT 461
| | | | |

RESULT 12
US-08-461-592B-5
; Sequence 5, Application US/08461592B
; Patent No. 5834425
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurigin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,592B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/340,539
; FILING DATE: 16-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CG-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-461-592B-5

Query Match 17.1% Score 385.2; DB 2; Length 531;
Best Local Similarity 99.2%; Pred No. 1.2e-103;
Matches 387; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 213 GATTTCCTGGACATCANGAAGCACTGACTTACCATTTATTTGAAAAACCCATG 272
| | | | |
Db 72 GATTTCCTGGACATCANGAAGCACTGACTTACCATTTATTTGAAAAACCCATG 131
| | | | |

QY 273 AACTGCAAGAGGCTTAGAGATTCTGCCGAGACAAATTACACATTAGTTGCAATACAA 332
| | | | |
Db 132 AACTGCAAGAGGCTTAGAGATTCTGCCGAGACAAATTACACATTAGTTGCAATACAA 191
| | | | |
QY 333 AACAAAGCGGAAATTTGATCTGAGAGACTCTGCCCTTACAGTGCTTTACTACTG 392
| | | | |
Db 192 AACAAAGCGGAAATTTGATCTGAGAGACTCTGCCCTTACAGTGCTTTACTACTG 251
| | | | |
QY 393 ATAGAAATCCGGAAGATAGAGAAATATGAGCTGGTGGGAACCAAAATCTCTACT 452
| | | | |
Db 252 ATAGAAATCCGGAAGATAGAGAAATATGAGCTGGTGGGAACCAAAATCTCTACT 311
| | | | |
QY 453 GAAGAACGACGAGAACTGGGAGATGTGAGCCCAACAAGAGAGAGAGAGACTGC 512
| | | | |
Db 312 GAAGAACGACGAGAACTGGGAGATGTGAGCCCAACAAGAGAGAGAGAGACTGC 371
| | | | |
QY 513 GTGAGATCTATATCAAGAGAAAGATGAGCAATGGAACGATGACGCTGCCAC 572
| | | | |
Db 372 GTGAGATCTATATCAAGAGAAAGATGAGCAATGGAACGATGACGCTGCCAC 431
| | | | |
QY 573 AAAGTAAGGACGACCTCTGTTACACAGCT 602
| | | | |
Db 432 AAAGTAAGGACGACCTCTGTTACACAGCT 461
| | | | |

RESULT 13
US-08-365-470-2
; Sequence 2, Application US/08365470
; Patent No. 5632991
; GENERAL INFORMATION:
; APPLICANT: Gimbrone, Jr., Michael A.
; TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,470
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,510
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/850,802
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0627.1350003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: nucleic acid
; LOCATION: 1-1833
; OTHER INFORMATION: / label = nucleic acid

```

; OTHER INFORMATION: /note - SEQ ID NO:2 begins at base pair position 117 and ends
; OTHER INFORMATION: base pair position 1949.
US-08-365-470-2

Query Match      13.7%: Score 310; DB 1; Length 1833;
Best Local Similarity 60.6%: Pred. No. 2.9e-81;
Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

OY 242 CTGGACTTACCATTTATCTGAAAAAACCATGAACCTGGCAAAAGGCTAGAAAGATTCTGCCG 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 CTGGCTCTTACAAACACCTCCAGAGACTATGACTTATGATGAGGCCAGTCTTATGTCTCA 122

OY 302 AGCAATTACACAGATTAGTGTCCATACAAAACAGCGGAAATTAGTATCTGGGAA 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 GCAAGGTACACACCTGTGTCAATTCAAAACAAAAGAGATTGAGTACCTAAATCTC 182

OY 362 GACTCTGCCCTTACGTCTTACTACTGATAGAAATCCGGAAGTTAGAGGAATATG 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183 CATATTGAGCTATTTCACCAAGTTATTACTGATTGGATAGAAAAGTCAACATGTGTG 242

OY 422 GAGCTGGGTGGGAACCAAAATCTCTCACTGAGAAGAGAGAACTGGGAGATGGTGA 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 GGTCTGGGTAGAAACCAACCAACCTCTGACAGAAAGAACCAAGACTGGCTCCAGGTGA 302

OY 482 GCCCAACAACAAGAACAGAGAGACTCGTGGAGATTATATCAAGAAACAAGA 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 303 ACCCAACAATAGGCAAAAMATAGAGACTCGTGGAGATTATACATAGAGAAAAAGA 362

OY 542 TGCAGCAAAATGGAGAGATAGCCCTGCCACAACCTAAAGCAGCCCTGTTACACAGC 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 363 TGTGGGCATGTGAATGATGATGAGAGTGCAGAGAAAGAACTGGCTTATGCTACAGC 422

OY 602 TTCTTCCAGCCCTGTGTCATGAGTGGCCATGAGAGATGTGTAAATCATATATCA 661
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 423 TGCCTGACCAATATACCTCTGAGTGGCCACGGTGAATGTGTAGAGCATCATATATTA 482

OY 662 CACTCTGCACTGTGATGTGGGGTACTATGGCCCCAGTGTGATTCATCACTGTGA 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 483 CACTTTCMACTGTGACCCCTGGCTTCACTGATGACTCAAGTGCMAATTTGTGAACCTGTAC 542

OY 722 GCTTTTGAAGCCCCAGAGTGGGTATACATGAGACTGACTACCCCTTGGAAACTTCAG 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 543 AGCCCTGGAATCCCTGAGATGATGAGAGCTGTGTTTGCATGCTACCCACTGGGAAACTTCAG 602

OY 782 CTTCACCTCAGACTGTGCTTCTGAGTGTCTGGAAGAAACAACCTTAACCTGGATGAGA 841
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 603 CTCAATATTCTTCTGCTATATCAGCTGTGATAGGGGTTTACTGGCAAGCAGCATGAGAC 662

OY 842 AACCACTGTGGACATTTTGGAAATGCTATCTCCAGAAACAACCTGTCAAGTGAATCA 901
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 663 CATTGAGTGTATGCTCTGTGAGAAATGAGTGTCTTATTCAGCTGCAGCTCAATGTGTGA 722

OY 902 GTGTGAGCTCTATTCAGACACAGATTTGGGATCATGAACTGAGCCATCCCTGGGCAG 961
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 723 GTGTGATGCTGTACAAATCCACCAATGAGGTGTGTGGAATGTTTCCAAAACCTGTGAAG 782

OY 962 CTTCACCTTACCTCTGATACCTTCTCATCTGCTCTCAGAAAGAACTGATTAATTGGGAA 1021
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 783 CTTCCTCATGSAACAACAACCTGTACATTTGACTGTGAAGAAAGATTTGAACATAATGGAGC 842

OY 1022 GAAGAAACCAATTTGTGATCATCTGGAATCTGTCTCAATCTTAATCTCAATATGTCA 1079
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 843 CCAGAGCCTTCACTGTACCTCATCTGTGGAAATTTGGACAACGAGAAAGCAACGTGTAA 900

RESULT 14
US-09-209-668-18
; Sequence 18, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
```

```

; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 3834
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (117)..(1949)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M24736/Genbank
; DATABASE ENTRY DATE: 1994-11-07
US-09-209-668-18

Query Match      13.7%: Score 310; DB 3; Length 3834;
Best Local Similarity 60.6%: Pred. No. 4.3e-81;
Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

OY 242 CTGGACTTACCATTTATCTGAAAAAACCATGACCTGGCAAAAGGCTTGAAGATTCTGCCG 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 ctggtcttaaacaccctcccgagagctatgactatgactgagctgctatgtca 238

OY 302 AGACAATTACACAGATTAGTGTCCATACAAAACAGCGGAAATTGATGTGAGAA 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 gcaaaagtlacacacactgltgcaaltcaaaacaaagaagatltgagtlaccctaaac 298

OY 362 GACTCTGCCCTTACGTCTTACTACTGATAGAAATCCGGAAGTTAGAGGAATATG 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 cataatgactatcaccaagattactatgatttgaaatcagaagaatcaaaatgtgtg 358

OY 422 GACTGGGTGGGAACCAAAATCTCTCACTGAGAAGAGAGAACTGGGAGATGGTGA 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 gtlctggtlagaacccagaacactctgcagaagaagccaagaactcgtggtccaaagtga 418

OY 482 GCCCAACAACAAGAAACAAGAGAGACTCGTGGAGATTATATCAAGAAACAAGA 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 419 acccaaaatcagaaaagaatgagactgcgtgagatctacatcaagaagaaaaaaga 478

OY 542 TGCAGCAAAATGAGACATGACGCTGCCACAACCTAAAGCAGCCCTGTGTTACACAGC 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 479 tltgtgcatgtlgaatgatagagtlgcagaagaagaagctltgcctatltgcacagac 538

OY 602 TTCTTGCACCCCTGTGTCATGAGTGGCCATGAGAGATGTGTAAATCATCATATATCA 661
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 539 tgcctgtaccaataacatccctgcagtlgcacagtlgtlgaagaccatcaataltca 598

OY 662 CACTCTGCACTGTGATGTGGGGTACTATGGGCCCACTGTCTGATTCAGTGTGA 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 599 caactlgaagtgtgaaacccgtgcttcaagtgaactaaagtgtgagcaaatltgtgaactgtac 658

OY 722 GCTTTTGAAGCCCCAGAGTGGGTATACATGAGACTGTACTACCCCTTGGAAACTTCAG 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 659 agccctlgaatccctlgaatgagacgtgtgttgagtcacccactgtgaaacttcag 718

OY 782 CTTCACCTCAGAGTGTGCTTCTGAGTGTCTGGAAGAAACAACCTTAACCTGGGATGAGA 841
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 719 ctcaaatcttccctgtcctatcagctltgataaggtlactctgcaagcagatgtgagac 778

OY 842 AACCACTGTGGACATTTTGGAAACCTGTATCTCCAGAAACAACCTGTCAAGTGAATCA 901
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 779 calgcagtlgatlgtcctctgtgagaaatgtgtccatcatccagccgtcaatgtgtlga 838

OY 902 GTGTGAGCTCTATTCAGACACAGATTTTGGGATCATGAACTGTAATCCCTGGGCAG 961
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 839 gtlgtatgctgtlgaacaaatccagcgaatgtgtgtgaaatgtltccaaaacctgtgaag 898

OY 962 CTTCACCTTACCTCTGATACCTTCTCATCTGTCTGAGAAAGAACTGAATTAATTGGGAA 1021
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:50:05 ; Search time 3458.26 Seconds
(without alignments)
9652.488 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259
Sequence: 1 GAATTCAGCTGCTGCTGCTT.....CGCCACGACACTGCAATTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA.Maln:*
1: /cgnl_7/ptodata/1/pna/PCTUS_COMB.seq:*
2: /cgnl_7/ptodata/1/pna/US07_COMB.seq:*
3: /cgnl_7/ptodata/1/pna/US07_COMB.seq:*
4: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
5: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
6: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
7: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
8: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
9: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
10: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
11: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
12: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
13: /cgnl_7/ptodata/1/pna/US08_COMB.seq:*
14: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
15: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
16: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
17: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
18: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
19: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
20: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
21: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
22: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
23: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
24: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
25: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
26: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
27: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
28: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
29: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
30: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
31: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
32: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
33: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
34: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
35: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
36: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
37: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
38: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
39: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
40: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
41: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
42: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*
43: /cgnl_7/ptodata/1/pna/US09_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2259	100.0	2259	US-09-119-209-1	Sequence 1, Appl 1
2	2161	95.7	2354	US-09-023-655-1154	Sequence 1154, Ap
3	2151.6	95.2	2385	US-60-243-521-18	Sequence 8, Appl 1
4	2150	95.2	2385	US-60-213-360-1118	Sequence 1118, Ap
5	2150	95.2	2564	US-09-396-970-8480	Sequence 8480, Ap
6	2146.8	95.0	2385	US-09-495-050A-292	Sequence 292, App
7	2146.8	95.0	2385	US-60-118-318-292	Sequence 292, App
8	2129.6	94.3	2387	US-60-172-373-15742	Sequence 15742, A
9	2087.6	92.4	2330	PCT-US92-03970-1	Sequence 1, Appl 1
10	2087.6	92.4	2330	PCT-US94-00909-1	Sequence 1, Appl 1
11	2087.6	92.4	2330	US-08-008-459-1	Sequence 1, Appl 1
12	2087.6	92.4	2330	US-08-340-539-1	Sequence 1, Appl 1
13	2087.6	92.4	2330	US-08-410-569-1	Sequence 1, Appl 1
14	1605.4	71.1	1788	US-60-164-285-5139	Sequence 5139, Ap
15	1605.4	71.1	1788	US-60-164-285-5139	Sequence 5139, Ap
16	1006.4	44.6	3238	US-60-212-659-816	Sequence 816, App
17	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
18	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
19	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
20	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
21	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
22	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
23	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
24	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
25	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
26	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
27	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
28	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
29	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
30	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
31	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
32	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
33	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
34	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
35	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
36	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
37	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
38	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
39	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
40	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
41	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
42	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
43	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
44	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
45	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App

ALIGNMENTS

RESULT 1
US-09-119-209-1

Sequence 1, Application US/09119209
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,209
FILING DATE: 20-Jul-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513278
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 6-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0565D1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-119-209-1

Query Match 100.0%; Score 2259; DB 15; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTTCTCACTGACACAGACACTCCCTTGGCAAGACT 60
DB 1 GAATTCAGTGTGCTTCTCACTGACACAGACACTCCCTTGGCAAGACT 60
QY 61 GAGACCCCTTGCTAGCAAGAGGCTCAATGGGCTGAGAAAGACTGAGAGACCAA 120
DB 61 GAGACCCCTTGCTAGCAAGAGGCTCAATGGGCTGAGAAAGACTGAGAGACCAA 120
QY 121 GCAAGCCATGATATTTCCATGGAATGTCAAGACCAAGGACTTATGGAACATCT 180
DB 121 GCAAGCCATGATATTTCCATGGAATGTCAAGACCAAGGACTTATGGAACATCT 180

DB 121 GCAAGCCATGATATTTCCATGGAATGTCAAGACCAAGGACTTATGGAACATCT 180
QY 181 TCAAGTTGTGGGGGTGACAAATGCTGTGATTTCTGGCAATCATGGAACACTACT 240
DB 181 TCAAGTTGTGGGGGTGACAAATGCTGTGATTTCTGGCAATCATGGAACACTACT 240
QY 241 GCTGACTTACCATTTATTTGAAAAAACCATGAACTGGCAAGGGCTAGAAATTTGCC 300
DB 241 GCTGACTTACCATTTATTTGAAAAAACCATGAACTGGCAAGGGCTAGAAATTTGCC 300
QY 301 GAGCAATTTACAGATTTGTTGCCATCAAAACAAAGGGGAAATGGTATCTGAGAA 360
DB 301 GAGCAATTTACAGATTTGTTGCCATCAAAACAAAGGGGAAATGGTATCTGAGAA 360
QY 361 AGACTGCCCCCTTCACTGCTTCTTACTGATAGAAATCCGAAATGAGAGAAATAT 420
DB 361 AGACTGCCCCCTTCACTGCTTCTTACTGATAGAAATCCGAAATGAGAGAAATAT 420
QY 421 GSAAGTGGGTGGGAAACCAAAATCTCTCACTGAAAGACAGAACTGGGAGATGTG 480
DB 421 GSAAGTGGGTGGGAAACCAAAATCTCTCACTGAAAGACAGAACTGGGAGATGTG 480
QY 481 AGCCCAACAACAAGAAAGAAAGAGAGACTGGTGAGATCTATATCAAGAAACAAG 540
DB 481 AGCCCAACAACAAGAAAGAAAGAGAGACTGGTGAGATCTATATCAAGAAACAAG 540
QY 541 ATGCAAGCAAAATGGAACGATGACGCTGACAAACTAAAGGACCCCTGTTACACAG 600
DB 541 ATGCAAGCAAAATGGAACGATGACGCTGACAAACTAAAGGACCCCTGTTACACAG 600
QY 601 CTTCCTGGCCAGCCCTGGTATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 CTTCCTGGCCAGCCCTGGTATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 ACACCTGCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 ACACCTGCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 AGCCTTGGAGGCCCCAGAGCTGGGTACCATGAGACTGATGATGATGATGATGATG 780
DB 721 AGCCTTGGAGGCCCCAGAGCTGGGTACCATGAGACTGATGATGATGATGATGATG 780
QY 781 GCTTACGCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 GCTTACGCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 AAACCACTGTGACCAATTTGGAACCTGATCTCCAGAACCAACCTGTCAGATGATTC 900
DB 841 AAACCACTGTGACCAATTTGGAACCTGATCTCCAGAACCAACCTGTCAGATGATTC 900
QY 901 AGTGTAGCCTCTATACAGCAGCATTTGGGATGATGAACTGTAGCCATCCCTGGCCA 960
DB 901 AGTGTAGCCTCTATACAGCAGCATTTGGGATGATGAACTGTAGCCATCCCTGGCCA 960
QY 961 GCTTACGCTTACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 GCTTACGCTTACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 AGAAGAAACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 AGAAGAAACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AATTGCAAAAGATTTCTCATGATTTAAGAGGGGTGATTAACCCCTCTTCAATTCGAG 1140
DB 1081 AATTGCAAAAGATTTCTCATGATTTAAGAGGGGTGATTAACCCCTCTTCAATTCGAG 1140
QY 1141 TGGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 TGGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 TAAAAAAGGCAAGAAATCCAAAGAAAGTATGATGATGATGATGATGATGATGATG 1260
DB 1201 TAAAAAAGGCAAGAAATCCAAAGAAAGTATGATGATGATGATGATGATGATGATG 1260

```
QY 1261 AAAGAAATCTTGAATCTATAAATCATGAGATCTTTAAATCCTTCATGAACGTT 1320
DB 1261 AAAGAAATCTTGAATCTATAAATCATGAGATCTTTAAATCCTTCATGAACGTT 1320
QY 1321 TTGTGTGGTGGACCTCCCTGCTCAAAACATGAAGTGTCTTCTTCACTGATCGGGAG 1380
DB 1321 TTGTGTGGTGGACCTCCCTGCTCAAAACATGAAGTGTCTTCTTCACTGATCGGGAG 1380
QY 1381 ATTTCTACCGACCAACAGATTCCTTCAGCTTCATTTGCGCCCTCATTTATCCCTAAC 1440
DB 1381 ATTTCTACCGACCAACAGATTCCTTCAGCTTCATTTGCGCCCTCATTTATCCCTAAC 1440
QY 1441 CCCAGCCCAAGAGTGTATATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAATAA 1500
DB 1441 CCCAGCCCAAGAGTGTATATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAATAA 1500
QY 1501 GACCATTAAGGGAAGATTAATGATGGAATATAAGATGGCTGATGCTCTTCTTCTGAC 1560
DB 1501 GACCATTAAGGGAAGATTAATGATGGAATATAAGATGGCTGATGCTCTTCTTCTGAC 1560
QY 1561 TCTTGTCTTCAATTCAGTGTCTTCACTTGTATGACAGACACTTCTAATGAAGTGC 1620
DB 1561 TCTTGTCTTCAATTCAGTGTCTTCACTTGTATGACAGACACTTCTAATGAAGTGC 1620
QY 1621 AAATTTGATACATATGATGAATATGAGACTGTTTCTGACATCAATTTCACTGCTC 1680
DB 1621 AAATTTGATACATATGATGAATATGAGACTGTTTCTGACATCAATTTCACTGCTC 1680
QY 1681 TTCTGATACATGATGAGTCACTCTTATGAAGTCAAAAGTCAAGCTCTCTTCTTTC 1740
DB 1681 TTCTGATACATGATGAGTCACTCTTATGAAGTCAAAAGTCAAGCTCTCTTCTTTC 1740
QY 1741 TTTCTACTCTCAATGAAGTAAATGGGCTCTGCTCAAGTTGAAAGTCTATTTGCACTG 1800
DB 1741 TTTCTACTCTCAATGAAGTAAATGGGCTCTGCTCAAGTTGAAAGTCTATTTGCACTG 1800
QY 1801 TACCTGCGCGCTGTGATGATGAGCACTCTATTTAACTGGCTTCAAGCTTCCACACTT 1860
DB 1801 TACCTGCGCGCTGTGATGATGAGCACTCTATTTAACTGGCTTCAAGCTTCCACACTT 1860
QY 1861 CTTCAGACACCTCTCTTTTTCAGTGGCTGACTTCCACACCTAGCATCTATGATGCCA 1920
DB 1861 CTTCAGACACCTCTCTTTTTCAGTGGCTGACTTCCACACCTAGCATCTATGATGCCA 1920
QY 1921 AGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
DB 1921 AGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 TTCTCTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
DB 1981 TTCTCTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
QY 2041 TTATGTAAGAAACATCACTGAATGCTAGTGAAGTGAATGCTCTTCTTCTTCTGAT 2100
DB 2041 TTATGTAAGAAACATCACTGAATGCTAGTGAAGTGAATGCTCTTCTTCTTCTGAT 2100
QY 2101 AAGAGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
DB 2101 AAGAGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
QY 2161 CCCCCAGAACTTTTATCACTTACATGATTTCAATATTTCTTAAATTTCACTCAGGC 2220
DB 2161 CCCCCAGAACTTTTATCACTTACATGATTTCAATATTTCTTAAATTTCACTCAGGC 2220
QY 2221 CTCCCTCAACCCACAGGAGGCGGCGAGACACTGGAATTC 2259
DB 2221 CTCCCTCAACCCACAGGAGGCGGCGAGACACTGGAATTC 2259
```

RESULT 2
US-09-023-655-1154
; Sequence 1154, Application US/09023655

```
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1154:
SEQUENCE CHARACTERISTICS:
LENGTH: 2354 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187182
US-09-023-655-1154

Query Match 95.7%; Score 2161; DB 14; Length 2354;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2200; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

QY 25 ACCTGACAGCAGACACCTCCCTTTGGCAAGAGACCTGAGACCTTGTGCTAAGTCAAGAG 84
DB 12 ACCGACAGCAGACACACTCTCTTGGGCAAGAGACCTGAGACCTTGTGCTAAGTCAAGAG 71
QY 85 GCTCAATGGGCTGAGAAAGAACTAGAGAGAGCAACGAAGCAATGATATTTCATGGA 144
DB 72 GCTCAATGGGCTGAGAAAGAACTAGAGAGAGCAACGAAGCAATGATATTTCATGGA 131
QY 145 AATGTACAGACACCAAGAGGACTTATGAACATCTTCAAGTTGTGGGGCTGAGCAATGC 204
DB 132 AATGTACAGACACCAAGAGGACTTATGAACATCTTCAAGTTGTGGGGCTGAGCAATGC 191
QY 205 TCTGTGTGATTTCTGCGACATCATGGAACCTACTGCTGAGCTTACCATTTATTCGAAA 264
DB 192 TCTGTGTGATTTCTGCGACATCATGGAACCGACTGCTGAGCTTACCATTTATTCGAAA 251
QY 265 AACCCATGAAGTGGCAAAAGGCTAGAGATTCGCGAGAACAAATTACAGAGATTAGTTC 324
DB 252 AACCCATGAAGTGGCAAAAGGCTAGAGATTTCTCCGAGAACAAATTACAGAGATTAGTTC 311
QY 325 CCATACAAACAAAGCGGAATTTAGTATCTGGAAGACTCTGCCCTTCAGTGTCTTCTT 384
DB 312 CCATACAAACAAAGCGGAATTTAGTATCTGGAAGACTCTGCCCTTTCAGTGTCTTCTT 371
```

QY 385 ACTACTGATAGGAATCCGGAAGATAGAGGAATATGAGACGTGGGTGGGAACCAAAAT 444
 |||||
 Db 372 ACTACTGATAGGAATCCGGAAGATAGAGGAATATGAGACGTGGGTGGGAACCAAAAT 431
 |||||
 QY 445 CTCACATGAAAGACGAGAACTGGGAGATGCTGAGCCCAACACAGAAAGCAAG 504
 |||||
 Db 432 CTCCTACTGAAAGACGAGAACTGGGAGATGCTGAGCCCAACACAGAAAGCAAG 491
 |||||
 QY 505 AGGACTGCTGAGATCTATATCAAGAAACAAAGATGCGCAATGGAATGGAACATGACG 564
 |||||
 Db 492 AGGACTGCTGAGATCTATATCAAGAAACAAAGATGCGCAATGGAATGGAACATGACG 551
 |||||
 QY 565 CCGGACCAAACTAAAGGACGCCCTCTGTTACACAGCTTTGCGACCCCTGTCATGCA 624
 |||||
 Db 552 CCGGACCAAACTAAAGGACGCCCTCTGTTACACAGCTTTGCGACCCCTGTCATGCA 611
 |||||
 QY 625 GTGGCCATGAGAACTGCTGAGAAATCATCAATATCACACCTGCACTGTGATGAGG 684
 |||||
 Db 612 GTGGCCATGAGAACTGCTGAGAAATCATCAATATCACACCTGCACTGTGATGAGG 671
 |||||
 QY 685 ACTATGGGCCCCAGTGTACCTGTGATGAGTGTGAGCCCTTGGAGGCCCCAGAGCTGG 744
 |||||
 Db 672 ACTATGGGCCCCAGTGTACCTGTGATGAGTGTGAGCCCTTGGAGGCCCCAGAGCTGG 731
 |||||
 QY 745 GTACCATGAGCTGTACTACCCCTTGGAACTTCAGCTTCAGCTCAGCTGTCCTTCA 804
 |||||
 Db 732 GTACCATGAGCTGTACTACCCCTTGGAACTTCAGCTTCAGCTCAGCTGTCCTTCA 791
 |||||
 QY 805 GCTGCTCTGAGGAACAACTTAACTGAGGATTTGAGAAACACCTGTGACCATTTGGA 864
 |||||
 Db 792 GCTGCTCTGAGGAACAACTTAACTGAGGATTTGAGAAACACCTGTGACCATTTGGA 851
 |||||
 QY 865 ACTGTCATCTCCAGAACCACTGTCAAGTGTGATGAGTGTGAGCCCTTTCAGCACCAG 924
 |||||
 Db 852 ACTGTCATCTCCAGAACCACTGTCAAGTGTGATGAGTGTGAGCCCTTTCAGCACCAG 911
 |||||
 QY 925 ATTTGGGGATCATGAACTGTAGCCATCCCTGGCCAGCTTCAGCTTCAGCTTCATGTA 984
 |||||
 Db 912 ATTTGGGGATCATGAACTGTAGCCATCCCTGGCCAGCTTCAGCTTCAGCTTCATGTA 971
 |||||
 QY 985 CCTTCATCTCTCAGAAAGAACTGATTAATTTGGAAAGAAACCATTTTGAATCAT 1044
 |||||
 Db 972 CCTTCATCTCTCAGAAAGAACTGATTAATTTGGAAAGAAACCATTTTGAATCAT 1031
 |||||
 QY 1045 CTGGAATCTGTCAATCTCACTGATCAATATGTCAAAATTTGCAAAAGTTTTCATGA 1104
 |||||
 Db 1032 CTGGAATCTGTCAATCTCACTGATCAATATGTCAAAATTTGCAAAAGTTTTCATGA 1091
 |||||
 QY 1105 TTAAAGAGGGGTATTAACCCCTCTTCATTCAGTGGCAGTCATGTTACTGATTC 1164
 |||||
 Db 1092 TTAAAGAGGGGTATTAACCCCTCTTCATTCAGTGGCAGTCATGTTACTGATTC 1151
 |||||
 QY 1165 CTGGGTTGGCATTTATCATTTTGGCTGGCAAGAGATTAATAAAGCAAGAAATCCACA 1224
 |||||
 Db 1152 CTGGGTTGGCATTTATCATTTTGGCTGGCAAGAGATTAATAAAGCAAGAAATCCACA 1211
 |||||
 QY 1225 GAAGTATGATGATCAATTAATATGAGCCCTTGGTGAAGAAATCTTGAATACTATA 1284
 |||||
 Db 1212 GAAGTATGATGATCAATTAATATGAGCCCTTGGTGAAGAAATCTTGAATACTATA 1271
 |||||
 QY 1285 AATCATGAGATCTTTAAATCTTCCATGAAAGCTTTTGTGTGGTGGACCTTCATGTC 1344
 |||||
 Db 1272 AATCATGAGATCTTTAAATCTTCCATGAAAGCTTTTGTGTGGTGGACCTTCATGTC 1331
 |||||
 QY 1345 AAACATGAAGTGTG- TTCCCTGAGTGCATCTGGAAAGATTTTACCCGCAACAGTTCC 1403
 |||||
 Db 1332 AAACATGAAGTGTGTTCTTCTGAGTGCATCTGGAAAGATTTTACCCGCAACAGTTCC 1391
 |||||
 QY 1404 TTCAGCTTCATTTGCCCCCTCATTTATCCCTCAACCCCCCAGCCACAGAGTCTTTATACA 1463
 |||||
 Db 1392 TTCAGCTTCATTTGCCCCCTCATTTATCCCTCAACCCCCCAGCCACAGAGTCTTTATACA 1451
 |||||

QY 1464 GCTCAGCTTTTGTCTTCTGAGGAGAAACAAATAGACCAT -AAGGGAAGATTCAT 1522
 |||||
 Db 1452 GCTCAGCTTTTGTCTTCTGAGGAGAAACAAATAGACCATTAAGGGAAGATTCAT 1511
 |||||
 QY 1523 GTGGAAATTAAGATGAGCTGATCTTGTCTCTTGTGACCTCTGTTTCACTTTCAATTTCA 1582
 |||||
 Db 1512 GTGGAAATTAAGATGAGCTGATCTTGTCTCTTGTGACCTCTGTTTCACTTTCAATTTCA 1571
 |||||
 QY 1583 GTGCTGACTGATGAGCAGACACTTCAATTAAGAGCAAAATTTGATACATATGTAATA 1642
 |||||
 Db 1572 GTGCTGACTGATGAGCAGACACTTCAATTAAGAGCAAAATTTGATACATATGTAATA 1631
 |||||
 QY 1643 TGGACTAGTTTCTTGCACATCAAAATTTACAGCTCTCTCTGATATCTGAGGAGTACA 1702
 |||||
 Db 1632 TGGACTAGTTTCTTGCACATCAAAATTTACAGCTCTCTCTGATATCTGAGGAGTACA 1691
 |||||
 QY 1703 CTCCTATAGAAAGTTCAAAAAGTCTACGCTCTCTCTTCTTCTTCACTCAGTGAATAT 1762
 |||||
 Db 1692 CTCCTATAGAAAGTTCAAAAAGTCTACGCTCTCTCTTCTTCTTCACTCAGTGAATAT 1751
 |||||
 QY 1763 GGGGCTCTGCTCAAGTTGAAAGAGCTCTATTTGACACTGTAAGCTGCGCTGTGAATTG 1822
 |||||
 Db 1752 GGGGCTCTGCTCAAGTTGAAAGAGCTCTATTTGACACTGTAAGCTGCGCTGTGAATTG 1811
 |||||
 QY 1823 GACCATCTATTTAACTGGCTTCAGGCTCCACCTCTTTCAGCCACCTCTCTTTTCA 1882
 |||||
 Db 1812 GACCATCTATTTAACTGGCTTCAGGCTCCACCTCTTTCAGCCACCTCTCTTTTCA 1870
 |||||
 QY 1883 GTTGGCTGACTTCACACCTAGCATCTCATGATGCGCAAGCAAAAGAGAGAGAGAGA 1942
 |||||
 Db 1871 GTTGGCTGACTTCACACCTAGCATCTCATGATGCGCAAGCAAAAGAGAGAGAGAGA 1930
 |||||
 QY 1943 ATAGCCTGGGCGTTTATAGTTTGGGGGTTTGTCTTCTTATAGACCCATTC 2002
 |||||
 Db 1931 ATAGCCTGGGCGTTTATAGTTTGGGGGTTTGTCTTCTTATAGACCCATTC 1990
 |||||
 QY 2003 TATTTCTTATGATCAATGTTCTTATACAGATATTTATAGAAACAACTACTGAA 2062
 |||||
 Db 1991 TATTTCTTATGATCAATGTTCTTATACAGATATTTATAGAAACAACTACTGAA 2050
 |||||
 QY 2063 ATGCTAGCTGCAAGTACATCTTTGATGTCATATGGAAGATTAAACAGGTGAGAA 2122
 |||||
 Db 2051 ATGCTAGCTGCAAGTACATCTTTGATGTCATATGGAAGATTAAACAGGTGAGAA 2110
 |||||
 QY 2123 ATTCCTGATTCACAATGAATGCTCTCTCTTCCCTGCCCCCAGACCTTTATCCACTT 2182
 |||||
 Db 2111 ATTCCTGATTCACAATGAATGCTCTCTCTTCCCTGCCCCCAGACCTTTATCCACTT 2170
 |||||
 QY 2183 ACCTAGATTCATCATATTTCTTAAATTTCAATCTCAGGCTCCCTCAACCCAC 2235
 |||||
 Db 2171 ACCTAGATTCATCATATTTCTTAAATTTCAATCTCAGGCTCCCTCAACCCAC 2223
 |||||

RESULT 3
 US-60-243-521-8
 ; Sequence 8, Application US/60243521
 ; GENERAL INFORMATION:
 ; APPLICANT: Hopkins, Christopher M.
 ; APPLICANT: Peterson, David P.
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Hawkins, Phillip R.
 ; TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS
 ; FILE REFERENCE: PA-0042 P
 ; CURRENT APPLICATION NUMBER: US/60/243,521
 ; NUMBER OF SEQ ID NOS: 2000-10-25
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 8
 ; LENGTH: 2385
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature

OTHER INFORMATION: Template ID: 331616.2
US-60-243-521-8

Query match	95.28;	Score 2151.6;	DB 56;	Length 2385;
-------------	--------	---------------	--------	--------------

OY	25	ACCTGCAGACACGACACTCTCCCTTT--GGCAAGAGACTGAGAGACCCCTGTGTCTAATGCACAA	83
Db	32	acctgcagacacgacacactctccctcttggcagaagaccctgagacccttgcgtactaagtcacaga	91
OY	84	GGCATATGGGCTGCGACGAACAACTATAGAGAAAGCGCAAGCAAAAGCCATGTATTTCCATGG	143
Db	92	ggctcaatbgygcctgcagaagaactatagaagaagcacaagcacaatgatattccaibg	151
OY	144	AAATGTGAGAGACCCGAGAGGACTTATGGAACATCTTCAAGTTGTGGGGGTGACAATG	203
Db	152	aaatgtcagagcaccacagagygactatgaaacattcaagttcgaigtggyggagcaatg	211
OY	204	CTCTGTGTGATTTTCCGCGACATCATGTGAACTACTGTGCGACTTACCATATTTCTGAA	263
Db	212	ctctgttgtatctccctgcgcacatcctggaacccgactctgtgactatcacattctgaa	271
OY	264	AAACCCATGAAGTGGCAAAAGGCTTAAGAATTTCTGCCGACAAATATACACAGATTAGTT	323
Db	272	aaacccatgaaactgcgcacaagygctatagaagatctgcgcgacacaattacacgaattagt	331
OY	324	GCCATACAAAACAAGGCCGGAATTTAGTATCTTGAGAGACACTCTGCCCTTCACTGCTTCT	383
Db	332	gcacatacaaaacaagcggaaatctgatactcgtagaagaagactcgtcttcagtcgtct	391
OY	384	TATACATGATGATGGAATCCGGGAAGATAGAGAGGAATATGACGTGGGTGGGAACCAAA	443
Db	392	tatacaccggataaggaatacccggaagataaggagaatactgagctggtgggaacacaaga	451
OY	444	TCCTCTACTAAGAGAGAGAGAACTGGGGGAGATGATGACCCCAACAAACAAGAAACAAG	503
Db	452	tctcttaactagaagaagaagaaactcgggagatggtgcgagccacaacaagaagaacaag	511
OY	504	GAGGACTGCGTGGAGATCTATATCAAGAGACAACAAAGATGCAAGCCAAATGGAAGCATGAC	563
Db	512	gaggactcgcctggagatctatacagaagaacaagaatgcagcacaatgcagacatgac	571
OY	564	GCCGCGCAACAACCTAAAGGCGACGCCCTGTGACAGCTTTGTCGACGCCCGGTGCATGC	623
Db	572	gctctgcacaacaactaaaggagccctctgttacaacagctctctgcagccctgcgcacagc	631
OY	624	AGTGGCCATGAGAAATGTGTAGAAATCATCAATAATCACACCTGCACACTGTGATGTGGG	683
Db	632	agtgcacatggagaaatgtgtagaataatcaataaattacacctgcacatcgtatgtggg	691
OY	684	TACTATGGGCCCCAGTGTCAAGCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCCACAGCTG	743
Db	692	tactatbgycccaagtctcagttctgtatctcagttgcagtcctctggaagcccccaagctb	751
OY	744	GGTTCATATGAGACGTACTCAACCCCTTTGGAACTTGAAGTTGACGTCAAGTGTGCTTTC	803
Db	752	ggttacaatcggacgttaactccctcttgggaaacttaagcttaagctccaagaatgctcttc	811
OY	804	AGCTGCTCTAAGAGAACAACTTAACTGGGATTTGAGAAACAACACCTGTGGACCATTTTGA	863
Db	812	agctgcctctgaagaaacaacttaacttggaatgtgaagaaaccaactctgtgacacattgga	871
OY	864	AACTGTGATCTCCAGAACCAACACTGTCAAGTGATTTCAAGTGTGAGCCTTATACAGACCA	923
Db	872	aaactgtcaatctccagaaaccaactctgcaagtattcagttgcagctctatcacaagaca	931
OY	924	GATTTGGGGGACATGAACCTGTAGCAATGCCCTGGCAGCTGACGTTTACGCTTCACTGATG	983
Db	932	gattttgggagatcaagaactgtagaacatccccctgcgcagcttaagctcttaaccctgcagct	991
OY	984	ACCTTCATCTGCTAGAAAGCACTGTGAATTAATTTGGCAAGAAAACCATTTGTGAATCA	1043

Db	992	accctcaccgctccagaaggaacgagatgaattcgggaagaagaacaaccattcgtaacca	1051
Oy	1044	tcctggaattctgctcgaatccctagctccaatatgatgcataaaatttgacaaaagtcttcantg	1103
Db	1052	tcgtgaatcctgctcaaatccctagtcacaatctgcaaaaatttgacaaaagtcttccaatg	1111
Oy	1104	atttaagagaggtgatatttaaaccccccttcttcantccagtcggcagtcgatgttaactgatttc	1163
Db	1112	attaaggaagggtgattataaaccctctcatccagtcgagtcgatgttactctgatttc	1171
Oy	1164	tcctgggtggcatttatcattttggctggcgaagagatttaaaaaaggcaaaattccacag	1223
Db	1172	tcctgggtggcatttatcattttggctggcgaagagatttaaaaaaggcaaaattccacag	1231
Oy	1224	agaaagtatgatgcaccctatttaataatgcgccttgatgaaagaaaattcttggaattactaa	1283
Db	1232	agaagtatgaatgagcccatataatcatgcctctggtgaagaagaaattcttggaattactaa	1291
Oy	1284	aaatcatgatgactccttttaaaatccttccatgaacgtttctggtggtggcactcctacgt	1343
Db	1292	aaatcatgaagatccctttaaataccctccacgaacgtttctggtggtggcactcctacgt	1351
Oy	1344	caaacatgaagagtgctg-cttccttgagtgcaatctgggaagattcttcaccgacacacagttc	1402
Db	1352	caaacatgaagatgctgcttcccttcagtgcaatctgggaagattcttcaccgacacacagttc	1411
Oy	1403	ctttcagcttcacatttcgcccctcatattatccctcaacccccccacagtggttataac	1471
Db	1412	cttcagcttcacatttcgcccctcatattatccctcaacccccccacagtggttataac	1471
Oy	1463	agctcagcttttctgtctttctgaggaagaaacaaatagaccat-aaaggaaaaggattca	1521
Db	1472	agctcagcttttctgtcttcttcaggaagaaacaaatagaccatlaaggaagattca	1531
Oy	1522	tcctggaattatgaagatggctgacttttgctcttttgatcctctgttttcagtttcaatttc	1581
Db	1532	tcgtgaataataaagaatgctgacttctgtccttcttgactctgttcttcagtttcaatttc	1591
Oy	1582	agctcctgacttgatgagacacacactttaaataagtcgaataatttgatataatgctgat	1641
Db	1592	agtgctgactctgtagcagacacactcttaagaagtgcaaatcttgatacatatgagatc	1651
Oy	1642	atgagactcagtttcttgtagcagatcaaatgctacgctcttctgatatctgtgaggtac	1701
Db	1652	atgagactcagtttcttgtagcagatcaaatgctacgctcttctgatatctgtgaggtac	1711
Oy	1702	actcttatgaaaagttcaaaaagttcagctccttcttcttaactcagtgagttaa	1761
Db	1712	actcttaagaagttcaaaaagttcagctccttcttcttaactcagtgagttaa	1771
Oy	1762	tggggctcctgcctcaagttgaaagagtcattttggcactgtacgctggcgccttggaatt	1821
Db	1772	tggggctcctgcctcaagttgaaagagttccatttgcaatgcaagcccgctcgatc	1831
Oy	1822	ggacacatcattatgactggtcttca-gcctccccacactcttcagcaacctctcttcttc	1881
Db	1832	ggacacatcattatgactggtcttca-gcctccccacactcttcagcaacctctcttcttc	1890
Oy	1882	agttggctgacttcacacactagcatctcatgagtcgcaagcaaaaagagagagaga	1941
Db	1891	agttggctgacttcacacactagcatctcatgagtcgcaagcaaaaagagagagaga	1950
Oy	1942	aatagcctgcgcgttcttctaagttctgggggttctgcttcccttccttcaggaaccaatc	2001
Db	1951	aatagcctgcgcgttcttctaagttctgggggttctgcttcccttccttcaggaaccaatc	2010
Oy	2002	ctattcttatagtcgaattgttcttcttaacagatatatactgtaagaagaaacatacagca	2061
Db	2011	ctattcttatagtcgaattgttcttcttaacagatatatactgtaagaagaaacatacagca	2070
Oy	2062	aatgcttagctgcaagtgacatccttttgatgtcatatggaagagtttaaaacagctgagca	2121

```

Db      2071  atgctagctgcgaagtgcacatccttccttgatgtcatattgtaagaaggtttaaaccaaggtgaga 2130
QY      2122  AATTCCTTGATTCAACATGAAATGCTCTCCCTTTCCCCTGGCCCCAGAACCTTATTCCACT 2181
        |||
Db      2131  aatccctgatccaagaagaatgcctccttcccctggccccagaactttataccact 2190
QY      2182  TACCCTAGATTCTACATATTCTTAATTTCACTCAGCGCTCCCTCAACCCCCAC 2235
        |||
Db      2191  tacttagattcataattcttctaatttcacctcgaagcctccccaaccac 2244

RESULT    4
US-60-213-360-1118
; Sequence 1118, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Tal, Preehl
; APPLICANT: Diep, Dihn
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 1118
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 331616.2
US-60-213-360-1118

Query Match          95.2%; Score 2150; DB 53; Length 2385;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2200; Conservative 0; Mismatches 10; Indels 4; Gaps 4;

QY      25   ACCGTGAGCACACACACTCCCTTT-GGCAAGAGACTGAGACCTTGTGCTAAGTCAAGA 83
        |||||
Db      32   acctgcagcacagcacactcccttggcgaagcactgagacccttgcctaagccaaga 91
QY      84   GGCTCATGGGCGTGCAGAAACAATACTAGAGAGGAGCCACCAAGCCATGATTTCCANG 143
        |||||
Db      92   ggctcaatgygcgcgaaagaactagaagaagaccaaagccaatgatatltccatgy 151
QY      144  AAATGTCAGAGCACCCAGAGAGGACTTATGAACATCTTCAGTTGTGGGGGAGCAATG 203
        |||||
Db      152  aaatgfcagagaccccgagaggaacttatgacaacttccaagtgtggyggtggaatg 211
QY      204  CTCCTGTGTGATTTCTCTGGCACATCATNGAACTTACTGCTGGACTTACCATTATTGTGA 263
        |||||
Db      212  cctctgttgtattcctctgcacatcalygaacgcgactgtgacttacattatctcga 271
QY      264  AAACCCATTAACCTGGCAAAAGGCTAGAGAGATTCTGCCGAGCAATTTACAGATTTAGT 323
        |||||
Db      272  aaacccatgaactgcgaagaaggtctagaagaattctgcgcgaacaatatcacagattagtt 331
QY      324  GCCATTACAAAACAGGCGGAAATTTAGTATCTGGAGAGAACTCTGCCCTTAGTGTTCT 383
        |||||
Db      332  gccatacaaaaacaaagcgysaaattgagtalctgysagaagactctgccttcagtcgttct 391
QY      384  TACTCTGGATTTGGATTCGGAGAGATAGAGAGSAAATAGSAGCTGGGTGGGAACCAACAA 443
        |||||
Db      392  tactctctggtatggaaatccgysaagataagsgaatataygaacgtgtgtygysgaaccaaaaa 451
QY      444  TCTCTCACTGAAGAACAGAGAACTGGGGAGATGSTAGGCCAACCAACAAGAACAG 503
        |||||
Db      452  tctctactgaagaagcagagaactgysgagatgtygtgagcccaacaacaagaagaacaaag 511
QY      504  GAGGACCTGGCTGTGATCTATATCAAGAGAAACAAGATCGAGGCAANAATGAGACGATGAC 563

```

Db	512	gagagctgcgttggagatctctataccaaggaacaaagatgcaggcaaatggaacgatgc	5711
OY	564	GCCTGCACAAACTAAAGGACGCCCTGTTTACACAGATCTGTCGAGCCCTGGTACATGC	623
Db	572	gacctccacaactaaaggcaagccctcglttacaagaactcttcgcagccctgltatgc	631
OY	624	AGTGGCCATGGAGACATGTTTAGAATAATCATCAATAATCACACCTGCACACTGTGATGTGGG	683
Db	632	agtcgcacatgagaaatgctgtagaataatcaataataatcacctgcactgtgtgtggg	691
OY	684	TACTATGGGCCCCAGTGCACGTTGATGATAGTGTGAGGCTTTGGAGGCCCCAGAGCTG	743
Db	692	tactatgaggccccaagtgltacgttctgaagtcagtcgacctgtggagcccaagactg	751
OY	744	GGTACCATGGACGTGACTCACCCCTTTGGAAACCTTCAGCTTCACACTCACAGTGTGCTTC	803
Db	752	gtfacatgactgttactacacccttgggaacttcagcttcagctcaagtgigtcttc	811
OY	804	AGCTGCTCGAAGAACAACTTAACCTGGATTTGAAGAAACACACTGTGGACATTTTGA	863
Db	812	agctgtctcgaaagaaacttaacttcgtggattgaagaacaccctgtgacatttga	871
OY	864	AACTGCTCAWCTCCGAAGAACCAACCGTCAAGTGAATGATAGTGAAGCCTATAGACACA	923
Db	872	aactgtcatctccagaaccacaacctgtcaagtgtctagtgtagtgcctcatcagaacca	931
OY	924	GATTTGGGATCATGACTGTAGCCATCCCTGGCCAGCTTCAGCTTACCTGTGCATGT	983
Db	932	gatttgggatalcatgaacttgaagcaatccctggcagacttcagcttacctgtcatgt	991
OY	984	ACCTTCATCTGCTCGAAGAACAGATGATTAATTTGGAAGAAACCAATTTGTAATCA	1043
Db	992	acctcatcctgcagaaggaagcaactcgagttaatttgggaagaagaacacatttgtatca	1051
OY	1044	TCGTGAACTGTGGTCAATCTGATGCCAATATGTCAAAAATTTGACAAAAGTTTCTCATG	1103
Db	1052	tctggaaactgttcaaatccctagcccaatatgtcaaaaatttggacaagaattcttcaatg	1111
OY	1104	ATTAAAGGAGGGGATTAATTAACCCCTCTCATTCACAGTGGCACTCATGTGTCGATTC	1166
Db	1112	attaaggagggtgtattataaaccccccttcaatccagtcagtcagtcagtctacgcacac	1177
OY	1164	TCGTGGTTGGCAATTAATCTTTGGCTTGGGCAAGATTTAAAAAAGCCAAAGAATCCAG	1222
Db	1172	tctgggttgcattatcatctatcttgcgtgcgaagatgttaaanaagcaagaatcccaag	1231
OY	1224	AGAACTATGATGACCCATTAATTAATGCGCCCTGTGGAAAGAAAATCTTGGAAATATCTA	1288
Db	1232	agaagtaagaaatgcccatataaactgcgacctgtgtgaagaanaattcttgaatactaa	1291
OY	1284	AAATCATGATGATCCCTTAAATCCTTCCATGAAACGTTTGTGTGGGACCTCCCTACGT	1343
Db	1292	aaatcatgagatctctttaaatcccttccatgaagaacgttttgttgtgtggaacctctaagt	1351
OY	1344	CAAACTGAATGTGG-TTCCTTCAGTGTCACTGTGGGAAGATTCTACCGACCAACAAGTTC	1402
Db	1352	caaaatgaaagtgtgttcttcttaagtgacatcgtggaagaattcttaactgcacaagaagtc	1411
OY	1403	CTTGAGCTTCATTTCCGCCCTCATATTATTCCTCAACCCCAAGCCACAGAGGTTTATAC	1462
Db	1412	cttcagcttccatttgcgccctcatattatccctcaaccccccaagcccaagtglttatcac	1471
OY	1463	AGCTCAGCTTTTGTCTCTTTCTGAAGAGAAACAATTAAGACAT-TAAGGAAAGGATTC	1521
Db	1472	agctccagcttltgtcttcttcttgaagagaacaacaataagaccataaaggaaagatltca	1531
OY	1522	TGTGGAATTAATTAAGATGGCGACTTTTGCGCTTTCCTTGATCTGTGTTTCAGTTTCAATTC	1581
Db	1532	tgttggaataaagaatgagctgcagcttgccttcttcagacctcgttccaatccaatcc	1591
OY	1582	AGTCTGTACTGATGACACACACTTCTAATGAATGAATGCAAAATTTGATACATATGTGAT	1641

Db	1592	atgtcgtacatctgatagacagacacatcttctaataagaagtgcanaatttgatatacatgtygaat	1651
Qy	1642	ATGACATCGATTTTCTTGTCAGATCAAAATTTTCACGTGCTTCTGTATCTGTGAGAGTAC	1701
Db	1652	atgagatcagtttctcttgacagatacaattccacagtcgtctctctgtaactgtgagagtcg	1711
Qy	1702	ACTGTATATGAAGAATTCAAAAGTGTACGCTGCTGCTTCTTCTTCTATACATCGAGTAAT	1761
Db	1712	atctctataagaagttcaaaaagctcagctccctctcttcttctaactcagygaaagtaa	1771
Qy	1762	TGGGGTCTCGTCAAGTTCGAAAGAGTCTCATTTTTCACATGTAGCCTTCGGCTGTGTAATT	1821
Db	1772	tggggctcgtcgaagtgtgaagagtcctattcttgacctgtagcctcgtcgtctgtgaatt	1831
Qy	1822	GGACCATCTCATTTTAACATGTGCTTCAGAGCCTCCCGACCTTCTTCAGCACCTGCTTTTTC	1881
Db	1832	ggaccatcctcatltaactgtgcttca-gcctcccaactcttctcagcacctctcttttc	1890
Qy	1882	AGTTGAGTCATCTCCACACCTAGCATCTCATAGTGTCCCAAGCAAAAGAGAGAAGAGA	1941
Db	1891	agtgtcgtgacttccacacctcagatctcatagtcagtcagaagcaaaagagagagagaga	1950
Qy	1942	AATPACCTGCGGGGTTTTTTTAACTTTGGGGGGTTTTGGCTGTTTCTTTTATGAGACCCATT	2001
Db	1951	aatgacgtcgtgcttttttttagttttagtgagggttttgctgttctctctttagagaccattc	2010
Qy	2002	CATTTTCTTATAGTCATATGTTCTTTTATCACAGATATTATTAGTAAGAAACATACCTGA	2061
Db	2011	catlctctatagtcataatgtcttcttcttatacagataattctagtaagaanaacatacctga	2070
Qy	2062	AATGCTAGCTGCAAGTGAACATCTCTTTTGATGTGCATATGGAAGAGTAAACAGTGGAGA	2121
Db	2071	aatgctagctgcaagtgcacatctctcttgatgacatgtaagaagtttaaacacagtcgaga	2130
Qy	2122	AATTCCTTGATTTACAAATGAAATGCTCTCTTCCCTGCTCCCGACCAACTTTTATCCACT	2181
Db	2131	aatctctgattcacaatgaaatgctctctcttccctcgccccagaactttatccact	2190
Qy	2182	TACCGAGATTTCACATATCTTAAATTTGCATCTCAGAGCCTCCCGCAACCCAC	2235
Db	2191	tacctagattcacaatcttctttaaattcatctcaggtcctccctcaaccacac	2244
RESULT 5			
US-09-396-970-8480			
; Sequence 8480, Application US/09396970			
; GENERAL INFORMATION:			
; APPLICANT: Gearling, David P.			
; APPLICANT: Kingsbury, William A.			
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A			
; TITLE OF INVENTION: MIXED LYMPHOCYTE LIBRARY			
; FILE REFERENCE: MUM98-40PA			
; CURRENT APPLICATION NUMBER: US/09/396,970			
; CURRENT FILING DATE: 1999-09-14			
; EARLIER APPLICATION NUMBER: 60/100,293			
; EARLIER FILING DATE: 1999-09-14			
; NUMBER OF SEQ ID NOS: 8756			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 8480			
; LENGTH: 2564			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)...(2564)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-396-970-8480			

Query Match	95.28;	Score 2150;	DB 17;	Length 2564;
Best Local Similarity	99.48;	Pred. No. 0;		
Matches 2200;	Conservative	0;	Mismatches 10;	Indels 4;
				Gaps 4;

QY	25	ACCTCGACGACAGCAGCACTCCCTTT -GGCAAGAGACCTCGAGACCCCTGTGCTCAAGTCAGA	83
Db	50	accctgcagcaagaagcaactccctcttggcagaaggacctctgaaacctctgtcctaagtcaga	109
QY	84	GGCTCAATGGCGTGCAGAGAAGCAATPAGAGAAGAGCACAAAGCAACCCATGTAATTTTCATGG	143
Db	110	ggctcaatcgggcctgcagaagaagcaatcagaagaagcgaagccaatgtatattccaa	169
QY	144	AAATGTGAGAGCACCCAGAGGAGCTTATGGAACATCTTCAGTTGTGGGGTGGAATG	203
Db	170	aaatgtcagagcaccacagagggaacttatggaacatctcaagtctgaggggcggagcaatg	229
QY	204	CTCTTGTGTGATTTCTGTGGCAGCATCATGAGAACTACTGCTGGACATTCACATTAATTCGAA	263
Db	230	ctctgtgtgtatcttccttgcgcatactgaaacccagatcctggaatccattatcttctgaa	289
QY	264	AAACCCATGAACTGGCAAAAGGGCTAGAGAAGATTCCTGGCGAGACAAATTAACACATATTAGTT	323
Db	290	aaacccaatgaactcggcaaaagggctagaagaattctgcgagaacaattacacagaatttagt	349
QY	324	GCCATCAAAAACAAGGCGGGAATTAAGTATCTGGAGAAGACTGTGCCCTTCAGTGTTCT	383
Db	350	gccatacaaaaacaaggcggaatttagtatctggagaagaacctgccttcaatctgcttc	409
QY	384	TACTACTGGATAGGATTCGGAGAGATPAGAGAAATPAGAGCTGGGTGGGAACAACA	443
Db	410	tactactgataagaaatccgaaagatagagaattgaaatcgtcggctggaaaccaacaa	469
QY	444	TCTCTCACTGAAGAAGCAAGAACTGGGGAGATGTGACCCCAACAACAAGAAAGAACAG	503
Db	470	tctcttactgaaagaagcagaagaactcgggagatcggtagcccaacaaagaagaacaag	529
QY	504	GAGGACTCCGTGGAGATCTATATCAAGAGAAACAAGATGACAGGCAAAATGGAACATATAC	563
Db	530	gaggacactcgtggagatcataataagaagaaacaaagatgcaaggcaaatggaaacgaatgac	589
QY	564	GCCCTCCACAACCTTAAGGCAAGCCCTCTGTTCACAGCTTCTTGCCAGCCCTGTGATGTC	623
Db	590	gacctccacaacataaaggcagccctctgttacaacagctctcttgcgaagccctgtcaatgc	649
QY	624	AGTGGCAATGAGAAATGTATGAATATCAATATACACACCGCAACCTGTGATGTTGGGG	683
Db	650	agtgagccatggaagaatcgtatgaagaaatcaataaataaacccgtcaacatcgtgaatgggg	709
QY	684	TACTATGGGCCCCAGTGTCAAGCTTGTATTCACATGTGACGCTTTGGAGGCCCAACAAGCTG	743
Db	710	tactatgggccccagatctcagtttgatattcaatcagatgtagagaccttggagggccccaaagctg	769
QY	744	GGTACCATGAGCTGTACTCACCCCTTTGGAACCTTGACGTTACGCTCACAGTGTGCTTTC	803
Db	770	ggtacacatgagactgtactcaaccttggaaacctcagcttcaagatcgaagcgtgccttc	829
QY	804	AGCTGCTTGAAGGAACAACTTAACCTGGGATTTGAAGAAACCACTGTGGACCATTTTGA	863
Db	830	agctgcttgaaggaacaaacttaactcgtggaattcgaagaacaacccgtggaaacatttgya	889
QY	864	AACTGTCATATCCAGAACCAACACTGTGCAAGTATTCAGTGTGAGGCTTATACACACCA	923
Db	890	aactggtcatctccagaaccaaacctgtcaagyaattcagatgtagagcctctatcagagaca	949
QY	924	GATTTGGGGATCATGAACGTAGGCATCCCGTGCCAGCTTGACGTTTAACCTTGACATGT	983
Db	950	gatttggggatcatgaactgtagcatalccctcgccagcttcagcttttaacctctgcagct	1009
QY	984	ACCTTCATCTGCTCAGAAAGCACTGAGTTAATTTGGGAAGAAACCACTTTGTGAATCA	1043
Db	1010	accttcacatctgtcagaagaagaaactggaattcgggaagaaagaaacaacttltgtgaatca	1069
QY	1044	TCTGGAATCTGTCAAAATCTTAGTCAAAATTTGTCAAAAATTTGGCAAAAAGTTTTCATGT	1103
Db	1070	ctctggaatcgtgtcaaatctcttagtccaatactgcanaaatctggaacaaaagtcttccaa	1129
QY	1104	ATTAAAGGAGGTATTAATTAACCCCTCTTCATTCAGTGGACATGAGTTACTGCATTC	1163

|||||
Db 1130 attaaaggagggataltataaccctctcatctcagtgagcatatggttacatctc 1189
QY 1164 TCTGGGTGGCATTTATCATTTGGCTGGCAAGAGATTAAAAAAGCAAGAATCCAA 1223
Db 1190 tctgggttgagcatctatcatcttgctgcaaggatataaaaaaagcaagaatccaa 1249
QY 1224 AGAATGTAATGAGCCATTTAAATCGCCCTGGTGAAGAAATCTTGGAATCTAA 1283
Db 1250 agaagtaagatgaccatataataatcgcccttgtagaagaanaatctctggaatctaa 1309
QY 1284 AAATCATGAGATCCCTTAAATCCCTCAATGAAGATTGTTGTGGTGACCTCTACGT 1343
Db 1310 aaataatgagatcccttaaacctccatcagaacgcttgtagtgctcactctcagct 1369
QY 1344 CAACATGAACTGTG-TTCCCTCAGTGCATCTGGAGAGATTTCACCGACCAACAGTTC 1402
Db 1370 caaacaagaagtgctctccctcagtgcatctggaagaattctactcctgcaacagctc 1429
QY 1403 CTTCAGCTTCATTTGCCCCCTCATTTATCCCTCAACCCCGACGACAGGTCTTATAC 1462
Db 1430 ctacagctcatcttgccctcctatctatccctcaaccccgacagctggtttatc 1489
QY 1463 AGCTCAGCTTTTGTCTTTTGTGAGAGAAACAAATTAAGCCAT-AAAGGAAAGATTCA 1521
Db 1490 agctcagcttttgctctctctctgaggaacaataaagaaccataaaggaaagattca 1549
QY 1522 TGTGGAATATTAAGATGGCTGACTTGTCTCTTTCTGACCTGTTTCAAGTTCAATC 1581
Db 1550 tgtggaatataaagaatgagctgactctctctctctgacccctgcttctcagttcaatc 1609
QY 1582 AGTCTCTACTTGATGACAGACACTCTTAATGAATGAAGTCAATTTGATATGTGAAT 1641
Db 1610 agtctctacttgatgacagacactcttaaatgaagtgcaattgtatcatatgtgaat 1669
QY 1642 ATGAGCTCAGCTTTCTTGAGATCAATTTACAGTCTCTTCTGTATCTGTGAGGTAC 1701
Db 1670 atggaactcagcttctctcagatcaaatctcaagctgctctctctctcagttctcaatc 1729
QY 1702 ACTCTTATGAAGATTCAAAAAGTCAAGCTCTCTTTCTTCTTAACTCCAGGAAGTAA 1761
Db 1730 acctatagaagaatcaaaaaagctcagctcctctctctctctctcagtggaagtaa 1789
QY 1762 TGGGGTCTGCTCAAGTTGAAGAAGTCTATTTGCACTGTAGGCTGCGCTGTGAAT 1821
Db 1790 tggggctcctgctcaagtgtaagaagctcctatctgcaactgagctcgctcgtaatt 1849
QY 1822 GGACCATCCATTTAACTGGCTCAGGCGCCCGACCTTCTTCAAGCACCCTGCTTTTC 1881
Db 1850 ggaacatctatcttaactggtctca-gccctccacactctctcaagcactctctcttc 1908
QY 1882 AGTTGGCTGACTTCACACCTAGCATCTCATGAGTCCCAAGAAAAAGAGAGAAGAGA 1941
Db 1909 agttgctgactctcacacactagcatcatgagtgcaagaagagagagagagaa 1968
QY 1942 AATAGCTCGGGGGTTTTTATTTGGGGGTTTTGTGTTCTTTTATGAACCCATTC 2001
Db 1969 aaagaagcctgagcttcttctagcttgagggttctgctctctctcttctatgagaccatc 2028
QY 2002 CTATTTCTTATAGTCAATGTTTCTTTTATCAGATATTTTATGAAGAAACATACGTA 2061
Db 2029 ctatctctatagctcaagctctcttcttctcaagataatactatgtaagaanaatcaacga 2088
QY 2062 AATGCTAGCTGCAAGTGCATCTTTTGTATGTCAATGGAAGAGTTAAACAGTGGAGA 2121
Db 2089 aatgtaagctgcaagtgacatctcttgatgcatatggaagatgtaaaacagtgagga 2148
QY 2122 AATTCCTGATTCACAAGTAATGCTCTCTTCTTCCCTGCCCCGAGAACTTTTATCACT 2181
Db 2149 aatctctgactcacaagaatgctctctctctccctgccccagagactttatccact 2208
QY 2182 TACCTAGATTCATATTTCTTTAAATTTCACTCAGGCTCCCGCAACGCCAC 2255
|||||

Db 2209 tactagatctcatatcttcttaaatctcatctcagggctccctcccaacccac 2262
RESULT 6
US-09-495-050A-292
Sequence 292, Application US/09495050A
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATE
FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: US/09/495, 050A
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 292
LENGTH: 2385
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID NO: 1876370CB1
US-09-495-050A-292

Query Match 95.0%; Score 2146.8; DB 18; Length 2385;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2198; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

QY 25 ACCTGAGACAGACACACTCCCTTT-GGCAGAGACCTGAGACCTTGTCTAAGTCAAGA 83
Db 32 acctgagacagacacactcccttgggcaaggacctgagacccttggctaaagtaaga 91
QY 84 GGCCTAATGGCTGCAAGAAAGTCTAGAGAGGACCAAGCAAGCATGATTTCCATGG 143
Db 92 ggcctaatggctgcaagaagaactagaagaagcaagaagcaagataatccatg 151
QY 144 AATGTACAGACCCAGAGGACTTATGAACATCTTCAAGTTGTGGGGTGAGCAATG 203
Db 152 aatgtacagacccagagacttatggaacatcttcaagcttgagggtgagcaatg 211
QY 204 CTTCTGTGATTTCTCTGCAATCATGGAACCTACTGCTTACCATTTATTTGAA 263
Db 212 ctctgtgtatctctctgagcatatcagaaacagactgtagcttaccatctatctgaa 271
QY 264 AAACCATGAACCTGGCAAGGGCTAGAAAGATTCTGCCGAGACAAATTACAGATTTAGTT 323
Db 272 aaacccatgaacctggcaaaaggtctagaagaatctgcgcgagaacaattacaagattagtc 331
QY 324 GCCATACAAAACAGCGCAATTGATGTGAGAGAAGACTTGCCCTTCACTGCTTCT 383
Db 332 gccatataaaacaaagcggaattgaglatctggaagaagactctgctcttcaatgctc 391
QY 384 TACTACTGATAGGAATCCGGAAGATGAGAGATATGAGACGTGGGGGGAACCAACAA 443
Db 392 tactactggaatagaaatccggaagaatagagggaatataagacgtgggtggaacaaacaa 451
QY 444 TCTCTCACTGAAGAAGAGAACTGGGAGATGAGTGGAGCCCAACAAGAGAGAAAG 503
Db 452 tctcttactgaagaagcagaagaactggggagatggtgagcccaacaacaagaagaagaag 511
QY 504 GAGAGCTGCGTGGAGATCTATATCAAGAGAAGAAAGATGCAGCAATGGAAGATGAG 563
Db 512 gaggaactgctggagatctatatacagaagaacaagaatgcaagcaaatggaacgtatgac 571
QY 564 GCCGCGCCACAAGCTAAAGGAGAGCCCTGTGTACACAGCTTTCAGCGCCCTGGTATGC 623
Db 572 ggcgcgccacaagcctaaagagagccctctgttacaagcttcttgcagccctggtatagc 631
QY 624 AGTGGCCATGAGAAATGTGTAGAAATCATCAATTAATCACACCTGCAACTGTGATGGGG 683
|||||

|||||
Db 632 agtggccatgaggaatgctgtagaataatcatcaataatcaaccctgcaactgtagatg999 691
QY 684 TACTATGGCCCCAGTGTGACGTTGTGATTGATGATGACGCTTTGGAGGCCCGAGACGTG 743
Db 692 tactatggtgccccagctgctagcttgatctagctgtagagcctcttgagggccccagagctg 751
QY 744 GGTACCATGTGACTGACCTCCCTTTGGAACCTTGACGTTGACCTGACAGTGGGCTTC 803
Db 752 ggtacacatgagctgtaactaccccttgaggaaactcagctcagctcacagctgacctc 811
QY 804 AGCTGCTCTAAGAGAACAACTTAACGTGATTGAGAAACACACCTGTGACATTGGA 863
Db 812 agctgctctgaaaggaaacaaacttaactcgtggaattgaaagaacacccctgtagacacattg99a 871
QY 864 AACTGCTCATCTCCAGAACCAACCTGTCAAGTGAATGATGAGCTTATCAGACACA 923
Db 872 aactgctcatctccagaaacacctgcaacgtgaatgtagtgcagctctacacga 931
QY 924 GATTTGGGATCATTGAACTGATGCAATCCCTGGCCAGCTTACCTTGACATGT 983
Db 932 gatttgggatactgaaactcgtgagcaccctggccagctcagcttcaactctgcaatg 991
QY 984 ACCCTCATCTGCTCAGAGAACGAGTAAATTGGAAGAAAGAAACCATTTGTGAATCA 1043
Db 992 acctctatctgctcagaagaagactggaattatgaggagaagaacacacattgtagaactca 1051
QY 1044 TCTGGAAATCTGTCAAACTCTAGTCAATATGTCAAAAAATTTGCAAAAGTTTCTCAATG 1103
Db 1052 tctggaaatctgttcaaaaactctagctcaatatgcaaaaaattgagcaaaagttcttcaatg 1111
QY 1104 ATTAAGAGAGGTGATTATTAACCCCTCTTATTTCAGATGGCAGTCAATGTTACGCAATTC 1163
Db 1112 attaaaggagggtgatttaaacccctctcattccagtgtagcagctgtagcattc 1171
QY 1164 TCTGGGTTGGCATTTATCATTTGGCTGGCAAGAGATTAAAAAAAGCAAGAAATCCAAAG 1223
Db 1172 tctgggtgtgcatattatcatctatctgctgcaagagatlaaaaaaggaagaaatccaag 1231
QY 1224 AGAAGTATGAATGACCCATATTAATGCGCTTGTTGTAAGAAATAATCTTGAATACTAA 1283
Db 1232 agaaatgtagatgaccatattatcaatcccttggtgtaagaataattcttgaaactaa 1291
QY 1284 AATTCATGAATCCTTTAATCCTTCATGAAGAGTTTGTGTGGTGGACCTCTCACT 1343
Db 1292 aaatcatgaatcccttaaatccctcctcctcagcttctgctgtagcaccctcctcgt 1351
QY 1344 CAACATGAGAGTGTG-TTCCTCAGTGCATCTGGAGAGATTTCACCCGACAGAGTGTATAC 1402
Db 1352 caaacatgaagtgcttctcctcctcagtgcatctcggaaagattctcactgacacacagctc 1411
QY 1403 CTTCAGCTTCATTTGCGCCCTCATTTATTCCTCAACCCCGACGACAGGTGTTATAC 1462
Db 1412 cttcagcttcattctgcccctcattatccctcaacccccagccagtggttattac 1471
QY 1463 AGCTCAGCTTTTGTCTTTTCTGAGGAAACAAATAAGACCAT-AAGGAAAGGATTCA 1521
Db 1472 agctcagcttctgtcttctcctcagtgagaaacaataagacatlaaagggaagaaatctca 1531
QY 1522 TGTGGAATTAAGAGATGGCTGACTTGTCTTCTTGTGACTCTTGTTCAGTTTCAATTC 1581
Db 1532 tgtggaataataaagatgagctgacttctcctccttgacacctgcttctcagtttcaatc 1591
QY 1582 AGTGTGTACTTGTATGACAGACACTCTTAATGAAGTGAATTTGATACATATGTGAAT 1641
Db 1592 agtgcgttacttgatgagcagacactcttaaaatgaagtgcaaatctgtataatgtagaac 1651
QY 1642 ATGGACTCAATTTTCTTGACAGATCAATTTACAGTCTCTTCTGTATACGTGAGAGTAC 1701
Db 1652 atggaactcaagttctctgagatcaaaattcacaagctgcttctcgtatcaactgtagaagctac 1711
QY 1702 ACCTTATTAAGAAAGTTCAAAAAGTCTACGCTCTCTTCTTCAATCTCAGTAAATAA 1761
|||||

Db 1712 actcttatagaagcttcaaaaagctcaacgctctcccttctcttcaactccagtgaa 1771
QY 1762 TGGGGTCTGCTCAAGTTGAAGAGTCTTATTGTGACATGATAGCTCGGCTGTGTAAT 1821
Db 1772 tgggtctctgctcaagtgaagaagctctattctgacgttagctcgcgtctgtagaatt 1831
QY 1822 GGACCATCTATTTTAACGTGCTCAGGCTCCCAACCTCTTTCAGCCACCTCTTTTTC 1881
Db 1832 ggaacatcccatcttaactgacctca-gcctcccaactctctcagccacacctcttcttc 1890
QY 1882 AGTTGGCTGACTTTCACACCTAGACATCTCATGAGTGGCCAGCAAAAGAGAGAGAGA 1941
Db 1891 agttgctgacttccacaacctagcatctcatgagtgccaagcaaaaggaggaagaga 1950
QY 1942 AATAGCCTGCGGGTTTTTTAGTTGGGGGTTTGTGCTTTTCTTTATGAGACCATTC 2001
Db 1951 aatagcctgcgtcttctttagtctgggggttctgctgcttctctttagagaccatctc 2010
QY 2002 CTATTCTTATGCAATGTTCTTTTATCAGADATTTATGTAAGAAACATCAGTGA 2061
Db 2011 ctattctctatagctaatgcttctcttcaacgacatattatgaagaacacacacvga 2070
QY 2062 AATGCTAGCTGCAAGTACATCTTTGATGTCAATATGAAGATTAACAGGTGAGAGA 2121
Db 2071 aatgctagctgcaagtgacatctctcttgatgctatgtaagagcttaaaacagtgtaga 2130
QY 2122 AATTCTTGTATTCACATGAATGCTCTCTTCTCCCTGCCCCAGAACTTTATCCACT 2181
Db 2131 aatcctctgattcacaatgaatgctctccttccctccctgccccagaaacttctacact 2190
QY 2182 TACCTAGATTCTACATATTTCTTAAATTTCTCATGTCAGGCGCTCCGTCAAACCCAC 2235
Db 2191 taactagattctacatattcttcttaattcaatctcaagcctccctcaacccac 2244

RESULT 7
US-60-118-318-292
; Sequence 292, Application US/60118318
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guejler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATE
; FILE REFERENCE: PR-0013 P
; CURRENT APPLICATION NUMBER: US/60/118,318
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: PERL Program
; SEQ ID NO 292
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1876370CB1
US-60-118-318-292

Query Match 95.0%; Score 2146.8; DB 43; Length 2385;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2198; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

OY 204 CTCTGTTGATTTCTGGCAGATCATGTGAACCTTGTGGAGTTTACCATTTATCTGAA 263
|||||
Db 212 ctctgttgatcttccttgccacatactgaaacccgactctggaacttaccatattctgaa 271
OY 264 AAACCCATGAGTGTGCAGAAAGGGCTGAGAAATTCGCGAGAACAAATTTACAGATTTAGTT 323
|||||
Db 272 aaaccatgaacttggcaaaaggtctagaagattctgcgagaacaattacacagatttagtt 331
OY 324 GCCATCAAAACAAAGGGGAAATGATGATCTGGAGAGACTGTCGCCCTTACAGTCGTTCT 383
|||||
Db 332 gccatacaaaaagggcgaaatttgagtaacctggagaagactctgaccttcaagtcttct 391
OY 384 TACTACTGATAGGAATCCGGAAGATAGAGAAATATGAGAGTGGGGGGAACCAACAA 443
|||||
Db 392 tactacttgataggaatcccgagaagataggaatactgaaagtggtggggaacaaacaa 451
OY 444 TCTCTCACTGAAAGAAAGCAGAGAACTGGGGAGATGTGAGCCCAACAAACAGAAACAG 503
|||||
Db 452 tctcttactgaagaagcaggaacttgggagatgtgtgagcccaacaagaagaacag 511
OY 504 GAGGACTGCGTGAGATCTATATCAAGAAAGAAAGATGCAAGCAATGGAAGAGATGAC 563
|||||
Db 512 gaggaacttgctggagatcatatataagaagaacaaagatgcaggcaaaatggaacgaatgac 571
OY 564 GCGTGGCAACAACTTAAAGCAGCCCTGTGTACACAGCTTCTTGGCCAGCCCTGGTCAATGC 623
|||||
Db 572 ggtcgcaacaacaataaagcagccctctgttaacacagcttcttgccagccctgtactgc 631
OY 624 AGTGGCATGGAAGATGTGTAAGAAATCATCAATATACACACCTGCAACTGTGATGGGG 683
|||||
Db 632 agtggccatggaagaaatgtctgagaatacatataatcacacttgcacactgtgagtggg 691
OY 684 TACTATGGGCCCAAGTGTGAGCTTGTGATTCAGTGTGAGGCTTGGAGGCCCAAGGCTG 743
|||||
Db 692 tactatggtgcccaagtgctgaatttgatctcagtgtgagaccccttgaggcccaagagctg 751
OY 744 GGTACCATGAGCTGTACTACCCCTTTGGAAACTTCACTTCACTCACAGTGTGCTTC 803
|||||
Db 752 ggtacatactgacttactaccccttgggaaacttgcagcttccagctccacagtgctgcttc 811
OY 804 AGCTGCTGTAAGGAAGAACTTAACTACGGGATGGAAGAAACCACTGTGACCATTTTGA 863
|||||
Db 812 agctgtctgaaagaaacaaacttaacgtggatctgaaagaacccacccgtgagacatttgg 871
OY 864 AACTGTGATCTTCAGAACCAACCTGTCAAGTGTGAGGCTGTATCAGCAGCA 923
|||||
Db 872 aactgtcatctccagaaacaaacttgcagatctcagtgtgagaccccttcatcagacaa 931
OY 924 GATTTGGGATCATGAACCTGTAGCCATCCCTGGCCAGCTTCACTTACCTGTGCATGT 983
|||||
Db 932 gatcttggaatactgaaacttgcacatcccttggccagcttcaacttacccttgcagt 991
OY 984 ACCCTGATCTGCAGAAAGAACTGATTAATTTGGGAAGAAACCACTTTGTGATATA 1043
|||||
Db 992 accttcatctgtccgaagaaacttgatctaaatctgggaagaaagaacacatctgttaata 1051
OY 1044 TCTGGAATCTGTCAAAATCTAGTCCAAATATGTCAAAAATTTGCAAAAATTTTCAATG 1103
|||||
Db 1052 tctggaatctgttcaaatctctagctcaataatgttcaaaaatctggacaaaagtcttcaatg 1111
OY 1104 AATTAAAGAGGAGATTTAAACCCCTCTTCAATTCAGTGGCAGTCATGGTATCTGCATTC 1163
|||||
Db 1112 attaaaggaagtgatataaaccccttcttcatctcagctgagcatgttactgcttc 1171
OY 1164 TCTGGTTGGCATTTATCATTTTGGCTGGCAAGGATTAATAAAGGAAGAAATCCAG 1223
|||||
Db 1172 tctgggttggaacttatacatcttgctggcaaggaatcttaaaaagcaagaaatccag 1231
OY 1224 AGAGTATGATGACCCATTTAAATTCGCCCTTGTGTAAGAAATTTTGGAAATATCTAA 1283
|||||
Db 1232 agaagatgaatgacccaataataatcgcccttggtaagaanaaatcttggaaataactaa 1291
OY 1284 AATATCATGAGATTCCTTTAAATTCCTTCCATGAACGCTTTTGTGTGTGGCACCTCTTACGT 1343

|||||
Db 1292 aaatcaagatccctttaaaatcccttccatgaaacgttttctgtgtggaacccctcaagt 1351
OY 1344 CAACATGAAGTGTG-TTCCCTGATGATCTGGGAAGATTTTACCACCAACAGTTTC 1402
|||||
Db 1352 caaacaatgaatgtgttcccttccatgacatctgggaagatcttctacatgacaacagctc 1411
OY 1403 CTTCAGCTTCCATTTGCGCCCTCATTTATTCCTCAACCCCAAGCCCAAGGTGTTATAC 1462
|||||
Db 1412 cttaagcttccatttgcgccctcatattatccctcaacccccccagcccaagtggttatac 1471
OY 1463 AGCTACACTTTTGTCTTTTCTGAGAGAAACAAATTAAGCAAT-AAGGAAAGATTTCA 1521
|||||
Db 1472 agcccaacttcttgccttcttctgaagaacaataaagacataaaggaagatca 1531
OY 1522 TGTGATATTAAGATAGGCTGACTTGTCTCTTCTTGTGACTTGTGTTTGTGATTAATTC 1581
|||||
Db 1532 tgtggaataataaagatgagctgacttgccttcttctgactctgttcttcaagttcaatlc 1591
OY 1582 AGTGTGTACTTGTATGACAGACACTTCTAATGAAGTGCATAATTTGATATCATGTGAT 1641
|||||
Db 1592 agtgcgtacttgaatgacagacacttcaatgaagtgcaaatgtgatacatatgtgat 1651
OY 1642 ATGACATCACTTTTCTTGGAGATCAAAATTTCAAGTGTCTGTCTGTATCTGTGAGTAC 1701
|||||
Db 1652 atggaacttgcttcttctgagatcaaatcttcaagctgtcttctgtatatacttgvgaagta 1711
OY 1702 ACTCTTATGAAGAAATTTCAAAAGTGTACGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTT 1761
|||||
Db 1712 actcttataagaagatcaaaaagcttaagctctctctcttcttcttcttcttcttcaacccaagtgaa 1771
OY 1762 TGGGCTCTGCTCAAGTGTGAAGAGTCCATTTGTGACATGTAGCCTGCGCTGTGAAAT 1821
|||||
Db 1772 tggggtcctgctcaagttgaagagttcattatgacgttagccctgcgcgtctgaaat 1831
OY 1822 GGACCATCTATTTTAACTGCGCTTCAAGGCTCCCAAGCTTCTTCAAGCCCAAGCTCTTTTTC 1881
|||||
Db 1832 ggaacatctctatttcaacgtgcttca-gcttcccaacttctcagccaactcttcttct 1890
OY 1882 AGTGGCTGTACTTCCACACCTAGATCATGATGAGTGCACCAAAAGAGAGAGAGAGA 1941
|||||
Db 1891 agtggcgtacttccacacacttagcatctcagtgagccaagcaaaaggaagagagaga 1950
OY 1942 AATAGCGTGGCGGTTTTTAACTTTGGGGTTTTGCTGTTTCTTTTATGAGACCCATTC 2001
|||||
Db 1951 aatagccgtgcgtcttctttagtttgggtgttgcgttcttcttcttctttagagaccatc 2010
OY 2002 CTATTTCTTATAGTCAATGTTCTTTTATACGATATTATATGATTAAGAAACATCACTGA 2061
|||||
Db 2011 ctatttctataagtaaatgttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2070
OY 2062 AATGTACTCTGAAGTGCATCTCTTTGATGTCAATGGAAGACTTAAACAGGTGAGAGA 2121
|||||
Db 2071 aatgtactctgcaagtgacatcttcttgaatgtcatatggaagagtttaaacaggtggaga 2130
OY 2122 AATTCCTGATTTCAAAATGATGCTCTTCCCTTCCCTGGCCCAAGAACTTTATGACAT 2181
|||||
Db 2131 aatcccttgatcccaatgaatgacttcccttcccttcccttcccttcccttcccttccact 2190
OY 2182 TACCTAGATTTCTACATATTTCTTTAAATTTTCAATCTCAGGCTCCCTCAACCCCA 2235
|||||
Db 2191 tacttagattctataatcttctttaaatttcatctcaggtcccttccctcaacccac 2244

RESULT 8
US-60-172-373-15742
; Sequence 15742, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequences, and Single Nucleotide Polym

FILE REFERENCE: GX-0006 P
CURRENT APPLICATION NUMBER: US/60/172.373
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 25, 772
SOFTWARE: PERL Program
SEQ ID NO 15742
LENGTH: 2387
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 331616.2
US-60-172-373-15742

Query Match 94.3%; Score 2129.6; DB 49; Length 2387;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2201; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

QY 25 ACCTGACGACACA-GCACACTCCCTT-GGCAAGACCTGAGACCCCTGTGTAGT-CAA 81
DB 32 accgcagcacaagcacactcccttggcagaagacctgaagcccttgcctaagtcctaa 91
QY 82 GAGGCTCAATGCGCTGCAGAGAAGACTAGAGAAGACCAGCAAGCCATGATTATTCAT 141
DB 92 gaggtcacaatgggctgcagaagaactagagaagaccaaagcacaatgatacttccat 151
QY 142 GAAATGTGAGAGCACCAGAGGACTTATGAAACATCTTCAAGTTGTGGGGTGACAA 201
DB 152 ggaatgtcagagacccagagaggaactatagaaactcttcaagcttgaggggcgaacaa 211
QY 202 TGGCTCTTGTGATTCTCTGGACATCATGGAACCTACTGCTGACTTACCATTTATCTG 261
DB 212 tgcctcttgcattcttcctgcgcacatcatcagaaacgactctggaactaccatattctg 271
QY 262 AAAAACCCATGAACCTGGCAAAAGGCTAGAAGATTCTCCGAGACATTTACACAGATTAG 321
DB 272 aaaaaccatgaactctgcagaaggtctagaagatctctgcagagaataataacagatttag 331
QY 322 TTGGCATACAAAACAGCGGAAATTGATATCTGAGAAAGACTCTGCCCTTCAGTGGTT 381
DB 332 ttgcatacaaaaacaagcggaattgatactctgagaagactctgccttccagtcgtc 391
QY 382 CTTACTCTGATTGATGAAATCCGAAAGTATGAGAGAATATGAGCTGGGTGGGAACCAACA 441
DB 392 cttaactctgataagaaatcccgagaagaatagagaataatagaaatctgaggaaacaca 451
QY 442 AATCTCTCATGAAGAGACAGAGAACTGGGAGATGGTGAGCCCAACAACAAGAAGACA 501
DB 452 aatctctcaactgaagaagaagagaaactggggagatggctgagcccaacaagaagaaca 511
QY 502 AGGAGACTGCGTGAGAGATCTATATCAAGAGAAACAAAGATGACGGCAAAATGGAACGATG 561
DB 512 aggaagactcgatgagaatctataatcaagaagaagaatgacggaataatgagaagatg 571
QY 562 ACCGCTGCCACAACCTAAAGGCAAGCCCTCTGTATACAGCTTCTTGGCAGCCCTGGTCAT 621
DB 572 accgcctgcacaacaactaaagcagccctctgttaacagactctcttgcaagccctggtcat 631
QY 622 GCAGTGCCATGAGATGTGTAGAAATCATCAATATACACACTGCAACTGATGTATGG 681
DB 632 gcagtgccatlgagaaatctgtagaaatcatcaataataataactgcaactgtatgttg 691
QY 682 GGTACTATGGGCCCCAGTGTACGTTGTGATTGAGTGAAGCCCTTGGAGGCCCCAGAGC 741
DB 692 ggtactatgggccccagtgctcagttgtgattcagtgtagcccttggaaggccccagagc 751
QY 742 TTGGTACCATGAGACTGATACACCCCTTGGAAACTCAGCTTACGCTACACAGTGTGCT 801
DB 752 ttgggtaccatgagactgatacactctcttggaataactcaactcaagctcagaatgtgctc 811
QY 802 TCAGCTCTCTGAAGAAACAACCTTAAGTGGATTGAGAAACCACTGTGACCATTTG 861
DB 811 tcagctctctgaagaaacaaccttaagtggaattgagaaacacactgtgacattttg 861

DB 812 tcagctgctcgaaggaacaaacttaactggaattgagaagaacacactgtgagaccattg 871
QY 862 GAAACTGCTCATCTCCAGAACCAACCTGTCAAGTGATTCAGCTGTGAGCCTCTATCAGCAC 921
DB 872 gaaactgctcatctccagaaacaaactgtcaagtgatctcagtgtagagctctcatcaagcac 931
QY 922 CAGATTTGGGGATCATGAACTGTAGCCATGCCCGGCGCAGCTTCAGCTTACGCTGCAT 981
DB 932 cagatctggggatcatgaaactgtagccatcccccgccagcttcaagcttcaactctgcac 991
QY 982 GTACCTTCATCTGCTCAGAAAGAACTGATTAATTTGGGAAGAAACCAATTTGTGANT 1041
DB 992 gtaccttcattctgctcagaagaactgagtaatttggaagaagaagaacacattgtgacat 1051
QY 1042 CATCTGGANCTGCTCAAAATCTTAGTCCAAATATGTCAAAAATGGACAAAAGTTCTCAA 1101
DB 1052 catctgaaatctgctcaaatccctagccaatgccaataatggaacaaaagttcttcaa 1111
QY 1102 TGATTAAAGAGAGTGATTAATTAACCCCTTCATTTCCAGTGGCAGTCAAGTTACTGCAT 1161
DB 1112 tgattaaagagtgatataaaccctctcatctcagtgagatgcaatgcttactgcacat 1171
QY 1162 TCTCTGGGTTGGCATTTATCATTTTGGCTGCAAGAGATTAAAAAAGGCAAGAAATCCA 1221
DB 1172 tctctgggttgcaattatcatcttgctgcagaagagatcaaaaaagcagaagaatcca 1231
QY 1222 AGAGAAGTATGATATGCCATATTAAATCGCCCTTGTGTGAAGAAATTTCTTGAATACT 1281
DB 1232 agagaagatgaaatgaaacccatataatcgcctctggtgaaagaagaattcttgaataact 1291
QY 1282 AAAATATGATGATCCTTTAAATCTCCAGTAAGAAACGTTTGTGGTGGACCTCCAC 1341
DB 1292 aaaaatcatgaaatccctttaaacccttccatgaaacgcttgatgagtggaacccctcac 1351
QY 1342 GTCAACATGAAAGTGTG-TTCCTTCAGTGCATCGGGAAGATTCTCCAGCCAGCAAGAGT 1400
DB 1352 gtcaaacatgaaagtgtgttccctcagtgatcctcggaaggttcttaactgacaaacgct 1411
QY 1401 TCGTTACGCTTCCATTTTCGCCCTTCATTTATCCCTCAACCCCAAGCCCAAGGTTTAT 1460
DB 1412 tccctcagctcccatctcgcgcccatatlatccctcaacccccagcccaagtgctatc 1471
QY 1461 ACAGCTCAGCTTTTGTCTTTCTTGAGAGAGAAACAATTAACAGCAT-AAGGGAAGAGATT 1519
DB 1472 acagctcagctcttcttcccttcgaagagaacaaaataacacataaggaagaagatt 1531
QY 1520 CATGTGGAATATAAGATGAGCTGACTTGTGCTTCTTGAATCTTGTGATTTCAAT 1579
DB 1532 catgtggaataataaagatgagcttgccttcttgcacttcttgcacttgcacttgcact 1591
QY 1580 TCACTGCTGATCTGATGACAGACACTTCTAATGAAGTGAATTTGATNACATATGTGA 1639
DB 1592 tcactgctgactgatagacagacactcttaaaagatgcaaaattgatacatatgga 1651
QY 1640 ATATGAGACTGAGTTTCTTGAGATCAAAATTTACAGTCGTCGTCGATACTGTGGAGGT 1699
DB 1652 atatgagactgagtttcttgagatcaaaatctcaagtcgctctctgtatactatgaggagc 1711
QY 1700 ACACCTTATAGAAAGTTCAAAAAGTCTACGCTTCCTCTTCTTCTTAATCTCAGTGAAGT 1759
DB 1712 acactcttatagaaagttcaaaaaagttcagcttcccttcttcttaactccagtggaat 1771
QY 1760 AATGGGCTCTGCTCAAGTTGAAAGAGTCTATTGCACTGTAGCCTGCGCCTGTGTGAA 1819
DB 1772 aatgggctctgctcaagttgaaagagttcattatgcaactgtagccctgcgcctgtgaa 1831
QY 1820 TTGGACCATCCTATTAACTGAGGCTTCAGGCTCCCAAGCTTCTTCAAGCAACCTCTTTT 1879
DB 1832 ttggaccatcctatttaactgaggtctcaagcttcccaagcttcttcaagcaacctctcttc 1880
QY 1880 TCAGTTGGCTGACTTCCACACACTAGATCTCATAGTGGCCAAAGCAAGAGAGAGAAGA 1939
DB 1891 tcagttggctgacttccacacactagatctcatatgagtgccaaagagagagaaga 1950

127 GGACTTATGGAACATCTTCAAGTGTGGGGGTGACAAATGCTCTTGTGATTTCTTGCC 186
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204
2205
2206
2207
2208
2209
2210
2211
2212
2213
2214
2215
2216
2217
2218
2219
2220
2221
2222
2223
2224
2225
2226
2227
2228
2229
2230
2231
2232
2233
2234
2235
2236
2237
2238
2239
2240
2241
2242
2243
2244
2245
2246
2247
2248
2249
2250
2251
2252
2253
2254
2255
2256
2257
2258
2259
2260
2261
2262
2263
2264
2265
2266
2267
2268
2269
2270
2271
2272
2273
2274
2275
2276
2277
2278
2279
2280
2281
2282
2283
2284
2285
2286
2287
2288
2289
2290
2291
2292
2293
2294
2295
2296
2297
2298
2299
2300
2301
2302
2303
23

QY	1244	TTAAATGCGCCCTGGTGAAGAAAATTCCTGGAAATACAAAAATCATAGAGATCCCTTTAA	1303
Db	1207	TTAAATGCGCCCTGGTGAAGAAAATTCCTGGAAATACAAAAATCATAGAGATCCCTTTAA	1266
QY	1304	TCCTTTCATGAAGCGTTTGTGTGTGGACACTCTCACTGTCMAACATGAAGTGTG - TTCC	1362
Db	1267	TCCTTTCATGAAGCGTTTGTGTGTGGACACTCTCTAGTCAACATGAAGTGTGTTC	1326
QY	1363	TTCAAGTCACATCGGGAAGATTTCTACCCGACCAACAGTTCTTACGTTCCATTTCCGCC	1422
Db	1327	TTCAAGTCACATCGGGAAGATTTCTACCTGACCAACAGTTCCCTTACGCTTCATTTTCACCC	1386
QY	1423	CTCATTTATCCCTCAACCCCCAGCCCAAGTGTATTACAGCTCAGATTTTGTCTTTT	1482
Db	1387	CTCATTTATCCCTCAACCCCCAGCCCAAGTGTATTACAGCTCAGATTTTGTCTTTT	1446
QY	1483	CTGAGGAGAAAACAATTAAGACAT - AAGGAGAAAGATTCATGTGGAATTATAAAGATGGCT	1541
Db	1447	CTGAGGAGAAAACAATTAAGACATTAAGGAGAAAGATTCATGTGGAATTATAAAGATGGCT	1506
QY	1542	GACCTTGCTCTTTCCTGACATCTGTGTTTCAAGTTTCATTCAGTGCCTGCTACTGTATGACAG	1601
Db	1507	GACCTTGCTCTTTCCTGACATCTGTGTTTCAAGTTTCATTCAGTGCCTGCTACTGTATGACAG	1566
QY	1602	ACACTTCTAAATGAAGTGCACAAATTTGATACATATGTAATGAGTACAGTTTCTTGCA	1661
Db	1567	ACACTTCTAAATGAAGTGCACAAATTTGATACATATGTAATGAGTACAGTTTCTTGCA	1626
QY	1662	GATCAAAATTCACAGTGTCTCTTCTGTATATCTGTGAGGTACACACTTATTACAAAGTTCAAA	1721
Db	1627	GATCAAAATTCACAGTGTGTCTGTGTGTATAC - GTGAGGTACACACTCT - - - ATGAGTCAAA	1680
QY	1722	AAGTCTACGCTCTCTCTTCTTCTTAACTCAGTGAATATGAGGCTGCTGCTCAAGTTGA	1781
Db	1681	AAGTCTACGCTCTCTCTTCTTCTTAACTCAGTGAATATGAGGCTGCTGCTCAAGTTGA	1740
QY	1782	AAGAGTCTAATTTGGCACTGTAGCCTGCGCGTCTGTGAATTTGAGCAATCTTAATTAACGTG	1841
Db	1741	AAGAGTCTAATTTGGCACTGTAGCCTGCGCGTCTGTGAATTTGAGCAATCTTAATTAACGTG	1800
QY	1842	CTTCAAGGCGCCGCCACCTCTTGAGCACACTCTCTTTTCAGTTGGCTGACTTCCACACC	1901
Db	1801	CTTCA - GCCCTCCACACTCTTGTAGCACACTCTCTTTTTCAGTTGGCTGACTTCCACACC	1859
QY	1902	TAGCATCTCATGAGTGCACAAGCAAGAAAAGAGAGAGAAATAGCCTGGCGGTTTTTT	1961
Db	1860	TAGCATCTCATGAGTGCACAAGCAAGAAAAGAGAGAGAAATAGCCTGGCGGTTTTTT	1919
QY	1962	AGTTTGGGGGTTTTGCTGTTTTCTTTTATGAGACCAATTCCTATTTCTTATAGTCAATGT	2021
Db	1920	AGTTTGGGGGTTTTGCTGTTTTCTTTTATGAGACCAATTCCTATTTCTTATAGTCAATGT	1979
QY	2022	TTCTTTTATCAGAGATTTATTTAGTAGAANAATCAGCTGAATGTAGAGTGCAGAGGACA	2081
Db	1980	TTCTTTTATCAGAGATTTATTTAGTAGAANAATCAGCTGAATGTAGAGTGCAGAGGACA	2039
QY	2082	TCCTTTTATGTCATATGGAAGAGTTAAACAAGTGGAGAAAATTCCTTATTTACACATGA	2141
Db	2040	TCCTTTTATGTCATATGGAAGAGTTAAACAAGTGGAGAAAATTCCTTATTTACACATGA	2099
QY	2142	AATGCTCTCTTTCCCGCTGCCCCAGAACTTTTATCCACTTACCTTAGATTTCAATATTTG	2201
Db	2100	AATGCTCTCTTTCCCGCTGCCCCAGAACTTTTATCCACTTACCTTAGATTTCAATATTTG	2159
QY	2202	TTTAAATTTTCATCTCAGGCGCTCCGCAACCCGAC 2235	
Db	2160	TTTAAATTTTCATCTCAGGCGCTCCGCAACCCGAC 2193	

RESULT 12
US-08-340-539-1
; Sequence 1, Application US/08340539

```

1 GENERAL INFORMATION:
2 APPLICANT: Tedder, Thomas F.
3 APPLICANT: Kansas, Geoffrey S.
4 TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
5 TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
6 NUMBER OF SEQUENCES: 11
7 CORRESPONDENCE ADDRESSES:
8 ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
9 STREET: Ten Post Office Square
10 CITY: Boston
11 STATE: MA
12 COUNTRY: USA
13 ZIP: 02109
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/340,539
22 FILING DATE: 16-NOV-1994
23 CLASSIFICATION: 514
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/008,459
27 FILING DATE: 25-JAN-1993
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/983,606
30 FILING DATE: 30-NOV-1992
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/862,483
33 FILING DATE: 02-APR-1992
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 07/770,608
36 FILING DATE: 03-OCT-1991
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 07/737,092
39 FILING DATE: 29-JUL-1991
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 07/730,503
42 FILING DATE: 08-JUL-1991
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: US 07/700,773
45 FILING DATE: 15-MAY-1991
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: US 07/313,109
48 FILING DATE: 21-FEB-1989
49 ATTORNEY/AGENT INFORMATION:
50 NAME: Heine, Holliday C.
51 REGISTRATION NUMBER: 34,346
52 REFERENCE/DOCKET NUMBER: DPCI-318XX
53 TELECOMMUNICATION INFORMATION:
54 TELEPHONE: (617) 542-2290
55 TELEFAX: (617) 451-0313
56
57 TELEX: 940675
58
59 INFORMATION FOR SEQ ID NO: 1:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 2330 base pairs
62 TYPE: nucleic acid
63 STRANDEDNESS: single
64 TOPOLOGY: linear
65
66 MOLECULE TYPE: CDNA
67 HYPOTHETICAL: NO
68 ANTI-SENSE: NO
69 FEATURE:
70 NAME/KEY: CDS
71 LOCATION: 53..1210
72 PUBLICATION INFORMATION:
73 DOCUMENT NUMBER: US 07/700,773
74 FILING DATE: 15-MAY-1991
75
76 US-08-340-539-1

```

Query Match 92.4%; Score 2087.6; DB 7; Length 2330;

Best Local Similarity 98.5%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

OY	44	CCCTTGGCAAGGACCGGACACCCCTTGCTGTAAAGTCAADAGGCTCAAGGGCTGCAAG	103
Db	7	CTTTTGGGCAAGGACCTGGAACCCCTTGCTGTAAAGTCAADAGGCTCAAGGGCTGCAAG	66
OY	104	AACTAGAAGAGGACCAAGCAAAAGCCATGATATTTTCATGGAATGTCAGAGCACCCAG	163
Db	67	AACTAGAAGAGGACCAAGCAAAAGCCATGATATTTTCATGGAATGTCAGAGCACCCAG	126
OY	164	GCACCTTAGAACAATCTTCAAGTTGTGGGGGTGACAAATGCTGTGTGATTTTCTGGC	223
Db	127	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGACAAATGCTGTGTGATTTTCTGGC	186
OY	224	ACATCATGGAACCTACTGCTGCACTTACCATTTATTTGTAAAAACCCATGAACTGGCAAG	283
Db	187	ACATCATGGAACCGACGACGCTGGACTTACCATTTATTTGTAAAAACCCATGAACTGGCAAG	246
OY	284	GGCTAGAGAATTCGCGGACACAATTAACAGATTTAGTTGGCATACAAAACAAAGCGGA	343
Db	247	GGCTAGAGAATTTCTGCCGAGACAAATTACACAGATTTAGTTGCCATACAAAACAAAGCGGA	306
OY	344	AATTGATATCTGGAGAAGACTCTGCCCTTCACTAGCTGTTCTACTACTGGATAGAAATCG	403
Db	307	AATTGATATCTGGAGAAGACTCTGCCCTTCACTAGCTGTTCTACTACTGGATAGAAATCG	366
OY	404	GAAATAGGAGGAATATGACGCTGGGTGGGAAACCAACAATCTTCACTGAAGAAGCAGA	463
Db	367	GAAATAGGAGGAATATGACGCTGGGTGGGAAACCAACAATCTTCACTGAAGAAGCAGA	426
OY	464	GAACTGGGGAGATGAGTGAGGCCCAACAACAAGAAGAAAGAGAGGACTGGTGGAGATGTA	523
Db	427	GAACTGGGGAGATGAGTGAGGCCCAACAACAAGAAGAGAGGAGACTGGTGGAGATGTA	486
OY	524	TATCAAGAGAACAAGATGACAGGCAAAATGGAACGATGACGCGCTCCACAATCTAAAGGC	583
Db	487	TATCAAGAGAACAAGATGACAGGCAAAATGGAACGATGACGCGCTCCACAATCTAAAGGC	546
OY	584	AGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGTGTATGCAATGGCCATGGAATGTGT	643
Db	547	AGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGTGTATGCAATGGCCATGGAATGTGT	606
OY	644	AGAAATCATCAATTAATCACACGTCGAACGTGTATGTTGGGGTCTATTTGGGCCCCAGTGTCA	703
Db	607	AGAAATCATCAATTAATTAACCTGTGCACATGTGTATGTTGGGGTCTATTTGGGCCCCAGTGTCA	666
OY	704	GCTTGTGATTCAGTGTGAGGCTTTTGGAGGCCCCAGAGAGCTGGGTATACATGAGACTGTACTCA	763
Db	667	GTTTGTGATTCAGTGTGAGGCTTTTGGAGGCCCCAGAGAGCTGGGTATACATGAGACTGTACTCA	726
OY	764	CCCCCTTTGGAACTTACAGCTTCAAGCTCACAGTGTGCTTCAAGCTGCTGTGAAGAACAA	823
Db	727	CCCCCTTTGGAACTTCAACTCAACGTACAGTGTGCTTCAAGCTGCTGTGAAGAACAA	786
OY	824	CTTAACTGGAGTTGAAGAAACACACTGTGACCATTTTGGAAACTGCTATCTCCAGAAC	883
Db	787	CTTAACTGGAGTTGAAGAAACCACTGTGACCATTTTGGAAACTGCTATCTCCAGAAC	846
OY	884	AACCTGTCAAGTATTCAGTGTGAGGCTTATCAGACACAGATTTTGGGATCATGAACTG	943
Db	847	AACCTGTCAAGTATTCAGTGTGAGGCTTATCAGACACAGATTTTGGGATCATGAACTG	906
OY	944	TAGCAATCCCCCTGGCCAGCTTCAAGCTTACCTGTGATGTACCTTCAATCTGTCCAGAAAG	1003
Db	907	TAGCAATCCCCCTGGCCAGCTTCAAGCTTACCTGTGATGTACCTTCAATCTGTCCAGAAAG	966
OY	1004	AACGAGATTAATTTGGGAAGAAAGAAACCAATTTGTGAATCATCTGGAATCTGGTCAAAATCC	1063
Db	967	AACGAGATTAATTTGGGAAGAAAGAAACCAATTTGTGAATCATCTGGAATCTGGTCAAAATCC	1026
OY	1064	TATGTCAATATGTCAAAAATTTGGACAAAAGTTTCTCAATGATTTAAGAGGCTGATTAATA	1123

D	b	1027	TAGTCCAAATATGTCAAAAAATTGGACAAAAGTTTCTCAATGATTTAAGAGGGGTGATTTAA	1086
Q	y	1124	CCCCCTCTCATTTCCAGTGGGACAGTCATGGTTACTGCATTTCTCTGGGTTGGCATTTATCAT	1183
D	b	1087	CCCCCTCTCATTTCCAGTGGGACAGTCATGGTTACTGCATTTCTCTGGGTTGGCATTTATCAT	1186
Q	y	1184	TTGGCTGGCAAGAGATTTAAAAAAGGCAAGAAATCCAAAGAAAGTATGAATGACCCATA	1243
D	b	1147	TTGGCTGGCAAGAGATTTAAAAAAGGCAAGAAATCCAAAGAAAGTATGAATGACCCATA	1206
Q	y	1244	TTAAATGCCCCCTTGGTGAAGAAAAATTCCTGGAAATACATAAATCATAGATTCCTTTAAA	1303
D	b	1207	TTAAATGCCCCCTTGGTGAAGAAAAATTCCTGGAAATACATAAATCATAGATTCCTTTAAA	1266
Q	y	1304	TCCCTTCATGAAAGCTTTTGTGTGGTGGCACCTCCCTACGTCAAAACATGAATGTGTG-TTCC	1362
D	b	1267	TCCCTTCATGAAAGCTTTTGTGTGGTGGCACCTCCCTACGTCAAAACATGAATGTGTGTCC	1336
Q	y	1363	TTTCAGTGCATCTGGGAAGATTTTCAACCCGACCAACAGTTCTCTCAGCTTCCATTTGGCC	1422
D	b	1327	TTTCAGTGCATCTGGGAAGATTTTCAACCCGACCAACAGTTCTCTCAGCTTCCATTTGGCC	1386
Q	y	1423	CTCATTTATCCCTCAACCCCAAGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTT	1482
D	b	1387	CTCATTTATCCCTCAACCCCAAGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTT	1446
Q	y	1483	CTGAGGACAAAACAAATTAAGACCAT-TAACGGAAAGGATTCATGTGGAAATTAAGATGGCT	1541
D	b	1447	CTGAGGACAAAACAAATTAAGACCATTAAGGGAAGGATTCATGTGGAAATTAAGATGGCT	1506
Q	y	1542	GACTTTGCTCTTTCTTGAAGCTCTGTGTTTTCAGTTTCAATTACAGTCTGTACTTGTATGACAG	1601
D	b	1507	GACTTTGCTCTTTCTTGAAGCTCTGTGTTTTCAGTTTCAATTACAGTCTGTACTTGTATGACAG	1566
Q	y	1602	ACACTTCTAAATGAAGTGCAAAATTTGATACATATATGTGAAATATGACATCAGTTTCTTGCA	1661
D	b	1567	ACACTTCTAAATGAAGTGCAAAATTTGATACATATATGTGAAATATGACATCAGTTTCTTGCA	1626
Q	y	1662	GATCAAAATTTACAGTCGCTCTGTATATCTGTGGAGGACACTCTTATAGAAAGTCCAAA	1721
D	b	1627	GATCAAAATTTACAGTCGCTCTGTATATCTGTGGAGGACACTCTTATAGAAAGTCCAAA	1680
Q	y	1722	AAGTCTACGCTCTCTCTTCTTCTTAACACGACGTGAAGTAAGGGGTCCTGCTCAAGTTGA	1781
D	b	1681	AAGTCTACGCTCTCTCTTCTTCTTAACACGACGTGAAGTAAGGGGTCCTGCTCAAGTTGA	1740
Q	y	1782	AAGAGTCTATTTGACAGTGTAGCCTCGCCCTGTCTGAATTTGGACCATCTATTTAACTGG	1841
D	b	1741	AAGAGTCTATTTGACAGTGTAGCCTCGCCCTGTCTGAATTTGGACCATCTATTTAACTGG	1800
Q	y	1842	CTTCAGGCTCCCAACCTCTTTCAGCCACGCTCTTTTTCAGTTGGGGTGCATTCACACC	1901
D	b	1801	CTTCA-GCCTCCCAACCTCTTTCAGCCACGCTCTTTTTCAGTTGGGGTGCATTCACACC	1859
Q	y	1902	TAGCATCTCATGAGTGGCCACAAAGAGAGAGAGAGAAATAGCCTGGCGGCTTTTTTT	1961
D	b	1860	TAGCATCTCATGAGTGGCCACAAAGAGAGAGAGAGAAATAGCCTGGCGGCTTTTTTT	1919
Q	y	1962	AGTTTGGGGGTTTGTGCTGTCTTTTATGAGACCATTCCTATTTCTTATATGCAATGT	2021
D	b	1920	AGTTTGGGGGTTTGTGCTGTCTTTTATGAGACCATTCCTATTTCTTATATGCAATGT	1979
Q	y	2022	TTCTTTTATCACGATATATATAGTAAGAAACATCACGAAATGCTATGCTGCAAGTACA	2081
D	b	1980	TTCTTTTATCACGATATATATAGTAAGAAACATCACGAAATGCTATGCTGCAAGTACA	2039
Q	y	2082	TCTCTTTATATCATATATGGAAGAGTTAAACAGGTGAGAAATTCCTTGATTCACAATGA	2141
D	b	2040	TCTCTTTATATCATATATGGAAGAGTTAAACAGGTGAGAAATTCCTTGATTCACAATGA	2099
Q	y	2142	AATGCTCTCTTTTCCCTGCCCCAGAACTTTTATCCACTTACCTAGATTCATATATTC	2201
D	b	2100	AATGCTCTCTTTTCCCTGCCCCAGAACTTTTATCCACTTACCTAGATTCATATATTC	2159

QY	1474	TTGTCCTTTCTGAGGAGAAACAATTAAGACAT - AAGGAAAGGATTCATGTGGAATATA	1532
Db	901	ttgtctttcttctgagagaaacaataagaacataaaggaaagatctctgagatata	960
QY	1533	AAGATGGCTGACTTTCCTCTTCTGACTCTTGTTCCTGATTTCATTTCAGTGCCTGACT	1592
Db	961	aagatgctgactttgtctctcttcttgactctctgtttcagttccaattcagtgctgact	1020
QY	1593	TCATGACAGACACTTCTAAATGAAGTGCAAATTTGATACATATGTGAATATGACTCAGT	1652
Db	1021	tgatcacagacacttctaataitgaatgcaaatltatatactatgtaataatgactcaat	1080
QY	1653	TTTCTTGACGATCAAAATTTACGCTGCTCTTGTATCTGATGAGAGTACACTTATAGA	1712
Db	1081	ttctctgagatcaaatlttcaactgctgtctctgtatctatgtaggtatcacttataga	1140
QY	1713	AAGTCAAAAAGTCTACGCTCTCTCTTCTTCTTAACTCCAGTGAATATGGGGTCTTGC	1772
Db	1141	aagttcaaaaagttcagctctctctcttcttctaactcagtgaaatggtgtctgc	1200
QY	1773	TCAACTGAAAAAGTCATTTGCACTGATGCTGCGCTGCTGTAAATTTGAGCAATCCGA	1832
Db	1201	tcaagtctgaagaagctcaatttgcactgttagcttcgctgcgtgaaatggaaccacta	1260
QY	1833	TTTAACTGGCTTCAGAGCCTTCCACACTTCTTCAGCACACTCTTCTTTCAGTTGAGCTGAC	1892
Db	1261	tttaactgcttca - gacctccacctctcttcagcacactctcttttcagtgtgctgac	1319
QY	1893	TTCCACACCTAGCATCTCATGATGTCGCAAGCAAAAGGAGAGAGAGAAATAGCTCGG	1952
Db	1320	ttccacacctgcatctatagtagtgcagaagaagagagagaaatagactctgc	1379
QY	1953	CGGTTTTTATGTTGGGGTTTTGCTGTTTTCTTCTTATGAGACCCATTCCTATTTCTTAT	2012
Db	1380	ctgttttttagtttgagggttttgcgttcttctttaaagagaccattccattcttat	1439
QY	2013	AGTCAATGTTCTTTATTCAGCATATTTATAGTAAGAAAACTCATGAAATGTAGCTG	2072
Db	1440	agtcactgttcttcttatacagatatattagtaagaacaactcactgaatgctagctg	1499
QY	2073	CAAGGACATCTCTTGAATGCATATGAGAGGTTAAACAGGTGAGAGAAATTCCTGAT	2132
Db	1500	caagtgacatctcttctgatagtcaatagaaaggttaacaacagtgagaaatctctgat	1559
QY	2133	TCACATGAATAGCTCTCTCTTCCCTGCCGCCACAGACCTTTATTCACATTTAGATTC	2192
Db	1560	tcaacaatgaatgctctctctcttccctgcgccacagacctttatccacttacctgattc	1619
QY	2193	TACATATCTTTAAATTCATATCTCAGGGCTCCCTCAACCCAC	2235
Db	1620	tacatatctttaaatttcattctcaggtccctccctaaccacac	1662
RESULT 15			
US-60-164-285-5456			
Sequence 5456, Application US/60164285			
GENERAL INFORMATION:			
APPLICANT: Ma, Xiao-Jun			
TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, treatment			
FILE REFERENCE: 3214			
CURRENT APPLICATION NUMBER: US/60/164,285			
CURRENT FILING DATE: 1999-11-05			
NUMBER OF SEQ ID NOS: 8259			
SEQ ID NO 5456			
LENGTH: 1788			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-60-164-285-5456			
Query Match 71.1%; Score 1605.4; DB 48; Length 1788;			
Best Local Similarity 99.4%; Pred. No. 0;			

	Matches 1653;	Conservative	0;	Mismatches	6;	Indels	4;	Gaps
QY	576	CTAAAGGACCCCTCMGTTCACACAGCTTCTTGCCACCCCTGGTCATGCAAGTGGCCATTGGA	635					
Db	1	ctaaaggcagccctcgtttacacagctctctgcagccctggcagcagtgccatgga	60					
QY	636	GAATGTGTGAATTCATCATATAATTCACACTGCAACTGCATGTGATGTGGGTACTATGGAGCCC	695					
Db	61	gaatgtgtgaataatcatataataataactgaactgtagtgggttaactatggccc	120					
QY	696	CAGTGTACGCTTGTGATTTACGTGTAGCCCTTTGGAGGCCCCAGAGCTGGGTACATTGAC	755					
Db	121	cagtgtaacgttgtgtatcagttgtagcccttbgagccccaagagcttggtaacatggagc	180					
QY	756	TGTACTCACCCCTTTGGAAACTTCACCTTCAGGTGCACATGAGGCCCTTCAGCTGCTTGA	815					
Db	181	tgtaactcaccccttgggaaacttcagcttcaagctccagtgtagcttccagctgcttgaa	240					
QY	816	GGAAACAACCTTAACCTGGATTTGAAGAAACACCTGTGTGACCAATTTGGAAACTGGTCATCT	875					
Db	241	ggaaacaacttaacttggatltgaggaacacaccttggagccatttggaaactggtcatct	300					
QY	876	CCAGAACCAACCTGTCAATGATTCAGTGTGAGCCCTTCATCAGACACCAATTTGGGAGAC	935					
Db	301	ccagaaaccaacctgtcaagltgacgttggagcccttaacagcaccagatlttggagtc	360					
QY	936	ATGAACGTGAGCCATCCCTGGGCCAG-CTTCAGCTTTACCTGTGCATGTACTTCATCTG	994					
Db	361	atgaactgttagccatccctctggccagcccttcaagcttactcttgaatgtaacttcatctg	420					
QY	995	CTCAGAGGAACTGACTTAATTGGGAGAGAAACCAATTTGTGAATCATCTGTGAATCTG	1054					
Db	421	ctcagaaggaactagtgtaatttgggagagagaaaccattlttgaatactcttgaatctg	480					
QY	1055	GTCAAAATCCTAGTCCCAATGTGTCAAAAATTTGGCAAAAATTTCTCAATATTAAAGAGGG	1114					
Db	481	gtcaaatctcagttccaatattgtccaaaatttggacaaaagttcctcaatgattaagagggg	540					
QY	1115	TGATTAATAACCCCTCTTCATTCCAGTGGCAGTCATGGTTACTGCATTCCTGGGTTGGC	1174					
Db	541	tgattaaacccctcttcattccacgttggcagtgcatgttactgcatctctcgggttggc	600					
QY	1175	ATTTAATCAATTTGGCTGGCGCAAGAGATTAAAAAGCAAGAAATCCAGAGAGAAATTA	1234					
Db	601	atttaacatttggcttggcgaagagatltaaaaaaggcaagaaatccaaagagatltgaa	660					
QY	1235	TGACCCATTTTAATCGCCCTTGGTGTAAGAAAGAAATTTCTTGGAAATCTAAAAATCATGAGA	1294					
Db	661	tgaaccataatlaatcgcccttggtaagaaaatltcttggataactaaataatcatgaga	720					
QY	1295	TCCCTTTAAATCCTTCATGATAACGTTTTGTGTGGTGGCACCTTCCTACGTCAACAATGAA	1354					
Db	721	tccctttaaactcttccatgaaacgttlttgttggtagccactcccaagtcaaacatgaa	780					
QY	1355	TGTGTG-TTCCCTTAGTGCATCTGGAAAGATTTTACCCCGCAACAAGTTCCTTCACACTTCC	1413					
Db	781	tgltgttcccttcaatgagcatcttggagaaatlttlaacttgcacaaagtttccctcagttcc	840					
QY	1414	ATTTCGCCCTCATTTATTCCTCAACCCCGACCCACAGAGTGTTAATACGTCAAGCTGTTT	1473					
Db	841	atttcgccctcatattatcccttcaaacccccaagcttcttatacaagctcagcttctt	900					
QY	1474	TTCGCTTTTGTGAGGAGAAACAATAATGACCAT-TAAGGAAAGATTCATGTGGAATTA	1532					
Db	901	ttgtctcttcttgaaggagaaacaataaagacccaataaaggaaaggttcaatcttggagaa	960					
QY	1533	AAGATGGCTGACTTTCGCTCTTTCTTGAGCTCTGTGTTTCAAGTTCAATTCAAGTGTACT	1592					
Db	961	aagatggctgacttgccttcttcttgactctgtttcagtttcaaatcagtgctgact	1020					
QY	1593	TGATACAGACACTTCTTAATGAAGTGCAAAATTTATATCATATGTGGAATATGAGACTCAGT	1652					
Db	1021	tgaatgacgaacactcttaatatgaatltgcaaatlttatcatatgtgaaatagactcagtt	1080					

QY 1653 TTCTGAGATCAATTTGACGTCGTCCTGTTATCTGAGAGTACACTCTTATAGA 1712
|||||
Db 1081 tctctgcagatcgaattcgaatcgcgtctctctgtatctcgtgaggtacaccttataga 1140
|||||
QY 1713 AAGTTCAAAAAGTCAAGCTCTCTCTTCTTCTTCACTCAAGTGAAGTAATGGGCTCTGC 1772
|||||
Db 1141 aagttcaaaaagttcagctctctctctctctctctcagtgaaatgaggtctctgc 1200
|||||
QY 1773 TCAAGTTGAAAAGAGTCTTATTTGACGTGAAGCTGCGCTGTGTGAATGGACCATCTA 1832
|||||
Db 1201 tcaagttgaaaagagttcctatttgacacgtagcctgcgctgtgaaatgagccatccta 1260
|||||
QY 1833 TTTTACGTGGCTTCAGGCTCCGCCACTTCTTTCACGCCACTCTCTTTTTCAGTTGGCTGAC 1892
|||||
Db 1261 tttaactggtctta-gctctcccaactctctcagccaactctctctcagtlgtgctgac 1319
|||||
QY 1893 TTCACACACATAGCATCTCATGAGTGCACAGCAAAAGAGAGAAATAGCTGCG 1952
|||||
Db 1320 ttccacacactagcatctcctcagtgagtgccaagcaaaagagagagaaatagcctgcg 1379
|||||
QY 1953 CGGTTTTTAAAGTTGGGGGTTTGGCTGTTCCCTTTTATGAGACCATTCCTATTCTTAT 2012
|||||
Db 1380 ctgtttttagttggtggtttgtctgttccctttatgagcccatctctattcttat 1439
|||||
QY 2013 AGTCAATGTTCTTTTATTCACGATATATTAGTAGAAGAAACATCACTGAATGCTAGCTG 2072
|||||
Db 1440 agtcaatgttctcttatacagatatattagtaagaataacatcatcgtaaatgctagctg 1499
|||||
QY 2073 CAAGTGACATCTCTTGTGATGTCATATGGAAGATTAAACAGTGAAGAAATTCCTTGAT 2132
|||||
Db 1500 caagtgacatctctctttagtgcataiggaagagttaaaacagtgaggaatctctgat 1559
|||||
QY 2133 TCACATGAAATGCTCTCTTCCCTGCCCCGAGAACTTTTATCACACTTACCTAGATTC 2192
|||||
Db 1560 tcaaatgaaatgctctctcttccctgcgccccagacctttatccaacttaactagatlc 1619
|||||
QY 2193 TACATATTCTTTAAATTCATTCACAGGCTCCCTCAACCCAC 2235
|||||
Db 1620 tacatatctttaaattcatctcagcctcctccaacccac 1662
|||||

Search completed: October 13, 2001, 02:42:35
Job time: 10350 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 13, 2001, 00:34:07 ; Search time 607.52 Seconds
(without alignments)
8893.734 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 1 GAATTCGAGTGTGCTGCTT.....CCGCAGACACTGGAATTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2230464 seqs, 119590913 residues

Total number of hits satisfying chosen parameters: 4460928

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_NA_New:*
1: /cgnl_7/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgnl_7/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgnl_7/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgnl_7/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgnl_7/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgnl_7/ptodata/2/pna/US09_NEW_COMB.seq:*
7: /cgnl_7/ptodata/2/pna/US09_NEW_COMB.seq:*
8: /cgnl_7/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2161	95.7	2354	US-09-880-107-2306	Sequence 2306, Ap
2	2140.6	94.8	2386	US-60-278-258-2358	Sequence 2538, Ap
3	2093.2	92.7	2339	US-09-760-475-377	Sequence 377, Ap
4	1117.2	49.5	1213	US-09-760-443-684	Sequence 684, Ap
5	1117.2	49.5	1213	US-09-760-475-1506	Sequence 1506, Ap
6	1107.8	49.0	1119	PCT-US01-26675-2	Sequence 2, Appl
7	1035	45.8	1298	US-09-758-449-424	Sequence 424, App
8	1035	45.8	1298	US-09-760-443-575	Sequence 575, App
9	969.8	42.9	27780	PCT-US01-26675-1	Sequence 1, Appl
10	775	34.3	1063	US-09-758-449-373	Sequence 373, App
11	562.2	24.9	579	US-09-796-692-210	Sequence 210, App
12	562.2	24.9	579	US-09-796-692-4884	Sequence 4884, Ap
13	549.2	24.3	579	US-09-796-692-5257	Sequence 5257, Ap
14	494.2	21.9	512	US-09-796-692-8471	Sequence 8471, Ap
15	436	19.3	491	US-09-824-518-7087	Sequence 7087, Ap
16	422	18.7	508	US-09-921-378-6114	Sequence 6114, Ap
17	401	17.8	435	US-09-909-627-13597	Sequence 13597, A
18	377.4	16.7	404	US-09-909-629-24942	Sequence 24942, A
19	353	15.6	510	US-09-796-692-8405	Sequence 8405, Ap
20	350.8	15.5	358	US-09-909-627-9774	Sequence 9774, Ap
21	345.8	15.3	458	US-09-796-692-6660	Sequence 6660, Ap
22	332	14.7	359	US-09-898-888-44935	Sequence 44935, A
23	327.2	14.5	332	US-09-823-301-9431	Sequence 9431, Ap
24	325.6	14.4	378	US-09-898-888-44963	Sequence 44963, A
25	325	14.4	337	US-09-898-888-44963	Sequence 44963, A

26	313	13.9	466	US-09-921-378-17022	Sequence 17022, A
27	310	13.7	3834	US-09-784-356-57	Sequence 57, Appl
28	310	13.7	3858	US-60-260-483-492	Sequence 492, Appl
29	295.6	13.1	326	US-09-796-692-2625	Sequence 2625, Ap
30	295.6	13.1	413	US-09-898-888-40487	Sequence 40487, A
31	294.8	13.1	3246	US-09-732-630-3860	Sequence 3860, Ap
32	277	12.3	358	US-60-252-833-40467	Sequence 40467, A
33	260.8	11.5	276	US-09-534-857-3295	Sequence 3295, Ap
34	253.8	11.2	274	US-09-534-857-3294	Sequence 3294, Ap
35	246.4	10.9	34	US-09-821-837-1743	Sequence 1743, Ap
36	235.2	10.4	869	US-09-760-498-456	Sequence 456, App
37	233.8	10.3	267	US-09-796-692-6345	Sequence 6345, Ap
38	233.8	10.3	735	US-09-732-630-1850	Sequence 1850, Ap
39	233	10.3	428	US-09-909-629-39432	Sequence 39432, A
40	199	8.8	204	US-09-796-692-6676	Sequence 6676, Ap
41	184.2	8.2	455	US-09-534-857-3257	Sequence 3257, Ap
42	167.8	7.4	193	US-09-796-692-6456	Sequence 6456, Ap
43	167.4	7.4	440	US-09-909-629-39348	Sequence 39348, A
44	165.8	7.3	241	US-60-253-651-20318	Sequence 20318, A
45	162.6	7.2	469	US-09-732-630-3050	Sequence 3050, Ap

ALIGNMENTS

RESULT 1
US-09-880-107-2306
; Sequence 2306, Application US/09880107
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles In Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2306
; LENGTH: 2354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. M25280
US-09-880-107-2306

Query Match 95.7%; Score 2161; DB 7; Length 2354;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2200; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

25 ACCTGCAGACACACACTCCCTTTGGCAAGACCTGAGCCCTTGCTAAGCAAG 84
|||||
12 accgtcagcagcagcactcccttcttggaagcagccttgagcccttggcctcaag 71
85 GCTCAATGGGCTGCAAGAACTAGAGAAAGCAACCAAGCCATGATTTTCCATGGA 144
|||||
72 gctcaatgggctgcaagaaactagagaaagcagcagcagcagcagcagcagcagc 131
145 AATGTCAGACACACAGAGGACTTATGAAACTCTTCAAGTTGTGGGCTGGAATGC 204
|||||
132 aatgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 191
205 TCTGTGTGATTTCTTGCAATCAGAACTAGAGAACTAGAGAACTAGAGAACTAG 264
|||||
192 tctgtgtgattcttccttgccatcatcatgaaacagcagcagcagcagcagcagc 251
265 AACCCATGAACACTGGCAAGAGGCTAGAAAGATTCTGCCAGACACTTACACGATT 324

D	252	aaccatgaactggaagaaggtctgaagaatctctgcgaagacaattacaagaatttgctg	311
Q	325	ccatTCAAAACAGGCGGAAATTGAGTATCTGGAGAAGACTCTGCCCTTCAGTGTCTT	384
D	312	ccatacaaaaagaagcggaaattgaglatcttggagaagactctgcctttcagtcgtctt	371
Q	385	ACTACTGGATNTGGAATCCGGAGAAGTATAGAGGAANTATGACGTGGGTGGGACCAACAATAAT	444
D	372	actacttgatcggaaatccggagaataagaaagaaataygaagctgggttgaggaaaccaaaat	431
Q	445	CTTCCTACTGAAGAAGCAGAGAACTGGGGAGATGGTGCACCAACAACAAGAACAAAG	504
D	432	ctcttactgaagaagcagagagactcggggagatggtgagcccaacaagaagaacaag	491
Q	505	AGGACTGCGTGGAGATCTATATCAAGAGAAACAAAGATGCAGGCCAAATGGAACGATGACG	564
D	492	aggaactcgtggagatcctatacaagaagaacaagaatgcaagcgaattgaacgatgacg	551
Q	565	CCTGCAACAACCTAAAGGACCCCTCGTTATACAGAGTTCTTCGACGCCCTGGTCAATGA	624
D	552	ccctgcacaacaactaaaggcagccctcgttacaagctcttgcgacctgtgtctga	611
Q	625	GTGGCCATGGGAATGTGTAGAAATCATCAATATCATCACTGCACCTGTGATGTGGGT	684
D	612	gtggccatgggaatctgtgtaaaatcaataataataataacttcgaactcgtgattggtggt	671
Q	685	ACTATGGGCCCCAGTGTACGCTTGATTCAGTGTAGACCCCTTGGAGGCCCCAGACCTGG	744
D	672	actatggccccagctgcagctgtgattcagtgtagcctttggagccccagactg	731
Q	745	GTACCATGAGATGTATACACACCCCTTGGAAACTTCAGCTTCAGCTACAGTGTGCTTCA	804
D	732	gtacacatgactgtcattccaccccttggaaacttcagcttcagcttcaagctgtgcttca	791
Q	805	GCTGCTCTGAAGGAACAACCTTAATCTGGATTGAAGAAACACACTGTGGACCATTTGGAA	864
D	792	gctgctctgaaggagaacaacttcaactcgtggttgaagaaacacactctggaaccaattgaa	851
Q	865	ACTGGTCACTCCAGAACCAACCTGTCAAGTGAATTCAGTGTGAGCCCTCATAGCACCG	924
D	852	actgctactctccagaaccaaccgtcaagtgattcagtgtagcctctatacagcaag	911
Q	925	ATTTTGGGATATGATACTGTATGCCATCCCTGGGCCAGCTTCAGCTTACTCTGCATGTA	984
D	912	attctgggatacgaactgtagcacatccctcgtgcacgtcttcagcttbaaccttgatgta	971
Q	985	CTTTCATCTGCTCAGAGGAAGTGAATTTGGGAAGAAACCAATTTTGATGATCAT	1044
D	972	cttcatctcgtcagaagaagactgagttaatttggagaagaagaacaacatttgtgaatct	1031
Q	1045	CTGGAATCTGGTCAAAATCTAAGTCCAATATGTCAAAATTTGGACAAAAGTTTCTCAATGA	1104
D	1032	ctggaactcgtgcaaacctcagtcacaatattgcaaaaatttggacaagaattctcaatga	1091
Q	1105	TTTAGAGAGCGGATTATTAACCCCTCTTCAATTTCAGATGCGCATGATGTTACTGCATCT	1166
D	1092	ttaagagagggatataaacccctcttcaatccagctggcagctcagtgttactgcatctc	1151
Q	1165	CTGCGTGGCGATTATATCTTGGCTGGCAAGGATTAAAAAAGCAAGAAATTCACAGA	1224
D	1152	ctgggtctggcaatttaacatttgcctggcagaaggatctlaaaaaaaggcaagaatccaga	1211
Q	1225	GAAGTATGAATGACCCATATTAAATGACCCCTTGCTGAAGAAAATTTGGAAATCTTAA	1284
D	1212	gaagtatgaatgacccatataatcgcctcgttggagaagaanaattcttggatactctaa	1271
Q	1285	AATCATGAGATCCTTTAAATCTTTCATGAAAGCGTTTGTGTGTGGACCTCTTAAGTTC	1344
D	1272	aatcatgaatcctttaaaccttccatgaaacgitttgttgggtggacccctcagtc	1331
Q	1345	AAACATGAATGTG-TTCCTTCAGTGCATCTGGGAAGATTTCTACCGCAACAACGTTCC	1403

[illegible]

QY	204	CTCTGTTGGATTTCCTGGCAATCATATGSAACCTACTCTGTGACTTACCATTTATTTGAA	263
Db	270	ctctgttgatgattctctgtgcacataatggaacccgactctgagcttaacattatctgaa	329
QY	264	AAACCCATTAACCGGCAAGGCGCTGGAAGATTCTCCGACGACATTTACAGATTTCGT	323
Db	330	aaacccaatgaactgycgaagaggtctagaagattctgcgcgagacattacaagattcagtl	389
QY	324	GCCATTCAAAACAGGCGGAAAATTGATCTGTGAGAAAGACTCGCCCTTCAGTCGTTCT	383
Db	390	gccaatacaaaaagcgcgaaatctgatactcgtgagaagactctgccttcagtcgtctc	449
QY	384	TACTACTGATTTGGAAATCCGGAAGTATAGGAGATTAATGACAGTGGGAGAACCAAA	443
Db	450	tactactcgtatagyaatcccgaaagataaggaagataatggaatgtagtgytggaaacaa	509
QY	444	TCTCTCACTGAAGAAGCAGAGAACTGGGGAATGGTAGGCCCAACACAGAAAGAACAG	503
Db	510	tctcttactgaagaagcagagaaactcgtgggaatgtagtgcacaaacaagaagaacag	569
QY	504	GAGGACTGCGTGGGAATCTATATCAAGAAACAAGATGACGAGCAATGGAAGATGAC	563
Db	570	gagagactcgttggagatctatatacaagaaacaagaatgcagcgaatgtaacagatgac	629
QY	564	GCCTCGCAAAACCTTAAAGGCGCCCTGTTACACACTCTTGGCAGCCCTGGTATACG	623
Db	630	gcctcgcaaaaactaaagcgcgcctctgttaacagctctctgcgcgcctgtgatagc	689
QY	624	AGTGGCATGGAAGATTGTGAAATCATCAATTAATCACACTGCAACTGTGATGGGG	683
Db	690	agtggccatgagaaatgtgtagaatacatcaataatacaaccctgcgaactgtgagtggg	749
QY	684	TACTATTTGGCCCCAGTGTACACTTGTATTCAGTGTAGCCTTTGAGGCCCGACAGCTG	743
Db	750	tactatggcccccagtgtaagytctgattcagtgatgtagcctcttgagagccccaagctg	809
QY	744	GGTACATGAGACTTACTACACCCCTTTGGAAACCTCAGCTTCAGCTTCACAGTGTGCTTC	803
Db	810	ggtacaatgagactgtactaccctcttgggaacttaagcttaagctccacaagtgtgcttc	869
QY	804	AGCTGCTCTGAAGAACAACTTAAGTGGGATTGAAGAAACCACTGTGGACCAATTTGGA	863
Db	870	agctgctctgaagaagaaacttaactacgtgatttgaagaacaacactgtgacacatttga	929
QY	864	AACGTGATCTCGAAGAACCAACTGTCAAGTATTCAGTGTAGGCTTTATCAGACCA	923
Db	930	aactggtcaatccagaacaacactgcgaagtattcagtgatgtagcctctatacaacaca	989
QY	924	GATTTGGGATCATGAACCTGTAGCAATCCCTGGCCAGCTTCAGCTTACTCTGACGT	983
Db	990	gatttgggatacatgaactctgagcatccctcctgcagcttcagcttaccctctcagat	1049
QY	984	ACCTTCATCTGCTCAGAGAAGAACTGAGTTAATTTGGAGAAGAAAAACATTTGTGAATCA	1043
Db	1050	aacctcatctgctcagagaagaaactgatttaattggaagaagaagaacacatttgaatca	1109
QY	1044	TCTGAATCTGTCAATCTTACTAGCCAATATGTGCAA	1080
Db	1110	tcctggaatctggtcaaatctctatgccaatatgtlcaaa	1146
RESULT 8			
: Sequence 575, Application US/09760443			
: GENERAL INFORMATION:			
: APPLICANT: Rosen et al.			
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
: FILE REFERENCE: P212			
: CURRENT APPLICATION NUMBER: US/09/760,443			
: CURRENT FILING DATE: 2001-01-16			
: Prior application data removed - refer to PAM or file wrapper			
NUMBER OF SEQ ID NOS: 2164			

Query Match	45.8%	Score 1035	DB 6	Length 1298
Best Local Similarity	99.2%	Pred. No. 2.2e-270		
Matches 1049	Conservative 1	Mismatches 6	Indels 1	Gaps 1
; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 575 ; LENGTH: 1298 ; TYPE: DNA ; ORGANISM: Homo sapiens ; US-09-760-443-575				
QY	25	ACCTGAGCAGCAGACACTCCCTTT-GGAAAGAGCCTTGAGACCTTGTGCTAAGTCAAGA	83	
Db	90	actgagcagcagcacactcccttgggaaagacctgagacctgtgctaagtaaga	149	
QY	84	GGCTCAATGGGCTGCAGAAAGAACTAAGAAGGACCAAGAACCATGTATTTCCATGG	143	
Db	150	ggctcaatggtctgcagaaagaaactaagaagaagccaagaagccatgatacttccatg	209	
QY	144	AAATGTCAGAGCAGCCAGAGGAGCTTATGAGCATTTCAAGTTGGGGGGGAGCAATG	203	
Db	210	aaatgtcagagagccccaagggagactatagaacatcttaagtgtgggggtggacaagt	269	
QY	204	CTCTGTGTGATTTCTCTGCAATCATGGAACCTACTGCTGAGCTTACCATTTCTGAA	263	
Db	270	ctctgtgtgattctcttgcacatcatgaaacagactgtgtgacttaccattatctga	329	
QY	264	AAACCCATGAGCTGGCAAGGGCTGAAATTTGCGCCGAGACATTTACAGATTTAGTT	323	
Db	330	aaacccaagaaactggcaaaaggtcagaagatcttcggagacaattacaagatlaagt	389	
QY	324	GCCATACAAACAAAGGCGGAAATTGATATCTGAGAGAGACTCTGCCCTTCAGTCTCT	383	
Db	390	gccatacaaaacaagcggaaattgagatcatcgggaagactcttccttaagtcgttct	449	
QY	384	TACTACTGATAGGAATCCGGAAGTATGAGGAAATATGAGACTGGGTGGGAACACAA	443	
Db	450	tactactgataagaatccggaaagataaggaatataygaaagtgtgttggaaaccaacaa	509	
QY	444	TCTTCACGAGAGAGAGAACTGGGGAGTGGTGAGCCCAACAAACAGAGAAACAG	503	
Db	510	tcttctactgaagaagcagagagactcggggagatgtgtgcccccaaaaagaagaacag	569	
QY	504	GAGGAGCTGCTGGAGATCTATATCAAGAAACAAAGATGAGGCAATGGAACGATGAC	563	
Db	570	gagagactcgttggagatcatataccaagaacaaagaatgaagaaatggaacgatgac	629	
QY	564	GGCTGCGCAAACTTAAAGGAGCCCTGTTACACAGTTCTTGCCAGCCCTGGTCATGC	623	
Db	630	gctctgccaaaactaaagcagccctccgttacaagaagctcttgcacccctgtctatgc	689	
QY	624	AGTGGCATGAGAAATGTGTAGAAATCATATATCATACACTGCACACTGTGATGTGGG	683	
Db	690	agtggccatgagaaatgtgtagaatacatcaatattacacctgcaactgtagatgtggg	749	
QY	684	TACTTTGGGCCCCAATGTCACCTTGTGATTTAGTGTGAGGCTTTGGAGGCCCCAGACTG	743	
Db	750	tactatgggccccagtgtcagtytcttgatctaaagtgtgagcctcttggagccccagagctg	809	
QY	744	GGTACATGAGACTGACTCACCCCTTTGGAAACTTCAGCTTCACCTCAACAGTGTGCCCTT	803	
Db	810	gttacatgagactgtactcacaccttgggaaactcgaactcgaactcaacagttgtcccttc	869	
QY	804	AGCTGCTTGAAGGAACAACTTAACTGGAATTGAAGAAACCAACTGTGAGCACTTTTGA	863	
Db	870	agctgcttgaaggaaacaaacttaactgtgaaatgaagaacacacctgtgacaatttga	929	
QY	864	AACGTGATATTCAGAAACCAACTGTCAAGTGTATGAGTGAAGCCTTATACAGACCA	923	
Db	930	aactgtgatactccaagaacaaactcttcaaaagtgtctaaagtgtgagcctctatagaacca	989	
QY	924	GATTGGGGATCATGAACCTGAGCAATCCCTGGCCAGCTTCAGCTTACTCTGCATGT	983	

Db	990	gatttgggagcatgacactgtagccatcccccgcgcagcttcagcttacccttcgacgt	1049
Db	994	ACCTTCATCTGCTCAGAGAACTAGTATATTTGGGAAAGAAAACCATTTTGTAATCA	10433
Db	1050	acctcatctgctcagaagaactgagtaattcggagaagaagaacatttgaatca	1109
Oy	1044	TCTGGAATCGTGCAATCCTAGTCCAAATATGTGCANA	1080
Db	1110	tctggaatctggtcaaatcctctagtcacaatcgtcaaa	1146

RESULT	9
PCT-US01-26675-1	
Sequence 1, Application PC/TUS0126675	
GENERAL INFORMATION:	
APPLICANT: Genaisance Pharmaceuticals, Inc.	
APPLICANT: Anastasio, Allison E	
APPLICANT: Blegiecki, Karyn M	
APPLICANT: Kilem, Stefanie E	
APPLICANT: Koshiy, Beena	
APPLICANT: Kumar, Anant Madan	
TITLE OF INVENTION: HAPLOYPES OF THE SELL GENE	
FILE REFERENCE: SELL MMH1116-PCT	
CURRENT APPLICATION NUMBER: PCT/US01/26675	
CURRENT FILING DATE: 2001-08-27	
PRIOR APPLICATION NUMBER: 60/428, 262	
PRIOR FILING DATE: 2000-08-25	
NUMBER OF SEQ ID NOS: 101	
SOFTWARE: PatentIn version 3.1	
SEQ ID NO 1	
LENGTH: 27780	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURE:	
NAME/KEY: allele	
LOCATION: (3349)..(3349)	
OTHER INFORMATION: PS1:	polymorphic base A or G
NAME/KEY: allele	
LOCATION: (3444)..(3444)	
OTHER INFORMATION: PS2:	polymorphic base T or C
NAME/KEY: allele	
LOCATION: (4206)..(4206)	
OTHER INFORMATION: PS3:	polymorphic base C or T
NAME/KEY: allele	
LOCATION: (5153)..(5153)	
OTHER INFORMATION: PS4:	polymorphic base G or A
NAME/KEY: allele	
LOCATION: (6682)..(6682)	
OTHER INFORMATION: PS5:	polymorphic base A or G
NAME/KEY: allele	
LOCATION: (6783)..(6783)	
OTHER INFORMATION: PS6:	polymorphic base C or G
NAME/KEY: allele	
LOCATION: (6784)..(6784)	
OTHER INFORMATION: PS7:	polymorphic base C or T
NAME/KEY: allele	
LOCATION: (6997)..(6997)	
OTHER INFORMATION: PS8:	polymorphic base T or C
NAME/KEY: allele	
LOCATION: (7027)..(7027)	
OTHER INFORMATION: PS9:	polymorphic base T or C
NAME/KEY: allele	
LOCATION: (8220)..(8220)	
OTHER INFORMATION: PS10:	polymorphic base T or C
NAME/KEY: allele	
LOCATION: (10868)..(10868)	
OTHER INFORMATION: PS11:	polymorphic base C or T
NAME/KEY: allele	
LOCATION: (12363)..(12363)	
OTHER INFORMATION: PS12:	polymorphic base G or A
NAME/KEY: allele	
LOCATION: (13838)..(13838)	

Db 24361 ccatcctatlaactgctca-gccloccaccctcttcagccaccctctcttcagt 24419
OY 1885 TGGGACCTTCACACACACATCTCATGAGTGGCCACCAAAAGAGAGAGAGAAAT 1944
Db 24420 tggcgactccacacccagatcctcagtgagtgccaaagagagagagaaat 24479
OY 1945 AGCCGCGCGGTTTTTGGTGGGGGTTTGGCTGCTTTTATGAGACCAATTCCTA 2004
Db 24480 agccgcgcgtttttttagtttggttggttggttggttggttggttggttggttggt 24539
OY 2005 TTTCTATAGTCATGTTCTTTTATGAGATATTATTAGTAAAGAAACATCACTGAAT 2064
Db 24540 ttctctatagtcacatgttctcttctatcagatattatagtaagaacacactgaat 24599
OY 2065 GCTAGCTCAGTACATCTTTGATGCTATGAGAAAGATTAAACAGTGGAGAAAT 2124
Db 24600 gctagctgcaagtgacatctctcttgatgacatgagaaagtaaacagtgagaaat 24659
OY 2125 TCTTGTATCAATGAATGCTCTCTTCCCTGCCCCAGAACTTTTATCCACTTAC 2184
Db 24660 tccctgattccaaatgaatgctctctctctccctgccccagacctttatccactac 24719
OY 2185 CTAGATCTACATATCTTTTAAATTTATGTCAGAGCTCCCTCAACCCAC 2235
Db 24720 ctgattctacatctctttaaattcatcagcctccctcaacccac 24770

RESULT 10
US-09-758-449-373/c
; Sequence 373, Application US/09758449
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PMO26
; CURRENT APPLICATION NUMBER: US/09/758,449
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 1478
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 373
; LENGTH: 1063
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (54)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-758-449-373

Query Match 34.3%; Score 775; DB 6; Length 1063;
Best Local Similarity 99.3%; Pred. No. 7.4e-200;
Matches 797; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

OY 1434 CTCACCCCCCAGAGAGGTGTATACAGCTGAGCTTTTGTCTTTTGTGAGAGAAA 1493
Db 1002 CAGAACCCCCCAGAGAGGTGTATACAGCTGAGCTTTTGTCTTTTGTGAGAGAAA 943
OY 1494 CAAATTAAGACAT-AAGGAAAGATTCATGTAATATAAGATGCTGACTTGCCT 1552
Db 942 CAAATAAGACATAAAGAAAGATTCATGTAATATAAGATGCTGACTTGCCT 883
OY 1553 TTTCTGACTCTTTGTTTGTGTTTCAATTCAGTCTGTAAGTGAAGACAGACTTTTAA 1612
Db 882 TTTCTGACTCTTTGTTTGTGTTTCAATTCAGTCTGTAAGTGAAGACAGACTTTTAA 823

OY 1613 TGAAGTCAAAATTTGATACATATGTAATGAGCTCAGTTTCTTGACATCAAAATTC 1672
Db 822 TGAAGTCAAAATTTGATACATATGTAATGAGCTCAGTTTCTTGACATCAAAATTC 763
OY 1673 ACGTGCCTCTGATATCTGTGAGGTACCTCTTATAGAAATTTAAAAAGCTACGCT 1732
Db 762 ACGTGCCTCTGATATCTGTGAGGTACCTCTTATAGAAATTTAAAAAGCTACGCT 703
OY 1733 CTCCTTCTTTTAACTCAGTAAATGAGGTGCTGCTCAAGTTGAAAGAGTCCAT 1792
Db 702 CTCCTTCTTTTAACTCAGTAAATGAGGTGCTGCTCAAGTTGAAAGAGTCCAT 643
OY 1793 TTGACAGTACGCTGCGCGCTGCTGATTTGACATCTTATTTAACTGCTTACGCTC 1852
Db 642 TTGACAGTACGCTGCGCGCTGCTGATTTGACATCTTATTTAACTGCTTACGCTC 584
OY 1853 CCCACCTTCTTACGACCTCTCTTTTCAAGTTGGCTGCTCCACACCTACATCTCAT 1912
Db 583 CCCACCTTCTTACGACCTCTCTTTTCAAGTTGGCTGCTCCACACCTACATCTCAT 524
OY 1913 GAGTGCACAAAGAGAGAGAGAGAAATAGCTGCGGTTTTTGTAGTTGGGGT 1972
Db 523 GAGTGCACAAAGAGAGAGAGAGAAATAGCTGCGGTTTTTGTAGTTGGGGT 464
OY 1973 TTTGCTGTTCTTTATGAGACCATTCCTATTTCTTATAGTCAATGTTCTTTATCA 2032
Db 463 TTTGCTGTTCTTTATGAGACCATTCCTATTTCTTATAGTCAATGTTCTTTATCA 404
OY 2033 CGATATTTATGAGAAACATCACTGAAATGCTAGCTGCAAGTACATCTTTGATG 2092
Db 403 CGATATTTATGAGAAACATCACTGAAATGCTAGCTGCAAGTACATCTTTGATG 344
OY 2093 TCATATGAGAGTTAAACAGTGGAGAAATCTCTTATTCACATGAATGCTCTCT 2152
Db 343 TCATATGAGAGTTAAACAGTGGAGAAATCTCTTATTCACATGAATGCTCTCT 284
OY 2153 TTCCCTGCCCCAGAACTTTTATCAGTACCTGATTTCAATATCTTAAATTTCA 2212
Db 283 TTCCCTGCCCCAGAACTTTTATCAGTACCTGATTTCAATATCTTAAATTTCA 224
OY 2213 TCTCAGGCTCTCTTAAACCCAC 2235
Db 223 TCTCAGGCTCTCTTAAACCCAC 201

RESULT 11
US-09-796-692-210/c
; Sequence 210, Application US/09796692
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077,001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22

```

; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(579)
; OTHER INFORMATION: n = A,T,C or G
US-09-796-692-210
```

```

Query Match          24.9%; Score 562.2; DB 6; Length 579;
Best Local Similarity 99.1%; Pred. No. 3.2e-142;
Matches 575; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
```

```

QY 1625 TTGATCATATGTGAATATGAGTCACTTTCTTTCGAGATCAATTTACAGTGTCTTCT 1684
    |||||||
DB 579 TTGATCATATGTGAATATGAGTCACTTTCTTTCGAGATCAATTTACAGTGTCTTCT 520

QY 1685 GTATACGTGTGAGAGTACACTCTTATAGAAAGTCAAAAGTCAAGCTCTCTTTCTTTC 1744
    |||||||
DB 519 GTATACGTGTGAGAGTACACTCTTATAGAAAGTCAAAAGTCAAGCTCTCTTTCTTTC 460

QY 1745 TAACTCCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTATTTGCACTGTAGC 1804
    |||||||
DB 459 TAACTCCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTATTTGCACTGTAGC 400

QY 1805 CTCGGCGTCTGTAATTTGGAGCCATCCATTTAATCTGCTCAGGCCCCCAGCTTCTTC 1864
    |||||||
DB 399 CTCGGCGTCTGTAATTTGGAGCCATCCATTTAATCTGCTCAGGCCCCCAGCTTCTTC 341

QY 1865 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGTAGTGCAGCA 1924
    |||||||
DB 340 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGTAGTGCAGCA 281

QY 1925 AAAGAGAGAGAGAGAAATAGCCTGGCGGTTTTTTAGTTGGGGTTTTGCTGTTTC 1984
    |||||||
DB 280 AAAGAGAGAGAGAGAAATAGCCTGGCGGTTTTTTAGTTGGGGTTTTGCTGTTTC 221

QY 1985 TTTTATGAGACCCATTCCTATTTCTTATATGATGTTTCTTTTATCAGATATTTAG 2044
    |||||||
DB 220 TTTTATGAGACCCATTCCTATTTCTTATATGATGTTTCTTTTATCAGATATTTAG 161

QY 2045 TAAGAAATCATCTCTAAATAGTAGCTCAAGAGCATCTCTTGTGATGTATGAGAGA 2104
    |||||||
DB 160 TAAGAAATCATCTCTAAATAGTAGCTCAAGAGCATCTCTTGTGATGTATGAGAGA 101

QY 2105 GTTAAAAAGAGTGAAGAAATTCCTTGATTCACAATGAATGCTCTCTTCCCTGCCCC 2164
    |||||||
DB 100 GTTAAAAAGAGTGAAGAAATTCCTTGATTCACAATGAATGCTCTCTTCCCTGCCCC 41

QY 2165 CAGAACTTTATCAGTCACTTACATGATTTCTATATTTCTTT 2204
    |||||||
DB 40 CAGAACTTTATCAGTCACTTACATGATTTCTATATTTCTTT 1
```

```

RESULT 12
US-09-796-692-4884/C
; Sequence 4884, Application US/09796692
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077, 001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4884
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (511)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-4884
```

```

Query Match          24.9%; Score 562.2; DB 6; Length 579;
Best Local Similarity 99.1%; Pred. No. 3.2e-142;
Matches 575; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
```

```

QY 1625 TTGATCATATGTGAATATGAGTCACTTTCTTTCGAGATCAATTTACAGTGTCTTCT 1684
    |||||||
DB 579 TTGATCATATGTGAATATGAGTCACTTTCTTTCGAGATCAATTTACAGTGTCTTCT 520

QY 1685 GTATACGTGTGAGAGTACACTCTTATAGAAAGTCAAAAGTCAAGCTCTCTTTCTTTC 1744
    |||||||
DB 519 GTATACGTGTGAGAGTACACTCTTATAGAAAGTCAAAAGTCAAGCTCTCTTTCTTTC 460

QY 1745 TAACTCCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTATTTGCACTGTAGC 1804
    |||||||
DB 459 TAACTCCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTATTTGCACTGTAGC 400

QY 1805 CTCGGCGTCTGTAATTTGGAGCCATCCATTTAATCTGCTCAGGCCCCCAGCTTCTTC 1864
    |||||||
DB 399 CTCGGCGTCTGTAATTTGGAGCCATCCATTTAATCTGCTCAGGCCCCCAGCTTCTTC 341

QY 1865 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGTAGTGCAGCA 1924
    |||||||
DB 340 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGTAGTGCAGCA 281

QY 1925 AAAGAGAGAGAGAGAAATAGCCTGGCGGTTTTTTAGTTGGGGTTTTGCTGTTTC 1984
    |||||||
DB 280 AAAGAGAGAGAGAGAAATAGCCTGGCGGTTTTTTAGTTGGGGTTTTGCTGTTTC 221

QY 1985 TTTTATGAGACCCATTCCTATTTCTTATATGATGTTTCTTTTATCAGATATTTAG 2044
    |||||||
DB 220 TTTTATGAGACCCATTCCTATTTCTTATATGATGTTTCTTTTATCAGATATTTAG 161
```

[illegible]

```

13 RESULT
14 US-09-796-692-5257/C
15 ; Sequence 5257, Application US/09796692
16 ; GENERAL INFORMATION:
17 ; APPLICANT: Gaiger, Alexander
18 ; APPLICANT: Algate, Paul A.
19 ; APPLICANT: Mannion, Jane
20 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
21 ; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
22 ; FILE REFERENCE: 2077 .001200
23 ; CURRENT APPLICATION NUMBER: US/09/796,692
24 ; CURRENT FILING DATE: 2001-03-01
25 ; PRIOR APPLICATION NUMBER: 60/186,126
26 ; PRIOR FILING DATE: 2000-03-01
27 ; PRIOR APPLICATION NUMBER: 60/190,479
28 ; PRIOR FILING DATE: 2000-03-17
29 ; PRIOR APPLICATION NUMBER: 60/200,545
30 ; PRIOR FILING DATE: 2000-04-27
31 ; PRIOR APPLICATION NUMBER: 60/200,303
32 ; PRIOR FILING DATE: 2000-04-28
33 ; PRIOR APPLICATION NUMBER: 60/200,779
34 ; PRIOR FILING DATE: 2000-04-28
35 ; PRIOR APPLICATION NUMBER: 60/200,999
36 ; PRIOR FILING DATE: 2000-05-01
37 ; PRIOR APPLICATION NUMBER: 60/202,084
38 ; PRIOR FILING DATE: 2000-05-04
39 ; PRIOR APPLICATION NUMBER: 60/206,201
40 ; PRIOR FILING DATE: 2000-05-22
41 ; PRIOR APPLICATION NUMBER: 60/218,950
42 ; PRIOR FILING DATE: 2000-07-14
43 ; PRIOR APPLICATION NUMBER: 60/222,903
44 ; PRIOR FILING DATE: 2000-08-03
45 ; PRIOR APPLICATION NUMBER: 60/223,416
46 ; PRIOR FILING DATE: 2000-08-04
47 ; PRIOR APPLICATION NUMBER: 60/223,378
48 ; PRIOR FILING DATE: 2000-08-07
49 ; NUMBER OF SEQ ID NOS: 9597
50 ; SOFTWARE: FastSeq for Windows Version 3.0
51 ; SEQ ID NO 5257
52 ; LENGTH: 577
53 ; TYPE: DNA
54 ; ORGANISM: Homo sapiens
55 ; FEATURE:
56 ; NAME/KEY: unsure
57 ; LOCATION: (497)
58 ; OTHER INFORMATION: n=A,T,C or G
59 ; US-09-796-692-5257

```

[illegible]

```

RESULT 14
US-09-796-692-8471/c
; Sequence 8471, Application US/09796692
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIORITY APPLICATION NUMBER: 60/186,126
PRIORITY FILING DATE: 2000-03-01
PRIORITY APPLICATION NUMBER: 60/190,479
PRIORITY FILING DATE: 2000-03-17
PRIORITY APPLICATION NUMBER: 60/200,545
PRIORITY FILING DATE: 2000-04-27
PRIORITY APPLICATION NUMBER: 60/200,303
PRIORITY FILING DATE: 2000-04-28
PRIORITY APPLICATION NUMBER: 60/200,779
PRIORITY FILING DATE: 2000-04-28
PRIORITY APPLICATION NUMBER: 60/200,999
PRIORITY FILING DATE: 2000-05-01
PRIORITY APPLICATION NUMBER: 60/202,084
PRIORITY FILING DATE: 2000-05-04
PRIORITY APPLICATION NUMBER: 60/206,201
PRIORITY FILING DATE: 2000-05-22
PRIORITY APPLICATION NUMBER: 60/218,950
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: 60/222,903
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: 60/223,416
PRIORITY FILING DATE: 2000-08-04
PRIORITY APPLICATION NUMBER: 60/223,378
PRIORITY FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSeq for Windows Version 3.0

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:18:21 ; Search time 2226.75 seconds
(without alignments)
9589.759 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259

Sequence: 1 GAATTCAGTGTGCTGCTT.....CCGCCAGCACACTGGAATTC 2259

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: gb_est41:*
42: gb_est42:*
43: gb_est43:*

44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_esthum29:*
64: em_esthum30:*
65: em_esthum31:*
66: em_esthum32:*
67: em_esthum33:*
68: em_esthum34:*
69: em_esthum35:*
70: em_esthum36:*
71: em_esthum37:*
72: em_esthum38:*
73: em_esthum39:*
74: em_esthum40:*
75: em_esthum41:*
76: em_esthum42:*
77: em_esthum43:*
78: em_esthum44:*
79: em_esthum45:*
80: em_esthum46:*
81: em_esthum47:*
82: em_esthum48:*
83: em_esthum49:*
84: em_esthum50:*
85: em_esthum51:*
86: em_esthum52:*
87: em_esthum53:*
88: em_esthum54:*
89: em_esthum55:*
90: em_esthum56:*
91: em_esthum57:*
92: em_esthum58:*
93: em_esthum59:*
94: em_esthum60:*
95: em_esthum61:*
96: em_esthum62:*
97: em_esthum63:*
98: em_esthum64:*
99: em_esthum65:*
100: em_esthum66:*
101: em_esthum67:*
102: em_esthum68:*
103: em_esthum69:*
104: em_esthum70:*
105: em_esthum71:*
106: em_esthum72:*
107: em_esthum73:*
108: em_esthum74:*
109: em_esthum75:*
110: em_esthum76:*
111: em_esthum77:*
112: em_esthum78:*
113: em_esthum79:*
114: em_esthum80:*
115: em_esthum81:*
116: em_esthum82:*

117: gb_estc48:*
118: gb_estc49:*
119: gb_estc50:*
120: gb_estc51:*
121: gb_estc52:*
122: gb_estc53:*
123: gb_estc54:*
124: gb_estc55:*
125: gb_estc56:*
126: gb_estc57:*
127: gb_estc58:*
128: gb_estc59:*
129: gb_estc60:*
130: gb_estc61:*
131: gb_estc62:*
132: gb_estc63:*
133: gb_estc64:*
134: gb_estc65:*
135: gb_estc66:*
136: gb_estc67:*
137: gb_estc68:*
138: gb_estc69:*
139: gb_estc70:*
140: gb_estc71:*
141: gb_estc72:*
142: gb_estc73:*
143: gb_estc74:*
144: gb_estc75:*
145: gb_estc76:*
146: gb_estc77:*
147: gb_estc78:*
148: gb_estc79:*
149: gb_estc80:*
150: gb_estc81:*
151: gb_estc82:*
152: gb_estc83:*
153: gb_estc84:*
154: gb_estc85:*
155: gb_estc86:*
156: gb_estc87:*
157: gb_estc88:*
158: gb_estc89:*
159: gb_estc90:*
160: gb_estc91:*
161: gb_estc92:*
162: gb_estc93:*
163: gb_estc94:*
164: gb_estc95:*
165: gb_estc96:*
166: gb_estc97:*
167: gb_estc98:*
168: gb_estc99:*
169: gb_estc100:*
170: gb_estc101:*
171: gb_estc102:*
172: gb_estc103:*
173: gb_estc104:*
174: gb_estc105:*
175: gb_estc106:*
176: gb_estc107:*
177: gb_estc108:*
178: gb_estc109:*
179: gb_estc110:*
180: gb_estc111:*
181: gb_estc112:*
182: gb_estc113:*
183: gb_estc114:*
184: gb_estc115:*
185: gb_estc116:*
186: gb_estc117:*
187: gb_estc118:*
188: gb_estc119:*
189: gb_estc120:*

190: gb_estl10:*
191: gb_estl11:*
192: gb_estl12:*
193: gb_estl13:*
194: gb_estl14:*
195: gb_estl15:*
196: gb_estl16:*
197: gb_estl17:*
198: gb_estl18:*
199: gb_estl19:*
200: gb_estl20:*
201: gb_estl21:*
202: gb_estl22:*
203: gb_estl23:*
204: gb_estl24:*
205: gb_estl25:*
206: gb_estl26:*
207: gb_estl27:*
208: gb_estl28:*
209: gb_estl29:*
210: gb_estl30:*
211: gb_estl31:*
212: gb_estl32:*
213: gb_estl33:*
214: gb_estl34:*
215: gb_estl35:*
216: gb_estl36:*
217: gb_estl37:*
218: gb_estl38:*
219: gb_estl39:*
220: gb_estl40:*
221: gb_estl41:*
222: gb_estl42:*
223: gb_estl43:*
224: gb_estl44:*
225: gb_estl45:*
226: gb_estl46:*
227: gb_estl47:*
228: gb_estl48:*
229: gb_estl49:*
230: gb_estl50:*
231: gb_estl51:*
232: gb_estl52:*
233: gb_estl53:*
234: gb_estl54:*
235: gb_estl55:*
236: gb_estl56:*
237: gb_estl57:*
238: gb_estl58:*
239: gb_estl59:*
240: gb_estl60:*
241: gb_estl61:*
242: gb_estl62:*
243: gb_estl63:*
244: gb_estl64:*
245: gb_estl65:*
246: gb_estl66:*
247: gb_estl67:*
248: gb_estl68:*
249: gb_estl69:*
250: gb_estl70:*
251: gb_estl71:*
252: gb_estl72:*
253: gb_estl73:*
254: gb_estl74:*
255: gb_estl75:*
256: gb_estl76:*
257: gb_estl77:*
258: gb_estl78:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Query Match	29.0%	Score 65.4	DB 155	Length 739
	Best Local Similarity	98.6%	Pred. No. 2.3e-174		
	Matches 702	Conservative	0	Mismatches 6	Indels 4
0Y	25	ACGTCACACAGCAGCACTCCCTTT	-GGCAAGSAGCTGAGACCCTTGTCTTAAGTCACAA	83	

Db	Accession	Gene	Species	Length (bp)	EST	EST ID	EST Length (bp)	EST Score	EST Description
Db	25	ACCTGACGACAGCAGCACTCCCTTTGGGCAAGACCTGTAACCCCTTGTGTAAAGTAA	84						
QY	84	GGCTCAATGGGCTGCAGAAAGAACTAGAGAAAGACCAAGCAAAAGCCATGATATTTCCATGG	143						
Db	85	GGCTCAATGGGCTGCAGAAAGAACTAGAGAAAGACCAAGCAAAAGCCATGATATTTCCATGG	144						
QY	144	AAATGTCAGAGCACCAGAGGACTTATGGAACATCTTCAAGTTGTGGGGTGGACATAG	203						
Db	145	AAATGTCAGAGCACCAGAGGACTTATGGAACATCTTCAAGTTGTGGGGTGGACATAG	204						
QY	204	CTCTTTGTGATTTCTTGGCAGATCATGAGAACACCTAGCTGGACTTACCATATTTCTGAA	263						
Db	205	CTCTCTGTGATTTCTTGGCAGATCATGAGAACACCTAGCTGGACTTACCATATTTCTGAA	264						
QY	264	AAACCCATGAACCTGGCAAAAGGGCTAGAAAGTCTGCCGAGACAAATTACACAGATTTAGTT	323						
Db	265	AAACCCATGAACCTGGCAAAAGGGCTAGAAAGTCTGCCGAGACAAATTACACAGATTTAGTT	324						
QY	324	GCCATACAAACCAAGGGGGAATTTGATATCTGAGAGAACCTTGCCCTTTCAGTGTGTT	383						
Db	325	GCCATACAAACCAAGGGGGAATTTGATATCTGAGAGAACCTTGCCCTTTCAGTGTGTT	384						
QY	384	TACTCTGTGATAGGAATCCGGAACATGAGAGAAATATGACGCTGGGTGGGAACCAACAA	443						
Db	385	TACTCTGTGATAGGAATCCGGAACATGAGAGAAATATGACGCTGGGTGGGAACCAACAA	444						
QY	444	TCTCTCACTGAAGAAGCAGAGAACTGGGGAGATGTGTAGGCCCAACAAAGAAACAAG	503						
Db	445	TCTCTCACTGAAGAAGCAGAGAACTGGGGAGATGTGTAGGCCCAACAAAGAAACAAG	504						
QY	504	GAGAGCTCCGCTGGAGATCTATATCAAGAAACAAAGATGCGACGAAATGGAACCATGAC	563						
Db	505	GAGAGCTCCGCTGGAGATCTATATCAAGAAACAAAGATGCGACGAAATGGAACCATGAC	564						
QY	564	GCTTCGCCAACAACAAAGGAGAGCCCTGTGTACACAGCTTCTTCCAGGCCCTGGTCAATGC	623						
Db	565	GCTTCGCCAACAACAAAGGAGAGCCCTGTGTACACAGCTTCTTCCAGGCCCTGGTCAATGC	623						
QY	624	AGTGGCCATGAGAGATGTGTAGAAATCATATATACACCTGCAACCTGTGATGTGGGG	683						
Db	624	AGTGGCCATGAGAGATGTGTAGAAATCATATATACACCTGCAACCTGTGATGTGGGG	682						
QY	684	TACTATGGGCCCCAGCTGACCTTGTGATCATGATGAGAGCCCTTTGGAAGCCC	735						
Db	683	TACTATGGGCCCCAGCTGACCTTGTGATCATGATGAGAGCCCTTTGGAAGCCC	733						

FEATURES	Location/Qualifiers
source	1. 621 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_11b="MAGE reserences, MAGA" /note="Vector: pbluescriptsm"
BASE COUNT	172 a 135 c 119 g 194 t 1 others
ORIGIN	
Query Match	26.2%; Score 592.8; DB 122; Length 621;
Best Local Similarity	99.4%; Pred. No. 6.6e-157;
Matches	616; Conservative 0; Mismatches 2; Indels 2; Gaps 2.
QY	1210 GCACAGAAATCCAGAGAGATGATGAATGACCCATATTAAATCGCCCTGGTGGAAGAAAT 1269
Db	1 GCACAGAAATCCAGAGAGAGATGATGAATGACCCATATTAAATCGCCCTGGTGGAAGAAAT 60
QY	1270 TCTTGGAAATCTAAATAATCATGAGATCCCTTTAAATTCCTTCATGGAACGTTTGTGTGT 1329
Db	61 TCTTGGAAATCTAAATAATCATGAGATCCCTTTAAATTCCTTCATGGAACGTTTGTGTGT 120
QY	1330 GGCACCTCTACGTGAACATGSAAGTGGG-TTCCCTTCAGTGCATCGGGAAGATTTTAC 1388
Db	121 GGCACCTCTACGTGAACATGSAAGTGGTGTCTTTCCTTCAGTGCATCGGGAAGATTTTAC 180
QY	1389 CCGACCAACAGTTCCTTCAGCTTCCATTTCCGCCCTCATTTATGCCCTCAACCCCAAGCCC 1448
Db	181 CCGACCAACAGTTCCTTCAGCTTCCATTTCCGCCCTCATTTATGCCCTCAACCCCAAGCCC 240
QY	1449 ACAGTGTATTATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAAATAAGACCAT-A 1507
Db	241 ACAGTGTATTATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAAATAAGACCATAA 300
QY	1508 AGGGAAGAGATTCAATGAGGAATATTAAGATGGCTACCTTTCCTTCAGTCTCTGT 1567
Db	301 AGGGAAGAGATTCAATGAGGAATATTAAGATGGCTACCTTTCCTTCAGTCTCTGT 360
QY	1568 TTCACTTTCAATTCAGTCTCTGACTTGTGATGACAGACACTTCCTAAATGAAGTCAAAATTGG 1627
Db	361 TTCACTTTCAATTCAGTCTCTGACTTGTGATGACAGACACTTCCTAAATGAAGTCAAAATTGG 420
QY	1628 ATACATATGTGAATATGAGACTCAGTTTCTTCGACATCAAAATTTCAAGCTGCTCTCTGA 1687
Db	421 ATACATATGTGAATATGAGACTCAGTTTCTTCGACATCAAAATTTCAAGCTGCTCTCTGA 480
QY	1688 TACCTGTGAGGATACCTCTTATAGAAAGTTCAGAAAGTCTACGCTCTCTCTTTCTTCAA 1747
Db	481 TACCTGTGAGGATACCTCTTATAGAAAGTTCAGAAAGTCTACGCTCTCTCTTTCTTCAA 540
QY	1748 CTCACGTAAGTAATAGGGGCTCCTGCTCAAGTTGGAAGAAGTCCCTATTTCGACTGTAGCCCTC 1807
Db	541 CTCACGTAAGTAATAGGGGCTCCTGCTCAAGTTGGAAGAAGTCCCTATTTCGACTGTAGCCCTC 600
QY	1808 GCCGTCTGTGAATTGGACCA 1827
Db	601 GCCGTCTGTGAATTGGACCA 620
RESULT 4	
AM408490	551 bp mRNA EST 16-FEB-2000
LOCUS	UI-HF-BKO-aldm-g-01-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION	IMAGE:3056832 5', mRNA sequence.
ACCESSION	AM408490
VERSION	AM408490.1 GI:6927547
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 551). NIH-MGC http://mgc.ncl.nih.gov/.
AUTHORS	

Y	1500	AGACC	1504
Y	1500	AGACC	1504

Db 547 AGACC 551

RESULT 5
BF790688 876 bp mRNA EST 12-JAN-2001
LOCUS 602250524F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338268 5',
DEFINITION mRNA sequence.
ACCESSION BF790688
VERSION BF790688.1 GI:12095742
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 876)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LNCM1213 row: 0 column: 05
High quality sequence stop: 549.
Location/Qualifiers
1. 876
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="NIH_MGC_81"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site:1: sfli (ggccgcctcgcc); Site:2: sfli
(ggccatagcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATAGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGGCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

BASE COUNT 229 a 205 c 250 g 192 t

ORIGIN

Query Match 22.6%; Score 511.4; DB 169; Length 876;
Best Local Similarity 94.2%; Pred. No. 9,6e-134;
Matches 585; Conservative 0; Mismatches 31; Indels 5; Gaps 5;

25 ACTGCAGCAGCAGCACTCCCTTGGCAAGACCTGAGCCCTTGCTAAGTCAAGAG 84
|||||
11 ACCTGAGCAGCAGCACTCCCTTGGCAAGACCTGAGCCCTTGCTAAGTCAAGAG 69
|||||
85 GCTCAATGGGCTGCGAGAGACTAGAGAGCAAGCAAGCCATGATATTTCCATGGA 144
|||||
70 GCTCAATGGGCTGCGAGAGACTAGAGAGCAAGCAAGCCATGATATTTCCATGGA 129
|||||
145 AATGTACAGCAGCAGCAGCACTTATGAGACATCTTCAAGTTGGGGGTGAGCAATGC 204
|||||
130 AATGTACAGCAGCAGCAGCAGGAGCTTATGAGACATCTTCAAG-TGTGGGGGTGAGCAATGC 188
|||||
205 TCTGTGTGATTTCTGGCAGCATCATGAACTACTGTGTGACTTACATTTATTCGAAA 264
|||||
189 TCTG-TGTGATTTCTGGCAGCATCATGAACTACTGTGTGACTTACATTTATTCGAAA 247
|||||

QY 265 AACCCATGACCTGGCAAGAGGCGTAGAATTTCTGCCAGCAATTAACAGATTAGTTG 324
|||||
Db 248 AACCATGAACTGGCAAGAGGCGTAGAATTTCTGCCAGCAATTAACAGATTAGTTG 307
|||||
QY 325 CCATACAAAACAAAGCGGAAATTGATATCTGAGAGAACTGTCCTTCACTGTTCT 384
|||||
Db 308 CCATACAAAACAAAGCGGAAATTGATATCTGAGAGAACTGTCCTTCACTGTTCT 367
|||||
QY 385 ACTACTGGATAGGAATCCGAGATAGAGAGAAATATGAGACGTGGTGGCAACAAAT 444
|||||
Db 368 ACTACTGGATAGGAATCCGAGATAGAGAGAAATATGAGACGTGGTGGCAACAAAT 427
|||||
QY 445 CTCTCACTGAAGACGAGAACTGGGAGATGTTGAGCCCAACAAGAAAGAAAG 504
|||||
Db 428 CTCTCACTGAAGACGAGAACTGGGAGATGTTGAGCCCAACAAGAAAGAAAG 487
|||||
QY 505 AGGACTGCGTGGAGATCTATATCAAGAAACAAAGATGAGGCAATGAGACATGAG 564
|||||
Db 488 AGGACTGCGTGGAGATCTATATCAAGAAACAAAGATGAGGCAATGAGACATGAG 546
|||||
QY 565 CCTGCCACAACATAAAGGCGCCCTCTGTTACACAGCTTCTTCCAGCCCTGTCTATGCA 624
|||||
Db 547 CCTGCCACAACATAAAGGCGCCCTCTGTTACACAGCTTCTTCCAGCCCTGTCTATGCA 605
|||||
QY 625 GTGGCCATGGAGAAATGTAG 645
|||||
Db 606 GTGGCCATGGAGAAATGTAG 626
|||||

RESULT 6
AM075834/c 632 bp mRNA EST 13-OCT-1999
LOCUS AM075834/c
DEFINITION xa80c03.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573092 3',
similar to gb:X10150_cds1 L-SELECTIN PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AM075834
VERSION AM075834.1 GI:6030832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 632)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/biopr/image/image.html
Seq primer: -40bp from Glibco
High quality sequence stop: 147.
Location/Qualifiers
1. 632
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL
rearrangement positive, includes both chronic phase and
myeloid blast crisis"
/lab_host="DH10B"
/note="Organ: whole blood; Vector: pCMV-Sport6; Site:1:
SalI; Site:2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Library constructed by Life Technologies."

BASE COUNT 175 a 126 c 130 g 201 t

QY	1731	----	CTCCGCTTCTTCTTCTTAACTCCAGTGAAGTAAATGGGGTCTCTGCTCAAGTTGAAGA	1785
Db	598	CTCTCCTTTCTTACTTAACTCCAGTGAAGTAAATGGGGTCTCTGCTCAAGTTGAAGA	657	
QY	1786	GTCCATATTCACACTAGCCCTCCGCTCTGTGTAATGGACATC	1829	
Db	658	GTTCATATTCACACTAGCCCTCCGCTCTGTGTAATGGACATC	701	
RESULT	8			
BS531689				
LOCUS	BS531689	946 bp	mRNA	EST
DEFINITION	602560237.1	NIH_MGC_61	Homo sapiens	CDNA clone IMAGE:4698320 5', mRNA sequence.
ACCESSION	BS531689			
VERSION	BS531689.1	GI:13523227		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 946)			
TITLE	NIH-MGC http://mhc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bhs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM1528 row: 1 column: 09 High quality sequence stop: 551. Location/Qualifiers 1. 946 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4698320" /clone_lib="NIH_MGC_61" /tissue_type="embryonal carcinoma" /lab_host="DH10B (TI phage-resistant)" /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1 SfiI (ggccgcctcgccc); Site_2: SfiI (ggccatcatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGGCCGACGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."			
FEATURES	source			
BASE COUNT	279 a	186 c	292 g	189 t
ORIGIN				
Query Match	19.0%;	Score 429.4;	DB 154;	Length 946;
Best Local Similarity	84.5%;	Pred. No. 1.9e-110;		
Matches 601;	Conservative 0;	Mismatches 96;	Indels 14;	Gaps 10;
QY	25	ACCTGACGACACGACACTCCCTTT-GGCAAGACCTGAGACCCCTTGCTAAGTCAGA	83	
Db	72	ACCTGACGACACGACACTCCCTTTGGGCAAGACCTGAGACCCCTTGCTAAGTCAGA	131	
QY	84	GGCTCAATGGGCTCGA-GAAGACATGAGAGGAGGACCAAGCAAGGCATGATTTCCATG	142	
Db	132	GGCTCAATGGGCTCGAAGACATGAGAGGAGGACCAAGCAAGGCATGATTTTCATG	191	

OY	143	GAATGTGACAGACACCCAGAGGACTTTGTGAAATCTTCAAGTTGTGGGGTGGAACAT	202
Db	192	GAATGTGACAGACACCCAGAGGACTTTGTGAAATCTTCAAGTTGTGGGGTGGAACAT	251
OY	203	GCTCTGTGTGATTTTCTGGCACAATCATGGAACCTACTGTCGAGCTTACCATTTATCTG	261
Db	252	GCTCTGTGTGATTTTCTGGCACAATCATGGAACCGAGCTGCGACTTACCATTTATCTGA	311
OY	262	AAAAACCATGAACCTGGCAAGGGCTAGAGAATTTCTGCCGAGACATTTACACAGATTTAG	321
Db	312	AAAAACCATGAACCTGGCAAGGGCTAGAGAATTTCTGCCGAGACATTTACACAGATTTAG	371
OY	322	TTGGCAATACAAAACAAGGGGGGAAATTGA--GTAATCTGGAGAAGAACTCTGCCCTTCACTGCT	380
Db	372	TTGGCAATACAAAACAAGGGGGGAAATTGAGTAATCTGGAGAAGAACTCTGCCCTTCACTGCT	431
OY	381	TCTTACTACTGATAGAGATCCGGAGAATAGAG--GAAATATGACGTGGGTGGGAACCA	439
Db	432	TCTTACTACTGATAGAGATCCGGAGAATAGAGCCGAAATATGAGCCTGGGTGGGAACCA	491
OY	440	CAAACTCTCACTG--AAGAAACAGAGAACTGGGGAGATGGTGAAGCCCAACAAGAGAG	497
Db	492	AAATCTCTTACTGGGAACGAAACAGAGAACTGGGGAGATGGTGAAGCCCAACAAGAGAG	551
OY	498	AACAAGAGAGACTGGGTGAGATCTATTTCAAG--AAACAAATGTCAAGCAATATG	554
Db	552	ACCGAGAGAGACTGGGTGAGATCTATTTAAAGAGAAACAGAAATTTCCAAGCAATATG	611
OY	555	AACGATGAGCGCTGGCACAAATCTAAAGCACCCCTCTGTAC--ACAGCTCTTGCGACAC	612
Db	612	GCAACGATAGCCTTGCACAAAAGTAAAGGGAGCCCTTGTGATACCGGACGCTTCTTCCAG	671
OY	613	CTGTGTCATGACAGTGGCCATGAGAAATGTGTAGAAATCATCAATATTCACACCTGCACT	672
Db	672	CC--GCTCGTAGTGACCATGGCCGAGCGCGGTGAATCTCAAGATTTGAACGGCAATG	730
OY	673	GTGA--TGTGGGCTACTATATGGCCCCAGTGTACGCTTGTGATTCAGTGTAG	722
Db	731	GTGAGCGTGTGGTACTGTGGCCACAGTGAAGTGTGATCGAGTACCTTGA	781

RESULT	9
LOCUS	AA669146/c
DEFINITION	AA669146 575 bp MRNA EST 20-NOV-1997
ACCESSION	AB94AC05.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
VERSION	IMAGE:854600.3, MRNA sequence.
KEYWORDS	AA669146
SOURCE	AA669146.1 GI:2630645
ORGANISM	EST. human.
REFERENCE	Homo sapiens Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini: Homnidae: Homo. 1 (bases 1 to 575)
AUTHORS	Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Krizman,D., Kucab,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin, J., Moore,B., Schellenberg,K., Stepcoe,M., Tan,F., Theisling,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
TITLE	Washu-NCI human EST Project
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.jnl.gov) for further information. Seq primer: -00mj fwd. Err from Amersham High quality sequence stop: 473.
FEATURES	
source	1..575 Location/Qualifiers /organism="Homo sapiens"

```

/db_xref="taxon:9606"
/clone_lib="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: lung; Vector: Bluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: oligo
dt, normal lung. Average insert size: 1.0 kb; Uni-2AP XR
vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
BASE COUNT      197 a      90 c      146 g      142 t
ORIGIN

```

```

Query Match      18.9%; Score 426.4; DB 10; Length 575;
Best Local Similarity 98.2%; Pred. No. 1.1e-109;
Matches 442; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

```

```

QY 1786 CTCCTATTGGCACTGACCTGCGCTGTGTGAATTGGACATCTTAACTGGCTTC 1845
|||||
DB 575 GTCCTATTGGCACTGACCTGCGCTGTGTGAATTGGACATCTTAACTGGCTTC 518
|||||
QY 1846 AGGCTCCACCTCTTTCAGCCACCTCTTTCAGTTGGCTGACCTCCACCTAGC 1905
|||||
DB 517 CAGCCCTCCACCTCTTTCAGCCACCTCTTTCAGTTGGCTGACCTCCACCTAGC 458
|||||
QY 1906 ATCTCATGATGCGCAAGCAAAAGAGAGAGAAATAGCCTGCGGTTTTTAACTT 1965
|||||
DB 457 ATCTCATGATGCGCAAGCAAAAGAGAGAGAAATAGCCTGCGGTTTTTAACTT 398
|||||
QY 1966 TGGGGTTTTGCTGTTTCTTTATAGAACCTATTCCTATTCTTTATAGCATGTTTC 2025
|||||
DB 397 TGGGGTTTTGCTGTTTCTTTATAGAACCTATTCCTATTCTTTATAGCATGTTTC 338
|||||
QY 2026 TTATACAGATATTATTAGTAAGAAACATCACTGAATGCTGCAAGTACATCTC 2085
|||||
DB 337 TTATACAGATATTATTAGTAAGAAACATCACTGAATGCTGCAAGTACATCTC 218
|||||
QY 2086 TTATGATGATATGAAGAGTTAAACAGGTGAGAAATTCCTTGATTCACATGAATG 2145
|||||
DB 277 TTATGATGATATGAAGAGTTAAACAGGTGAGAAATTCCTTGATTCACATGAATG 218
|||||
QY 2146 CTCCTCTTCCCTGCGCCAGACATTTATACACTTACCTAGATTCATATTCCTTA 2205
|||||
DB 217 CTCCTCTTCCCTGCGCCAGACATTTATACACTTACCTAGATTCATATTCCTTA 158
|||||
QY 2206 AATTTCACTCAAGGCTCCCTCAACCCAC 2235
|||||
DB 157 AATTTCACTCAAGGCTCCCTCAACCCAC 128

```

```

RESULT 10
BG236008/c 567 bp mRNA EST 12-FEB-2001
LOCUS na120h11.x1 Soares_NPBMc Homo sapiens cDNA clone IMAGE:4141700 3',
DEFINITION mRNA sequence.
ACCESSION BG236008
KEYWORDS BG236008.1 GI:12749855
SOURCE EST.
ORGANISM human.

```

```

REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCT-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
Tumor Gene Index
Unpublished (1997)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

```

```

JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs.fda.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima

```

```

Bonardo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Seq primer: -40UP from G1bco
High quality sequence stop: 479.
location/Qualifiers
1. 567
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4141700"
/clone_lib="Soares_NPBMc"
/tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pTZ19-D-Pac; Site_1: NotI;
Site_2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTCACATCTGAACTGGAGGAGCGCGCGGTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTZ19 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."
BASE COUNT      191 a      88 c      142 g      146 t
ORIGIN

```

```

Query Match      18.6%; Score 419.8; DB 175; Length 567;
Best Local Similarity 99.3%; Pred. No. 8.1e-108;
Matches 432; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

```

QY 1801 TACCTGCGCGTGTGAATGGACATCTTAACTGCTTCAGCCCTCCACCTT 1860
|||||
DB 567 TACCTGCGCGTGTGAATGGACATCTTAACTGCTTCAGCCCTCCACCTT 509
|||||
QY 1861 CTCACGACCTCTCTTTTTCAGTGGCTGCTTCACACCTAGCATCTATGATGCCA 1920
|||||
DB 508 CTCACGACCTCTCTTTTTCAGTGGCTGCTTCACACCTAGCATCTATGATGCCA 449
|||||
QY 1921 AGCAAAAGAGAGAGAGAAATAGCCTGCGGTTTTTATGTTGGGGTTTGCTGT 1980
|||||
DB 448 AGCAAAAGAGAGAGAGAAATAGCCTGCGGTTTTTATGTTGGGGTTTGCTGT 369
|||||
QY 1981 TTCTTTTATGAGACCATCTATTTCTTATAGTCAATGTTCTTTTATCAGATATTA 2040
|||||
DB 388 TTCTTTTATGAGACCATCTATTTCTTATAGTCAATGTTCTTTTATCAGATATTA 329
|||||
QY 2041 TTATGTAAGAAACATCATGTAATGCTAGCTGCAAGTACATCTCTTATGATGATG 2100
|||||
DB 328 TTATGTAAGAAACATCATGTAATGCTAGCTGCAAGTACATCTCTTATGATGATG 269
|||||
QY 2101 AAGAGTTAAACAGGTGAGAAATTCCTTGATTCACATGAATGCTTCCTTCCCTG 2160
|||||
DB 268 AAGAGTTAAACAGGTGAGAAATTCCTTGATTCACATGAATGCTTCCTTCCCTG 209
|||||
QY 2161 CCCCAGAACTTTTATCAGTACCTAGATTCATATCTTTTAAATTCATCTCAGGC 2220
|||||
DB 208 CCCCAGAACTTTTATCAGTACCTAGATTCATATCTTTTAAATTCATCTCAGGC 149
|||||
QY 2221 CTCCTCAACCCAC 2235
|||||
DB 148 CTCCTCAACCCAC 134

```

```

RESULT 11
N72396 465 bp mRNA EST 02-APR-1996
LOCUS YV39c11.r1 Soares fetal liver spleen INF5 Homo sapiens cDNA clone
DEFINITION IMAGE:245108 5' similar to gb:U16150_cds1 L-SELECTIN PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION N72396

```

VERSION	N72396.1	GI:1229500
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 465)	
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman , M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maitis,M., Parsons,J. Riffin,L., Roifling,T., Soares,M., Tan,F., Trevaaskis,E., Waterston , R., Williamson,A., Woldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: reverse ET High quality sequence stop: 369.	
FEATURES	Location/Qualifiers	
Source	1..465	
	/organism="Homo sapiens"	
	/db_xref="GDB:3794354"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:245108"	
	/clone_lib="Soares fetal liver spleen INFUS"	
	/sex="male"	
	/dev_stage="20 week post conception fetus"	
	/lab_host="DH10B (ampicillin resistant)"	
	/note="Organ: Liver and Spleen; Vector: pTR13d (Pharmacia with a modified polylinker; Site.1: Pac I; Site.2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGGAGAAATTAATAAAGACTCTTTTCTTTTTTTTTTTT 3'] double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT	123 a 107 c 103 g 127 t	5 others
ORIGIN		
Query Match	18.0%; Score 406.4; DB 159; Length 465;	
Best Local Similarity	97.6%; Pred. No. 4.8e-104;	
Matches 454; Conservative	0; Mismatches 4; Indels 7; Gaps 4;	
OY	709 TGAATCAGTGAGCGCTTTGGAGGCCCAAGACGTGGTACCATTGACGTACTACCCCT	768
Db	4 TGATTCAGTGTGAGCCTTTGGAGG-COCAGAGCTGGGTACCATGGACGTACTCA-CCCT	61
OY	769 TTGGAACCTTCAGCTTCAGCTCACAGTGTGCCTTCAGCTGCTGGAAGAACAACCTTAA	828
Db	62 TTGGAACCTTCAGCTTCA-NTCACAGTGTGCCTTCAGCTGCTGGAAGAACAACCTTAA	120
OY	829 CTGGGATTTGAGAACCAACCCGTGTGACCATTTGGAAAACGTGTCATCTCAGAACCAACT	888
Db	121 CTTGGATTTGAGAACCAACCCGTGTGACCATTTGGAAAACGTGTCATCTCAGAACCAACT	180
OY	889 GTCAAGTATTCAGTGTGAGCCTTATCAGCAGCAGATTTGGGGATCATGTAAGTGTAGCC	948
Db	181 GTCAAGTATTCAGTGTGAGCCTTATCAGCAGCAGATTTGGGGATCATGTAAGTGTAGCC	240
OY	949 ATCCCCCGGCAGCTTACGCTTTACCTCTGCATGTA---CCTTCATCTGCTCAGAAAGA	1004
Db	241 ATCCCCCGGCAGCTTACGCTTTACCTCTGCATGNACNTTCATCTGCTCATTAAGA	300
OY	1005 ACTGAGTAAATTTGGAGAAAGAAACCATTTGTAATCATCTGGAATCTGGTCAAATCT	1064
Db	301 ACAGAGTAAATTTGGAGAAAGAAACCATTTGTAATCATCTGGAATCTGGTCAAATCT	360

QY	1065	AGTCCAAATATGCAAAAATTGCGACAAAAGTTTCCAAATGATTAAGGAGGCGATATATAC	1124
Db	361	AGTCCAAATATGCAAAAATTGCGACAAAAGTTTCCAAATGATTAAGGAGGCGATATATAC	420
QY	1125	CCCCCTTCATTCAGTGGCAGTCATGTTACTGCATTTCTGGG	1169
Db	421	CCCCCTTCATTCAGTGGCAGTCATGTTACTGCATTTCTGGG	465
RESULT	12		
LOCUS	AV737434	552 bp	mRNA
DEFINITION	AV737434	CB Homo sapiens cDNA clone CBCCE10	5', mRNA sequence.
ACCESSION	AV737434		
VERSION	AV737434.1	GI:10855015	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 552)		
TITLE	Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M., and Chen,Z.		
JOURNAL	Homo sapiens CB library cDNA clones		
COMMENT	Unpublished (2000)		
CONTACT	Contact: Zhu Chen		
	Shanghai Institute of Hematology, Rui-jin Hospital		
	197 Rui-jin II Road, Shanghai 200025, P. R. China		
	Tel: 86-21-64740490		
	Fax: 86-21-64743206		
	Email: mbs@hems.sh.cn		
	This clone is available at Shanghai Hematology Institute in Shanghai.		
	Chinese National Human Genome Center at Shanghai		
	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.		
FEATURES	Location/Qualifiers		
SOURCE	1..552		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="CBCEP10"		
	/clone_11b="CB"		
	/tissue_type="cord blood"		
	/cell_type="CD34+ hematopoietic stem/progenitor cell"		
	/lab_host="BM25.8"		
	/note="Vector: plasmid; Site: 1: EcoRI. The insert is cloned randomly with the EcoRI digestion"		
BASE COUNT	166 a 120 c 149 g 112 t 5 others		
ORIGIN			
Query Match	17.8%; Score 403.2; DB 110; Length 552;		
Best Local Similarity	93.8%; Pred. No. 4.2e-103;		
Matches 496; Conservative	0; Mismatches 21; Indels 12; Gaps		
QY	87	TCATGGGCGTCGAGAACTGAGAAAGGACCAAGCAAGCCATGATTTCCATGGAAA	146
Db	15	TCGATGCGGTCGACAGAGACGACAAAGGCGCAAGCAAGCCATGATTTCCATGGAAA	74
QY	147	TGTACAGACACCAGAGGAGCTTATGAAACATCTTCAAGTTGTGGGGGTGACATGTC	206
Db	75	TGTACAGACACCAGAGGAGCTTATGAAACATCTTCAAGTTGTGGGGGTGACAAAGTC	134
QY	207	TGTTTGATTTTCTGTGGCAGCATGAGAACTGACTGTGGACCTTACCATTTATTTGAAAA	266
Db	135	TGTTTGATTTTCTGTGGCAGCATGAGAACTGACTGTGGACCTTACCATTTATTTGAAAA	194
QY	267	CCCATGACATGCAAAAGGCTGAGAGATTTCGCGAGACAAATTACACAGATTAGTTGCC	326
Db	195	CCCATGACATGCAAAAGGCTGAGAGATTTCGCGAGACAAATTACACAGATTAGTTGCC	254
QY	327	ATACAAACAGCGAAATTGATCTGAGAGAACTCTGCCCTTCAGTGGTTCTTAC	386

Db	384	GGTGAAGAAATTTCTTGGATACACTGAAATCATGATGCTTTAAATCCTTCCATGAA	325
OY	1317	CGTTTGTGTGTGGACCTCCTACGTAAACATGAGTGTG-TTCCTTCAGTGCATCTG	1375
Db	324	CGTTTGTGTGTGGACCTCCTACGTAAACATGAGTGTGTCNTTCAAGTGATCTG	265
OY	1376	GGAACATTTCTACCCGACCAACAGTCTTCAAGCTTCATTTCCGCTCATTTATCCCT	1435
Db	264	GGAAATTTCTACCCGACCAACAGTCTTCAAGCTTCATTTCCGCTCATTTATCCCT	205
OY	1436	CAACCCCAAGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTTGAGGAAACA	1495
Db	204	CAACCCCAAGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTTGAGGAAACA	145
OY	1496	AATAAGACCAT-AAGGGAAGGATTCATGTGGAATATATAAGATGGCTACCTTGTCTTT	1554
Db	144	AATAAGACCATTAAGGGAAGGATTCATGTGGAATATATAAGATGGCTACCTTGTCTTT	85
OY	1555	CTTGACTCTGTTTTCAGTTTCATTCATTCAGTGTCTACTTGTATGACAGCACTTCAATG	1614
Db	84	CTTGACTCTGTTTTCAGTTTCATTCATTCAGTGTCTACTTGTATGACAGCACTTCAATG	25
OY	1615	AAGTCAAAATTTGATACATATGTG 1638	
Db	24	AAGTCAAAATTTGATACATATGTG 1	
RESULT 14			
LOCUS	AI694304	566 bp mRNA	EST 17-DEC-1999
DEFINITION	w45c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone		
ACCESSION	AI694304		
VERSION	AI694304.1	GI:4971644	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 566)		
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1429 Std Error: 0.00 Seq primer: -40UP from Glbco High quality sequence stop: 458. Location/Qualifiers 1..566 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:231078" /clone_id="Soares_NFL_T_GBC_S1" /lab_host="DH10B" /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH119W, testis NT1, and B-cell NCI-GARP GCB1) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."		
FEATURES	Source		
BASE COUNT	189 a	86 c	139 g 152 t
ORIGIN			

Query Match 17.7%; Score 399.8; DB 23; Length 566;
 Best Local Similarity 99.1%; Pred. No. 3.9e-102;
 Matches 423; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

1810 CCTGCTGTAATGGGACCATCTATTAACTGGCTGAGGCTCCCACTCTCTTCAGCCA 1869
 |||||||
 Db 566 CCTGCTGTAATGGGACCATCTATTAACTGGCTGAGGCTCCCACTCTCTTCAGCCA 508
 1870 CCTCTCTTTTCACTGCTGCTGACTTCCACACCTAGCATCTCATGAGTGGCAAGCAAGG 1929
 |||||||
 Db 507 CCTCTCTTTTCACTGCTGCTGACTTCCACACCTAGCATCTCATGAGTGGCAAGCAAGG 448
 1930 AGAGAAGAGAAATAGCTGCGCGCTTTTATGTTGGGGGTTTGGCTTCCCTTTA 1989
 |||||||
 Db 447 AGAGAAGAGAAATAGCTGCGCGCTTTTATGTTGGGGGTTTGGCTTCCCTTTA 388
 1990 TGAGACCCATCTCTTATTTCTTATGCAATGTTCTTTATCAGCATTTATTAGTAAGA 2049
 |||||||
 Db 387 TGAGACCCATCTCTTATTTCTTATGCAATGTTCTTTATCAGCATTTATTAGTAAGA 328
 2050 AATCATCTGTAATGCTAGTGCAGTGCAGATCTCTTGTATGTCATATGGAAGCTTAA 2109
 |||||||
 Db 327 AATCATCTGTAATGCTAGTGCAGTGCAGATCTCTTGTATGTCATATGGAAGCTTAA 268
 2110 AACAGTGGAGAAATTCCTTGTATGTCATATGGAAGCTTCTCTT -CCCTGCGCCCA 2168
 |||||||
 Db 267 AACAGTGGAGAAATTCCTTGTATGTCATATGGAAGCTTCTCTT -CCCTGCGCCCA 208
 2169 ACTTTTATCCTTACCTTACATTTCTTAAATTTCAATCAGGCTCCCTCA 2228
 |||||||
 Db 207 CCTTTATTCATCTTACTTACTTATGATTTCAATATTTCTTAAATTTCAATCAGGCTCCCTCA 148
 2229 ACCCCAC 2235
 |||||||
 Db 147 ACCCCAC 141

RESULT 15
 BF902611 403 bp mRNA EST 18-JAN-2001
 LOCUS CMI-MT0238-141200-653-a12 MT0238 Homo sapiens cDNA, mRNA sequence.
 DEFINITION CMI-MT0238-141200-653-a12 MT0238 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF902611
 VERSION BF902611.1 GI:12294070
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 403)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPERB/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CMI6t2-CMI-MT0238-
 141200-653-a12&t3=2000-12-14&t4=1)

Seq primer: puc 18 forward
 High quality sequence stop: 403.
 FEATURES
 source
 1. 403
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MT0238"
 /dev_stage="Adult"
 /note="organ: marrow; Vector: puc18; Site.1: SmaI; Site.2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 ,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 104 a 95 c 100 g 104 t
 ORIGIN

Query Match 17.6%; Score 396.6; DB 171; Length 403;
 Best Local Similarity 99.0%; Pred. No. 2.8e-101;
 Matches 399; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

624 AGTGGCATGAGAAATGTGTAGAAATCATCAATATACACCTGCACTGTGATGGG 683
 |||||||
 Db 1 AGTGGCATGAGAAATGTGTAGAAATCATCAATATACACCTGCACTGTGATGGG 60
 684 TACTATGGGCCCCAGGTGACGTTGATTGATGAGGCTTTGGAGGCCACAGCTG 743
 |||||||
 Db 61 TACTATGGGCCCCAGGTGACGTTGATTGATGAGGCTTTGGAGGCCACAGCTG 120
 744 GGTACCATGAGTGTACTACCCCTTTGGAACTTCAGCTCAGCTCAGCTGTCCTTC 803
 |||||||
 Db 121 GGTACCATGAGTGTACTACCCCTTTGGAACTTCAGCTCAGCTCAGCTGTCCTTC 180
 804 AGCTGCTGGAAGGAAACAATTAAGTGGGATTGAAGAAACACCTGTGGACATTGGA 863
 |||||||
 Db 181 AGCTGCTGGAAGGAAACAATTAAGTGGGATTGAAGAAACACCTGTGGACATTGGA 240
 864 AACGTGCTATCCGGAACCAACCTGTCAAGTATGATGAGGCTTATCAGACCA 923
 |||||||
 Db 241 AACGTGCTATCCGGAACCAACCTGTCAAGTATGATGAGGCTTATCAGACCA 300
 924 GATTGGGATCATGAACCTGTAGCCATCCCTGGCCAGCTTACGTTTAACTGTGCATGT 983
 |||||||
 Db 301 GATTGGGATCATGAACCTGTAGCCATCCCTGGCCAGCTTACGTTTAACTGTGCATGT 360
 984 ACCTTCATCTGCTCAGAGGAACCTGAGTTAATTGGGAGAGAA 1026
 |||||||
 Db 361 ACCTTCATCTGCTCAGAGGAACCTGAGTTAATTGGGAGAGAA 403

Search completed: October 13, 2001, 00:33:41
 Job time: 4520 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:18:25 ; Search time 3951.8 Seconds
(without alignments)
8841.957 Million cell updates/sec

Title: US-09-119-209-1
Perfect score: 2259
Sequence: 1 GAATTCAGCTGCTGCTGCTT.....CCGCCAGCACACTGGATTTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_hcgo_hum:*
20: em_hcgo_inv:*
21: em_hcgo_rod:*
22: em_hcgo_hum1:*
23: em_hcgo_hum2:*
24: em_hcgo_hum3:*
25: em_hcgo_hum4:*
26: em_hcgo_hum5:*
27: em_hcgo_hum6:*
28: em_hcgo_hum7:*
29: em_hcgo_hum8:*
30: em_hcgo_inv1:*
31: em_hcgo_inv2:*
32: em_hcgo_other:*
33: em_hcgo_rod:*
34: em_hum1:*
35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*

44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
48: em_rod:*
49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_v1:*
53: gb_sts1:*
54: gb_sts2:*
55: gb_sts3:*
56: gb_sy:*
57: gb_un:*
58: gb_v11:*
59: gb_v12:*
60: gb_hcgo1:*
61: gb_hcgo2:*
62: gb_hcgo3:*
63: gb_hcgo4:*
64: gb_hcgo5:*
65: gb_hcgo6:*
66: gb_hcgo7:*
67: gb_hcgo8:*
68: gb_hcgo9:*
69: gb_hcgo10:*
70: gb_hcgo11:*
71: gb_hcgo12:*
72: gb_hcgo13:*
73: gb_hcgo14:*
74: gb_hcgo15:*
75: gb_hcgo16:*
76: gb_hcgo17:*
77: gb_hcgo18:*
78: gb_hcgo19:*
79: gb_hcgo20:*
80: gb_hcgo21:*
81: gb_hcgo22:*
82: gb_hcgo23:*
83: gb_hcgo24:*
84: gb_hcgo25:*
85: gb_pr1:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_pr10:*
95: gb_pr11:*
96: gb_pr12:*
97: gb_pr13:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2259	100.0	2259	9 AR060685	AR060685 Sequence
2	2258	100.0	2259	97 MIMPLNHR	X16070 Human mRNA
3	2161	95.7	2354	97 HUMTLNR	M25280 Human lymph
4	2127.8	94.2	2323	93 HSLDEU8	X17519 Human mRNA
5	2087.6	92.4	2330	9 AR016679	AR016679 Sequence
6	2087.6	92.4	2330	9 AR040718	AR040718 Sequence
7	2087.6	92.4	2330	9 AR054061	AR054061 Sequence
8	2087.6	92.4	2330	10 I70140	I70140 Sequence 1

D	b	61	GAGACCCCTTGTCCTAAGTCAAGAGGCTCAATTGGGCTCAGAGAACTAGAGGAAGACCA	120
Q	y	121	GCAAGGCATATATTTTCCATGGAATAAGTACAGACACCCAGAGGAGCTTATGGAACATCG	180
D	b	121	GCAAGGCATATATTTTCCATGGAATAAGTACAGAGCACCCAGAGGAGCTTATGGAACATCG	180
Q	y	181	TCAAGTTGTGGGGTGCACATGCTCTGTTGTGATTTCTGGCACATCATGGAACCTACT	240
D	b	181	TCAAGTTGTGGGGTGCACATGCTCTGTTGTGATTTCTGGCACATCATGGAACCTACT	240
Q	y	241	GCTGACCTTACCATTTATCTGAAAAACCCATGSAACGGCAAGGGCATAGAAAGTTCTGGCC	300
D	b	241	GCTGACCTTACCATTTATCTGAAAAACCCATGSAACGGCAAGGGCATAGAAAGTTCTGGCC	300
Q	y	301	GAGACATTTACAGAGATTAGTGGCATACAAAAACAAGGGGAAATTGATATCTGGAGA	360
D	b	301	GAGACATTTACAGAGATTAGTGGCATACAAAAACAAGGGGAAATTGATATCTGGAGA	360
Q	y	361	AGACTCGCCCTTCAGTCGTTCTTACTACTGATAGGAATCCGGAAGATTAGAGAGAAAT	420
D	b	361	AGACTCGCCCTTCAGTCGTTCTTACTACTGATAGGAATCCGGAAGATTAGAGAGAAAT	420
Q	y	421	GGAGCTGGGTGGGAGACCAAAATCTCTCACTAABAAGCAGAGAACTGGGAGATGGTG	480
D	b	421	GGAGCTGGGTGGGAGACCAAAATCTCTCACTAABAAGCAGAGAACTGGGAGATGGTG	480
Q	y	481	AGCCCAACACAAGAAAGAACAGSAGAGCTGCTGGAGATCTTTATCAGAGAGAAACAAG	540
D	b	481	AGCCCAACACAAGAAAGAACAGSAGAGCTGCTGGAGATCTTTATCAGAGAGAAACAAG	540
Q	y	541	ATGCAAGGCAAAATGGAACGATGACGCTGCACAAACTAAAGGCAAGCCCTCTTTACACAG	600
D	b	541	ATGCAAGGCAAAATGGAACGATGACGCTGCACAAACTAAAGGCAAGCCCTCTTTACACAG	600
Q	y	601	CTTCTTGCCACAGCCCTGTATGCAATGGGCCATGAGAAATGTGCAAAATCATCAATATATC	660
D	b	601	CTTCTTGCCACAGCCCTGTATGCAATGGGCCATGAGAAATGTGCAAAATCATCAATATATC	660

4

QY	721	AGTTTTGAGAGGCCCGAGAGCTGGGTACACATGAGACCTGTACTACCCCTTTGGAAACTTCA	780
Db	721	AGCTTTTGGAGGCCCCAGAGCTGGGTACATGAGACTGTACTACCCCTTTGGAAACTTCA	780
QY	781	GCTTCAGCTCACAGTGTGGCTTCAGCTGCCTCGAAGGAACAACCTTAACCTGGATTGAAG	840
Db	781	GCCTTCAGCTCACAGTGTGGCTTCAGCTGCCTCGAAGGAACAACCTTAACCTGGATTGAAG	840
QY	841	AAACCACTGTGGACCATTTGGAACTGTCATCTTCAGAACCAACCTGTCAAGTATTC	900
Db	841	AAACCACTGTGGACCATTTGGAACTGTCATCTTCAGAACCAACCTGTCAAGTATTC	900
QY	901	AGGTGAGGCTCATGAGACCAAGATTTGGGATCATATGAACGTGAGCATCCCTGGGCA	960
Db	901	AGGTGAGGCTCATGAGACCAAGATTTGGGATCATATGAACGTGAGCATCCCTGGGCA	960
QY	961	GCCTCAGCTTACCTTCGCATGTACCTTCATCTGCTCAGAAAGAACTAGTTAATTGGGA	1020
Db	961	GCCTCAGCTTACCTTCGCATGTACCTTCATCTGCTCAGAAAGAACTAGTTAATTGGGA	1020

1021	AGAGAAACCATTTGTGATCATCTGGAATCTGTCAAATCCTACGCCAATATGTCAAA	1080
------	--	------

[illegible]

QY	1201	TAAAAAAGGCAAGAAATCCAGAGAAGTATGAATGACCATATTAATATGCCCTTGCTG	1260
Db	1201	TAAAAAAGGCAAGAAATCCAAAGAGATATGAATGACCATATTAATATGCCCTTGCTG	1260
QY	1261	AAAGAAATATCTTGGAATACTAAAAATCATGACATCCCTTAATCCCTTCATGAAAGCTT	1320
Db	1261	AAAGAAATATCTTGGAATACTAAAAATCATGACATCCCTTAATCCCTTCATGAAAGCTT	1320
QY	1321	TGTGTGTGGGCACTCCTCAAGCTCAAAACATGAAGTGTGTCTTCAGTGCATCGGGAG	1380
Db	1321	TGTGTGTGTGGCACTCCTCAAGCTCAAAACATGAAGTGTGTCTTCAGTGCATCGGGAG	1380
QY	1381	ATTTCATCCCGGACCAACAGTTCCTTAGCTTCATATTTGCCCTCATTTATCCCTCAAC	1440
Db	1381	ATTTCATCCCGGACCAACAGTTCCTTAGCTTCATATTTGCCCTCATTTATCCCTCAAC	1440
QY	1441	CCAGGCCCAAGGTGTTTATACAGCTCAGCTTTTGTCTTTCGAGGACAAACAAATA	1500
Db	1441	CCAGGCCCAAGGTGTTTATACAGCTCAGCTTTTGTCTTTCGAGGACAAACAAATA	1500
QY	1501	GACCATAAAGGAAAGGATTCATGTGAATTAAGAATGCGTGACTTGTCTTTCTTGAC	1560
Db	1501	GACCATAAAGGAAAGGATTCATGTGAATTAAGAATGCGTGACTTGTCTTTCTTGAC	1560
QY	1561	TCTGTGTTTACGTTTCAATTCAGTGCCTGTACTTGTATGACAGACACTTCTAATGAAGTGC	1620
Db	1561	TCTGTGTTTACGTTTCAATTCAGTGCCTGTACTTGTATGACAGACACTTCTAATGAAGTGC	1620
QY	1621	AAATTTGATACATATGTAATATGACACTAGTTTCTTGAGATCAAAATTTTCAGCTGTC	1680
Db	1621	AAATTTGATACATATGTAATATGACACTAGTTTCTTGAGATCAAAATTTTCAGCTGTC	1680
QY	1681	TTCTGTATACTGGAGAGTACACTCTTAATGAAGTTCAAAAAGTCAAGCTCCTCTTC	1740
Db	1681	TTCTGTATACTGGAGAGTACACTCTTAATGAAGTTCAAAAAGTCAAGCTCCTCTTC	1740
QY	1741	TTTTCTAAGTCCAGTGAAGTAAATGGGGCTCGCTCAAGTTGAAAAGAGTCCATTTGCACTG	1800
Db	1741	TTTTCTAAGTCCAGTGAAGTAAATGGGGCTCGCTCAAGTTGAAAAGAGTCCATTTGCACTG	1800
QY	1801	TAGCCCTGGCGCTGTGGAATTTGGACCATCTATTTAAGTGGCTTCAGGCTCCCCACTT	1860
Db	1801	TAGCCCTGGCGCTGTGGAATTTGGACCATCTATTTAAGTGGCTTCAGGCTCCCCACTT	1860
QY	1861	CTTCAGCCACCTCTCTTTTTCAGTTGGGCTACTTCCACACCTTAGCATATGAGTGC	1920
Db	1861	CTTCAGCCACCTCTCTTTTTCAGTTGGGCTACTTCCACACCTTAGCATATGAGTGC	1920
QY	1921	AGCAAAAGAGAGAAAGAGAAATAGCCCTGCGGGTTTTTACTTTGGGGGTTTTGCTGT	1980
Db	1921	AGCAAAAGAGAGAAAGAGAAATAGCCCTGCGGGTTTTTACTTTGGGGGTTTTGCTGT	1980
QY	1981	TTTCCTTTTATGAGACCATTTCCATTTTCTATATGTCAAATGTTTTCTTTTATCAGATATTA	2040
Db	1981	TTTCCTTTTATGAGACCATTTCCATTTTCTATATGTCAAATGTTTTCTTTTATCAGATATTA	2040
QY	2041	TTAGTAAAGAAACATACAGTGAATGGTAGGTGGAAGGACATCTCTTTGATGTGCATATGG	2100
Db	2041	TTAGTAAAGAAACATACAGTGAATGGTAGGTGGAAGGACATCTCTTTGATGTGCATATGG	2100
QY	2101	AAGAGTTAAAGAGTGTGAGAAATTCCTTGATTCACAAATGAATGCTCTTCCTCCCTG	2160
Db	2101	AAGAGTTAAAGAGTGTGAGAAATTCCTTGATTCACAAATGAATGCTCTTCCTCCCTG	2160
QY	2161	CCCCAGAACTTTTATCCACTTACCTAGATTTCTACATATCTTTAAATTTCACTCAGGC	2220
Db	2161	CCCCAGAACTTTTATCCACTTACCTAGATTTCTACATATCTTTAAATTTCACTCAGGC	2220
QY	2221	CTCCCTCAACCCACGGGGCCGCGACACACACTGTGAATTC	2259
Db	2221	CTCCCTCAACCCACGGGGCCGCGACACACACTGTGAATTC	2259
QY	2259	CTCCCTCAACCCACGGGGCCGCGACACACACTGTGAATTC	2259
Db	2259	CTCCCTCAACCCACGGGGCCGCGACACACACTGTGAATTC	2259

RESULT	2
LOCUS	MPLNLR 2259 bp mRNA PRI 31-DEC-1990
DEFINITION	Human mRNA for pln homing receptor homologue (peripheral lymph node).
ACCESSION	X16070.1 GI:38092
VERSION	X16070
KEYWORDS	Lymphocyte adhesion receptor; Lymphocyte homing receptor; transmembrane protein.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 2259)
AUTHORS	Bowen,B.R., Nguyen,T. and Laaky,L.A.
TITLE	Characterization of a human homologue of the murine peripheral lymph node homing receptor
JOURNAL	J. Cell Biol. 109 (1), 421-427 (1989)
MEDLINE	89308881
FEATURES	
source	Location/Organisms 1..2259 /organism="Homo sapiens" /db_xref="taxon:9606"
mRNA	/feature_type="peripheral lymph node"
s1g_peptide	/cell_type="Lymphocyte"
CDS	/clone_id="cDNA In lambda gt10"
	1..>2259
	129..242
	129..1247
	/codon_start=1
	/product="pln homing receptor"
	/protein_id="CAA34203.1"
	/db_xref="GI:38093"
	/db_xref="SWISS-PROT:P14151"
	/translation="MIPMKQSTYKRLMIIFKLGMWTMLCDFLAHNGTYCWTYNHS EKPNMSARFRCNDNTDLVAIONKAIELEKTLPESYYWIGIRKGITGGLTWVG TKNKLTDEAENMGDGEPPNNKKKNKECYETIKRNKDGNDDACHLKALCLYTASC QNPKSGSHGEVEELIINNHCNCSDVGYIGPOQLYIQEPYLEAELEGMDTHPRGNS FSSCAFCSSEGINVLGLETCGFPEAMSSPETCVICICEPUSADLLIMCSHL ASFESTACTPICTEGTELIGKRRTTEESSGISNPSPICOKLDKSFMREKDYNFL FIPLAVMTATPSGLAFILWIILARRLKKRKSRSMDNY"
	FIPAAVMATAFPSGLAFILWIILARRLKKRKSRSMDNY"
	243..1244
mat_peptide	/product="pln homing receptor"
	BASE COUNT 635 a 517 c 487 g 619 t 1 others
ORIGIN	
Query Match	100.0%; Score 2258; DB 97; Length 2259;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2258; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 GAATTCCAGTGCGTTGGCTTCCTCACGTGCAGCAGCAACAACCCTTGGCAAGACCT 60
Dd	1 GAATTCCAGTGCGTTGGCTTCCTCACGTGCAGCAGCAACAACAACCCTTGGCAAGACCT 60
Oy	61 GAGACCCTTGGCTTAAGCAAGAAGGCCGAATGGGTGAGAAAGAACCTGAGAAGACCAA 120
Dd	61 GAGACCCTTGGCTTAAGCAAGAAGGSTCAATGGGTGAGAAAGAACCTGAGAAGACCAA 120
Oy	121 GCAAAAGCATGATATTTCCATGGAATATGCAAGACCAACGAGGACTTATGGAACATCT 180
Dd	121 GCAAAAGCATGATATTTCCATGGAATATGCAAGACCAACGAGGACTTATGGAACATCT 180
Oy	181 TCAAGTTGTGGGGGTGACAAATGCTGTGTGTGATTTCTGGCAATCAGAACTACT 240
Dd	181 TCAGTTGTGGGGGTGACAAATGCTGTGTGTGATTTCTGGCAATCAGAACTACT 240
Oy	241 GCTGCACTTACCATTATCTGAAAAAACCCAAGCAAGCAAGGCAATGATTTGCCC 300
Dd	241 GCTGCACTTACCATTATCTGAAAAAACCCAAGCAAGGCAATGATTTGCCC 300
Oy	301 GAGACAATTACAGATTAGTTGCCATACAAAACAAAGGCGGAATTAGATCTGGAGA 360

```

|||||
Db 301 GAGCAGATTTACAGAGATTTAGTGGCCATACAAAACAGGGGAAATGAGATCTGGAGA 360
OY 361 AGACTGGCCCTCAGCTGCTTCTTACTAGTATAGAAATCCGGAGATATGAGGAATAT 420
Db 361 AGACTGGCCCTCAGCTGCTTCTTACTAGTATAGAAATCCGGAGATATGAGGAATAT 420
OY 421 GGAAGTGGTGGGACCAACAAATCTCTCACTAGAGAGAGAGAACTGGGGAGATGGT 480
Db 421 GGAAGTGGTGGGACCAACAAATCTCTCACTAGAGAGAGAGAACTGGGGAGATGGT 480
OY 481 AGCCCAACAACAAGAAAGAACAGAGAGACTGCGTGGAGATCTATATCAGAGAAACAAAG 540
Db 481 AGCCCAACAACAAGAAAGAACAGAGAGACTGCGTGGAGATCTATATCAAGAAACAAAG 540
OY 541 ATGCAGGCAAAATGGAAGATGAGCGCTGCCACAACAACTAAAGGAGCCCTGTATACAG 600
Db 541 ATGCAGGCAAAATGGAAGATGAGCGCTGCCACAACAACTAAAGGAGCCCTGTATACAG 600
OY 601 CTTCCTTGCCAGCCCTGCTATGCAATGAGAGATGAGAAATGTAATCATCATATATC 660
Db 601 CTTCCTTGCCAGCCCTGCTATGCAATGAGAGATGAGAAATGTAATCATCATATATC 660
OY 661 ACACCTGCAACTGTATGTGGGGTACTATAGGGCCCAAGTGTGAGCTTGTGATTCAGTGTG 720
Db 661 ACACCTGCAACTGTATGTGGGGTACTATAGGGCCCAAGTGTGAGCTTGTGATTCAGTGTG 720
OY 721 AGCCTTTGAGGGCCCGAGAGCTGGGATACCATGAGTGTACTACCCCTTTGAGAACTTCA 780
Db 721 AGCCTTTGAGGGCCCGAGAGCTGGGATACCATGAGTGTACTACCCCTTTGAGAACTTCA 780
OY 781 GCTTCAGCTCAGAGTGTGCTTCACTGTCTGAAAGAAACAACTTAACTGGGATTTGAAG 840
Db 781 GCTTCAGCTCAGAGTGTGCTTCACTGTCTGAAAGAAACAACTTAACTGGGATTTGAAG 840
OY 841 AAACCAACCTGTGACATTTTGAATGCTGCTATCTCCAAACCAACCTGTCAAGTATTC 900
Db 841 AAACCAACCTGTGACATTTTGAATGCTGCTATCTCCAAACCAACCTGTCAAGTATTC 900
OY 901 AGTGTAGGCTCTATCAGACACAGATTTGGGGATCATGAACTGTAAGCCATCCCTGGCCA 960
Db 901 AGTGTAGGCTCTATCAGACACAGATTTGGGGATCATGAACTGTAAGCCATCCCTGGCCA 960
OY 961 GCTTCAGCTTAACTCTGTCATCTACCTTCATCTGCTCAGAGAACTGATTAATTTGGA 1020
Db 961 GCTTCAGCTTAACTCTGTCATCTACCTTCATCTGCTCAGAGAACTGATTAATTTGGA 1020
OY 1021 AGAAGAAACCAATTTGTGAATCATGGAATGTCGAAATCTGTGCTCAATATGTCAAA 1080
Db 1021 AGAAGAAACCAATTTGTGAATCATGGAATGTCGAAATCTGTGCTCAATATGTCAAA 1080
OY 1081 AATTGGACAAAAGTTTCTCAATGATTAAGSAGSAGTATTAACCCCTTCATTTCCAG 1140
Db 1081 AATTGGACAAAAGTTTCTCAATGATTAAGSAGSAGTATTAACCCCTTCATTTCCAG 1140
OY 1141 TGGCAGTATGTTACTGCTCATTTCTCGGGTTGGCATTTATCATTTTGGCTGSCAAGAGAT 1200
Db 1141 TGGCAGTATGTTACTGCTCATTTCTCGGGTTGGCATTTATCATTTTGGCTGSCAAGAGAT 1200
OY 1201 TAAAAAAGGCAAGAAATCCAAAGAGATATGAATGACCAATTAATTCGCTTGGTG 1260
Db 1201 TAAAAAAGGCAAGAAATCCAAAGAGATATGAATGACCAATTAATTCGCTTGGTG 1260
OY 1261 AAAGAAATTTCTTGAATACTAAAAATCATGAGATCTTTAAATCCCTTCATGAAACGTT 1320
Db 1261 AAAGAAATTTCTTGAATACTAAAAATCATGAGATCTTTAAATCCCTTCATGAAACGTT 1320
OY 1321 TTGTGTGGTGGCACTCTCTAGTCAAAATGAGTGTCTTCTTCAAGTCACTGGGAG 1380
Db 1321 TTGTGTGGTGGCACTCTCTAGTCAAAATGAGTGTCTTCTTCAAGTCACTGGGAG 1380
OY 1381 ATTTCACCCAGCAACAGTTCCTTCACTTCATTTGGCCCTCATTTATCCGCAACC 1440
|||||

```

```

Db 1381 ATTTCACCCAGCAACAGTTCCTTCACTTCATTTGGCCCTCATTTATCCCTCAACC 1440
OY 1441 CCCAGCCACAGTGTTTATACAGCTCAGCTTTTGTCTTTCTGTGAGAAACAAATTA 1500
Db 1441 CCCAGCCACAGTGTTTATACAGCTCAGCTTTTGTCTTTCTGTGAGAAACAAATTA 1500
OY 1501 GACCATTAAGGAAAGATTCATGTGGAATATTAAGATGGCTGACCTTGTCTTGTGAC 1560
Db 1501 GACCATTAAGGAAAGATTCATGTGGAATATTAAGATGGCTGACCTTGTCTTGTGAC 1560
OY 1561 TCTTGTTCAGTTTCAATTCAGTGTCTGATGATGACAGACACTTCTAAATGAAGTGC 1620
Db 1561 TCTTGTTCAGTTTCAATTCAGTGTCTGATGATGACAGACACTTCTAAATGAAGTGC 1620
OY 1621 AATTTGATACATATGTGAAATATGAGTACAGTTTCTTGACATCAAAATTCAGCTGTC 1680
Db 1621 AATTTGATACATATGTGAAATATGAGTACAGTTTCTTGACATCAAAATTCAGCTGTC 1680
OY 1681 TTCTGTATACCTGTGGAGTACACTCTTATAGAAAGTCAAAAAGCTPAGGCTGCTTTC 1740
Db 1681 TTCTGTATACCTGTGGAGTACACTCTTATAGAAAGTCAAAAAGCTTACGCTTCTTTC 1740
OY 1741 TTTCTAATCTCAGTGAATATGAGGCTCTGCTCAAGTTGAAGAGTCTATTGCACTG 1800
Db 1741 TTTCTAATCTCAGTGAATATGAGGCTCTGCTCAAGTTGAAGAGTCTATTGCACTG 1800
OY 1801 TAGCCCTGGCGTGTGATGATGAGCAATCTATTTAACTGTGCTTCAAGCCCTCCACCTT 1860
Db 1801 TAGCCCTGGCGTGTGATGATGAGCAATCTATTTAACTGTGCTTCAAGCCCTCCACCTT 1860
OY 1861 CTTCAGCCACCTCTTTTTCAGTTGGCTGACTTCCACAGCTAGACATCTATGAGTGC 1920
Db 1861 CTTCAGCCACCTCTTTTTCAGTTGGCTGACTTCCACAGCTAGACATCTATGAGTGC 1920
OY 1921 AGCAAAAGAGAGAAAGAGAAATAGCTGCGCGGTTTTTTAGTTGGGGTTTTGCTGT 1980
Db 1921 AGCAAAAGAGAGAAAGAGAAATAGCTGCGCGGTTTTTTAGTTGGGGTTTTGCTGT 1980
OY 1981 TTCCCTTTATGAGACCCATTCCTTATTTCTATAGCAATGTTCTTTATAGATATTA 2040
Db 1981 TTCCCTTTATGAGACCCATTCCTTATTTCTATAGCAATGTTCTTTATAGATATTA 2040
OY 2041 TTAGTAAAGAAACATCACTGAATGCTAGCTGCAAGTACATCTTTGATGATATAG 2100
Db 2041 TTAGTAAAGAAACATCACTGAATGCTAGCTGCAAGTACATCTTTGATGATATAG 2100
OY 2101 AAGAGTTAAACAGGTGAGAAATTCCTGTGATTCACATGAATAGCTCTTCCCTG 2160
Db 2101 AAGAGTTAAACAGGTGAGAAATTCCTGTGATTCACATGAATAGCTCTTCCCTG 2160
OY 2161 CCCCAGAACTTTTATCCACTTACCTAGATTCATATTTCTTTAAATTCATCTCAGGC 2220
Db 2161 CCCCAGAACTTTTATCCACTTACCTAGATTCATATTTCTTTAAATTCATCTCAGGC 2220
OY 2221 CTCCCTCAACCCCAAGGGGCCGCCAGCACACTGGAATTC 2259
Db 2221 CTCCCTCAACCCCAAGGGGCCGCCAGCACACTGGAATTC 2259

RESULT 3
HOMLNR 3
LOCUS 2354 bp mRNA PRI 07-OCT-1998
DEFINITION Human lymph node homing receptor mRNA, complete cds.
ACCESSION M25280
VERSION M25280.1 GI:187182
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2354)
AUTHORS Siegelman, M.H. and Weissman, I.L.
TITLE Human homologue of mouse lymph node homing receptor: evolutionary

```

conservation at tandem cell interaction domains
Proc. Natl. Acad. Sci. U.S.A. 86 (14), 5562-5566 (1989)

JOURNAL

89315837

MEDLINE

Draft entry and computer-readable sequence for [1] kindly provided
by M.H. Siegelman, 02-JUN-1989.

Location/Qualifiers

FEATURES

source

1. .2354

/organism="Homo sapiens"

/db_xref="taxon:9606"

gene

1. .2354

/gene="LNRH"

116. .229

/note="Lymph node homing receptor precursor"

/note="Lymph node homing receptor signal peptide"

116. .1234

/gene="LNRH"

/note="Lymph node homing receptor precursor"

/codon_start=1

/db_xref="GDB:G00-118-834"

/protein_id="AAC63053.1"

/db_xref="GI:307134"

/translation="MIFPMKQSTQDRLNMIKILMGWMLCDFLAHGGIDCWTHYS
EKPMNQBARPCRDNTDLVAIONKAEIYLEKTFPSRSYVIGIRKIGITWVG
TKNSLEAEANMGDEBNKKNKEDVEIYIKRNDKKNNDACHLKALCTYASC
QPMSCGHECEVELINNYTNCNDYGYPCOLYIOCEPLEAPELGMDCHPLGNS
FSSOCARFSCSEGTNIGIEETGCGPENGMSPEPTCOVICELPSADLIMNSHPL
ASRFTSACTFICSEGTIELLIGKKTKTCESSGINSNPSPTICOKLDKFSMKIEGDYNFL
PIPVAVVNTVFSLSIAFLIWLARLIRKGRKSKRSNDY"

BASE COUNT 663 a 531 c 498 g 662 t

ORIGIN

Query Match 95.7% Score 2161; DB 97; Length 2354;
Best Local Similarity 99.4% Pred. No. 0;
Matches 2200; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

25 ACCGACGACAGACACTCCCTTTGGCAAGACCTGAGACCTTGTCTAAGTCAAG 84
12 ACCGACGACAGACACTCCCTTTGGCAAGACCTGAGACCTTGTCTAAGTCAAG 71
85 GCTCAATGGCTGCAAGAACTAGAGAAAGCAAGCAAGCAAGCAAGCAAGCAAG 144
72 GCTCAATGGCTGCAAGAACTAGAGAAAGCAAGCAAGCAAGCAAGCAAGCAAG 131
145 AATGTGAGAGACCCAGAGGACTTATGAACTCTTCAAGTTGGGGGTGGAACATGC 204
132 AATGTGAGAGACCCAGAGGACTTATGAACTCTTCAAGTTGGGGGTGGAACATGC 191
205 TCTGTGTGATTTCTGGACATCATGGAACCTGCTGACATTTACATTTATCTGAAA 264
192 TCTGTGTGATTTCTGGACATCATGGAACCTGCTGACATTTACATTTATCTGAAA 251
265 AACCCATGAACCTGGCAAGGCTAGAGATCTGCGGAGCAATTTACAGATTTAGTTG 324
252 AACCCATGAACCTGGCAAGGCTAGAGATTTCTGCGGAGCAATTTACAGATTTAGTTG 311
325 CCATACAAAACAGCGGAAATAGATCTGAGAAAGACTCTGCCCTTTCAGTGGTCTT 384
312 CCATACAAAACAGCGGAAATAGATCTGAGAAAGACTCTGCCCTTTCAGTGGTCTT 371
385 ACTACTGATAGGAATCCGGAAGATAGGAGAAATATGAGACGTGGTGGAAACAAT 444
372 ACTACTGATAGGAATCCGGAAGATAGGAGAAATATGAGACGTGGTGGAAACAAT 431
445 CTCACAGTGAAGAGAGAACTGGGAGATGGAGACCCCAACAACAAGAAAGCAAG 504
432 CTCACAGTGAAGAGAGAACTGGGAGATGGAGACCCCAACAACAAGAAAGCAAG 491
505 AGGACTGCTGGAGATCTATATCAAGAGAAACAAGATGACGAGCAATGGAACGATGACG 564
492 AGGACTGCTGGAGATCTATATCAAGAGAAACAAGATGACGAGCAATGGAACGATGACG 551
565 CTTGCCACAACCTAAAGGACGCTCTGTTACACAGCTTTTGGCAGGCTTGATGATCA 624

|||||
Db 552 CTTGCCACAACCTAAAGGACGCTCTGTTACACAGCTTTTGGCAGGCTTGATGATCA 611
625 GTGGCCATGAGAAATGTGTAGAAATCATCAATATACACCTGCAAGCTGTGTGGGT 684
612 GTGGCCATGAGAAATGTGTAGAAATCATCAATATATACACCTGCAAGCTGTGTGGGT 671
685 ACTATGGGCCCCAGTGTAGCTTGTGATTCAGTGTGACCTTTTGGAGGCCCCAGAGCTGG 744
672 ACTATGGGCCCCAGTGTAGCTTGTGATTCAGTGTGACCTTTTGGAGGCCCCAGAGCTGG 731
745 GTACCATGAGCTGTACTACCCCTTTGGAAACTTGTAGCTGAGCTCACAGTGTGCTTCA 804
732 GTACCATGAGCTGTACTACCCCTTTGGAAACTTGTAGCTGAGCTCACAGTGTGCTTCA 791
805 GCTGCTGTGAAGAAACAACCTTAACTGGGAAATGGAAGAAACCAACCTGTGGACATTTGGAA 864
792 GCTGCTGTGAAGAAACAACCTTAACTGGGAAATGGAAGAAACCAACCTGTGGACATTTGGAA 851
865 ACTGTCATCTTCAGAAACCAACCTGTCAAGTATTCAGTGTGAGGCTCTATTCAGACCCAG 924
852 ACTGTCATCTTCAGAAACCAACCTGTCAAGTATTCAGTGTGAGGCTCTATTCAGACCCAG 911
925 ATTTGGGATCATGAACCTGTAGCCATCCCTGGCCAGCTTCACTTACCTGTGATGTA 984
912 ATTTGGGATCATGAACCTGTAGCCATCCCTGGCCAGCTTCACTTACCTGTGATGTA 971
985 CTTTCATCTCTCAGAGAAACCTGAGTAAATTTGGAGAGAAACAACCTTGTGATGATCAT 1044
972 CTTTCATCTCTCAGAGAAACCTGAGTAAATTTGGAGAGAAACAACCTTGTGATGATCAT 1031
1045 CTGGAATCTGTGCAAAATCTCTAGTCCCAATATGTCAAAATTTGGCAAAAGTTTCTAATGA 1104
1032 CTGGAATCTGTGCAAAATCTCTAGTCCCAATATGTCAAAATTTGGCAAAAGTTTCTAATGA 1091
1105 TTAAGGAGGATATATTAACCCCTTCAATTCAGTGTGAGTCACTGATCTGATCTCT 1164
1092 TTAAGGAGGATATATTAACCCCTTCAATTCAGTGTGAGTCACTGATCTGATCTCT 1151
1165 CTGGTGTGGCAATTTATCTTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGA 1224
1152 CTGGTGTGGCAATTTATCTTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGA 1211
1225 GAAATATGAATGACCAATTAATTAATCGCCCTTGTGAAAGAAATTTCTGGAATCTAAA 1284
1212 GAAATATGAATGACCAATTAATTAATCGCCCTTGTGAAAGAAATTTCTGGAATCTAAA 1271
1285 AATCATGATGATCTTAAATCCTTCATGAAGAAAGTTTGTGGTGGGACCTCCATAGCTC 1344
1272 AATCATGATGATCTTAAATCCTTCATGAAGAAAGTTTGTGGTGGGACCTCCATAGCTC 1331
1345 AAACATGAAGTGTG-TTCCCTCAGTGCATCTGGAGAAATTTCTACCCGACCAACAGTTTC 1403
1332 AAACATGAAGTGTGTTCTTCATGATGCATCTGGAGAAATTTCTACCCGACCAACAGTTTC 1391
1404 TTAAGCTTCATTTGCCCCCTCATATTTATTCCTCAACCCCCAGCCACAGGTTTATACA 1463
1392 TTAAGCTTCATTTGCCCCCTCATATTTATTCCTCAACCCCCAGCCACAGGTTTATACA 1451
1464 GCTCAGCTTTTGTCTTTCTTGGAGAGAAACAATTAAGACAT -AAGGAAAGATTCAT 1522
1452 GCTCAGCTTTTGTCTTTCTTGGAGAGAAACAATTAAGACATTAAGGAAAGATTCAT 1511
1523 GTGCAATATAAGATAGGCTGACCTTGTCTTCTTGAATCTTGTGATGAGTTCAATTTCA 1582
1512 GTGCAATATAAGATAGGCTGACCTTGTCTTCTTGAATCTTGTGATGAGTTCAATTTCA 1571
1583 GTGCTGACTTGTATGACAGACACTTCTAATGAAGTGAATTTGATATCATATGTGAATA 1642
1572 GTGCTGACTTGTATGACAGACACTTCTAATGAAGTGAATTTGATATCATATGTGAATA 1631
1643 TGGAATGATTTCTTGGAGATCAAAATTTCAAGTGTCTGATGATGAGGATGATCA 1702
|||||

Db	1632	TGAGCTACAGTTTTTCTTGCGAGATCAAAATTTCAACGTCGCTCTTGTATATCTGTGAGGTACA	1691
QY	1703	CTCTTATAAAGAGTTCAAAAAAGCTTACGCTCTCTCTCTTTCTTTTCAACTCCAGTGAAGTAAT	1762
Db	1692	CTCTTATAAAGAGTTCAAAAAAGCTTACGCTCTCTCTCTTTCTTTTCAACTCCAGTGAAGTAAT	1751
QY	1763	GGGGTCTCTCTCAATTTAAAGAGAGTCGTAATTTGGAGCTGTAGCCCTGGCGCTGTGAATTG	1822
Db	1752	GGGGTCTCTCTCAATTTAAAGAGAGTCGTAATTTGGAGCTGTAGCCCTGGCGCTGTGTGAATTG	1811
QY	1823	GACCAATCCATTTTAACTGGCTTCAGGCGCTCCCACTCTCTCTGTAGCCACCTCTTTTTC	1882
Db	1812	GACCAATCCATTTTAACTGGCTTCAGGCGCTCCCACTCTCTCTGTAGCCACCTCTTTTTC	1870
QY	1883	GTGTGCTGACTTCCACACCTTACATCTCATGAGTGGCCAAACAAAGAGAGAGAGAGA	1942
Db	1871	GTGTGCTGACTTCCACACCTTACATCTCATGAGTGGCCAAACAAAGAGAGAGAGAGA	1930
QY	1943	ATAGCCTGCGGGGTTTTTTAGTTTGGGGGTTTTGCTGTTCCTTTTATGAGACCCATTCC	2002
Db	1931	ATAGCCTGCGGGGTTTTTTAGTTTGGGGGTTTTGCTGTTCCTTTTATGAGACCCATTCC	1990
QY	2003	TATTTCTATATAGTCAATGTTTCTTTTATPACAGATATATATAGTAAAGAAACATCACTGAA	2062
Db	1991	TATTTCTATATAGTCAATGTTTCTTTTATPACAGATATATATAGTAAAGAAACATCACTGAA	2050
QY	2063	ATGTAGCTGCAAGTGCATCTCTTTGATGTCAATGTAGAAAGAGTTAAACAGGTGAGAA	2122
Db	2051	ATGTAGCTGCAAGTGCATCTCTTTGATGTCAATGTAGAAAGAGTTAAACAGGTGAGAA	2110
QY	2123	ATTCCTTGATTCACAATGAATAGTCCTCCCTTCCTCCCTGCCCCAGACATTTTATCCACTT	2182
Db	2111	ATTCCTTGATTCACAATGAATAGTCCTCCCTTCCTCCCTGCCCCAGACATTTTATCCACTT	2170
QY	2183	ACGTAGATTTCATATTTCTTTAAATTTGATCATCGAGGCTCCCTCAACCCGAC	2235
Db	2171	ACGTAGATTTCATATTTCTTTAAATTTGATCATCGAGGCTCCCTCAACCCGAC	2223
RESULT	4		
FEATURE			
LOCUS	HSLEU8	2323 bp mRNA	PRI
DEFINITION	Human mRNA for Leu-8 pan leukocyte antigen.		27-MAY-1999
ACCESSION	X17519		
VERSION	X17519.1	GI:34344	
KEYWORDS	antigen; glycoprotein; receptor; transmembrane protein.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 2323)		
TITLE	Camerini,D., James,S.P., Stamenkovic,I. and Seed,B. Leu-8/T01 is the human equivalent of the Mel-14 lymph node homing receptor		
JOURNAL	Nature 342 (6245), 78-82 (1989)		
MEDLINE	90044046		
FEATURES			
source		Location/Qualifiers	
		1..2323	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		1..2323	
		/note="long form"	
		/evidence=experimental	
		join(1..1078,1515..2323)	
		/note="short form"	
		/evidence=experimental	
		join(50..1078,1515..1577)	
		/codon_start=1	
		/product="Leu-8 antigen short form"	
		/protein_id="CAB43537.1"	
		/db_xref="GI:4902830"	
		/translation="MGCRPTREGSPKAMIFPKKQSTORDLIMNIFKLMGFMILCCDEL	
		AHHGTDCWTHYSEKPRPMNRRARFRGRDNYTLDLVALYONKAELEIYEKTLPSRSYTWI	
CDS			

	CDS	/note="Leu-8 antigen" /codon_start=1 /protein_id="CAB43536.1" /db_xref="GI:4902829". /translation="MGCRTRREBPSKAMIPFWKCOSTORDIMNIFKLGMWTMLCDPLAHGDDCWYHYHSEKPMWMOARAPRCRDNVYDLAIQNKAEIYLETFLSPRSYWI GJRKIGGLTWGTGWKSLTEBAENMGGDEINNTCKNDGVYGPQCPIYOCEPLEAPL HIKIKALCYTAACQPWSCSGHGEVEIJNNTCNDGVYGPOCPYOCEPLEAPL GMDDCTHSIGNSFSSQCAFSCSBETNLRTGETCGPFGWSSPEPTCOVIOCEPLS APDLGIMNCSHPLASFSTACTFCSGECSTELGKKTKICSSGISWSNPSPICOKLDK SFEMKEGDFLTIVFSFNVLVLMDTSK" 50...1207
	sig_peptide	join(203..1078,1515..1574)
	mat_peptide	/note="Leu-8 is the human homologue of the mouse Mel-14 receptor" /product="Leu-8 antigen short form" 203..1204 /note="Leu-8 is the human homologue of the mouse Mel-14 receptor"
	mat_peptide	/note="Leu-8 is the human homologue of the mouse Mel-14 receptor"
BASE COUNT	652 a	520 c 490 g 661 t
ORIGIN		
Query Match	94.2%;	Score 2127.8; DB 93; Length 2323;
Best Local Similarity	99.3%;	Prod. No. 0;
Matches 2179; Conservative	0;	Mismatches 12; Indels 4; Gaps 4;
OY	44	CCCTTGCCAAGACTGAGACCCTTGTCGAAGCAAGAGGCATCATGCGGTGCAGAAG 103
Db	4	CCTTGGGCAAGAGACTGAGACCCTTGTCGCTAAGTCAAGAGGCTCAATGGGTGCAGAAG 63
OY	104	AACATGAGAGAGAACCAAGCAAAAGCCATGATATTCCATGAAATGTCAAGACCAAGAG 163
Db	64	AACATGAGAGAGAACCAAGCAAAAGCCATGATATTCCATGAAATGTCAAGACCAAGAG 123
OY	164	GGACTATAGAACATCTTCAAGTTGGGGGGTGGACAATGCTGCTGTGATTTCTCGGC 223
Db	124	GGACTTATAGAACATCTTCAAGTTGGGGGGTGGACAATGCTGCTGTGATTTCTCGGC 183
OY	224	ACATCATGGAACCTTACTCTGACTTACCATTTATTCGAAAAAACCATGAACTGGCAAG 283
Db	184	ACATCATGGAACCGACTCTGACTTACCATTTATTCGAAAAAACCATGAACTGGCAAG 243
OY	284	GGCTGAGAGATTTCGCCAGACATTTACACAGATTTAGTTGCCATACAAAACAAGCGGA 343
Db	244	GGCTGAGAGATTTCGCCAGACATTTACACAGATTTAGTTGCCATACAAAACAAGCGGA 303
OY	344	AATTGAGTATCTGGAGAAGACTGACCCTTCAGTCGTCTTACTAGGATAGGAATCGG 403
Db	304	AATTGAGTATCTGGAGAAGACTGACCCTTCAGTCGTCTTACTAGGATAGGAATCGG 363
OY	404	GAACTAGAGAGAAATATGAGACGTGGTGGGAACCAACAAATCTCTCATGAAAGACAGA 463
Db	364	GAACTAGAGAGAAATATGAGACGTGGTGGGAACCAACAAATCTCTCATGAAAGACAGA 423
OY	464	GAACTGGGGGAGATGATGAGCCCAACCAAGAGAAACAAGGAGAGACTGCTGGAATCTA 523
Db	424	GAACTGGGGGAGATGATGAGCCCAACCAAGAGAAACAAGGAGAGACTGCTGGAATCTA 483
OY	524	TATCAAGAGAAACAAGATGCAGGCAAATGGAAGATGAGCGCTGCGACAAACTAAAGC 583
Db	484	TATCAAGAGAAACAAGATGCAGGCAAATGGAAGATGAGCGCTGCGACAAACTAAAGC 543
OY	584	AGCCCTCTGTTCACACAGCTTCTTGCCAGCCCTGTCATGCACTGGCCATGGAAGATGTG 643
Db	544	AGCCCTCTGTTCACACAGCTTCTTGCCAGCCCTGTCATGCACTGGCCATGGAAGATGTG 603

QY 644 AGAATCATCATATACACCTGCAACCTGTGATGTGGGGTACTATGAGGCCCAAGTGTCA 703
 DB 604 AGAAATCATCAATTAATTAACCTGCAACCTGTGATGTGGGGTACTATGAGGCCCAAGTGTCA 663
 QY 704 GCTTGTGATTCAGTGTGAGGCTTTGGAGGCCCAAGAGCTGGTACATGTGACTGTACTCA 763
 DB 664 GTTGTGATTCAGTGTGAGGCTTTGGAGGCCCAAGAGCTGGTACATGTGACTGTACTCA 723
 QY 764 CCCCTTTGGAACTTCAGCTTCAGCTCACAGTGTGCTTCAGCTGCTCTGAAGAACAAA 823
 DB 724 CTCTTTGGGAACTTCAGCTTCAGCTCACAGTGTGCTTCAGCTGCTCTGAAGAACAAA 783
 QY 824 CTTAAGTGGATGAGAAACCAACCTGTGACCATTTGGAACTGTGATCTCCAGAAC 883
 DB 784 CTTAAGTGGATGAGAAACCAACCTGTGACCATTTGGAACTGTGATCTCCAGAAC 843
 QY 884 AACCTGTCAAGTATTCAGTGTGAGCTTCATGACACAGATTTGGGATTCATGAACTG 943
 DB 844 AACCTGTCAAGTATTCAGTGTGAGCTTCATGACACAGATTTGGGATTCATGAACTG 903
 QY 944 TAGCATCCCTGGCCAGCTTCAGCTTCATGACATGTACCTTCATCTGTGACGAAG 1003
 DB 904 TAGCATCCCTGGCCAGCTTCAGCTTCATGACATGTACCTTCATCTGTGACGAAG 963
 QY 1004 AACTGAGTTAATTTGGGAGAAAGAAACATTTGTGAATCTCTGGAATCTGTCTCAATTC 1063
 DB 964 AACTGAGTTAATTTGGGAGAAAGAAACATTTGTGAATCTCTGGAATCTGTCTCAATTC 1023
 QY 1064 TACTGCAATTTGCAAAATTTGGACAAAGTTCTCAATGATTAAGAGGGGTATTATA 1123
 DB 1024 TACTGCAATTTGCAAAATTTGGACAAAGTTCTCAATGATTAAGAGGGGTATTATA 1083
 QY 1124 CCCCTTCCTTCATTCAGTGTGACATGTGTTACTGCAATTCCTGTGGTGGCATTTATCAT 1183
 DB 1084 CCCCTTCCTTCATTCAGTGTGACATGTGTTACTGCAATTCCTGTGGTGGCATTTATCAT 1143
 QY 1184 TTGGCTGGCAGAGAGATTAAAAAGGCAAAATCCAGAGAGATGTAGTAAATCCATA 1243
 DB 1144 TTGGCTGGCAGAGAGATTAAAAAGGCAAAATCCAGAGAGATGTAGTAAATCCATA 1203
 QY 1244 TTAAATCGCCCTTGGTGAAGAAATTTCTGSAATCTAAATCTAGATCCCTTTAA 1303
 DB 1204 TTAAATCGCCCTTGGTGAAGAAATTTCTGSAATCTAAATCTAGATCCCTTTAA 1263
 QY 1304 TCCCTTCATGAAAGTTTGTGTGTGTGGCACTCTACGTCAAAACATGAAGTGTG-TTCC 1362
 DB 1264 TCCCTTCATGAAAGTTTGTGTGTGTGGCACTCTACGTCAAAACATGAAGTGTGTCC 1323
 QY 1363 TTCAAGTGCATCTGGGAAAGATTTCTACCCGACCAAGTTCCTTCAGCTTCATTTGGCCC 1422
 DB 1324 TTCAAGTGCATCTGGGAAAGATTTCTACCTGACCAAGTTCCTTCAGCTTCATTTGGCCC 1383
 QY 1423 CTCAATTTATCCCTCAACCCCGACCCCAAGGTTTATACAGCTTCAGCTTTTGTCTTTT 1482
 DB 1384 CTCAATTTATCCCTCAACCCCGACCCCAAGGTTTATACAGCTTCAGCTTTTGTCTTTT 1443
 QY 1483 CTGAGAGAGAAACAAATAGACCAT-AAGGAAAGATTCATGTGGAATATAGAGATGCT 1541
 DB 1444 CTGAGAGAGAAACAAATAGACCATTAAGGAAAGATTCATGTGGAATATAGAGATGCT 1503
 QY 1542 GACTTGTCTCTTCTTGTGACTCTTGTGTTTCAAGTTCAATTCAGTGTGCTGATGACAG 1601
 DB 1504 GACTTGTCTCTTCTTGTGACTCTTGTGTTTCAAGTTCAATTCAGTGTGCTGATGACAG 1563
 QY 1602 ACCTCTTAAGTGAAGTGAATTTATACATGTGGAATAGGACCTCACTTTCTTGA 1661
 DB 1564 ACCTCTTAAGTGAAGTGAATTTATACATGTGGAATAGGACCTCACTTTCTTGA 1623
 QY 1662 GATCAATTTTACAGTGTCTTCTGTATACTGTGAGGATACACTTTATAGAAAGTTCAAA 1721
 DB 1624 GATCAATTTTACAGTGTGTCTGTATACTGTGAGGATACACTTTATAGAAAGTTCAAA 1683

QY 1722 AAGTCTAGGCTTCCTTCTTCTTACTCCAGTGAAGTAATGGGGCTGCTCAAGTTGA 1781
 DB 1684 AAGTCTAGGCTTCCTTCTTCTTACTCCAGTGAAGTAATGGGGCTGCTCAAGTTGA 1743
 QY 1782 AAGAGTCTATTTTGCACGTAGAGCTCCGCGTGTGTGAATTTGACATCTATTTAACTGG 1841
 DB 1744 AAGAGTCTATTTTGCACGTAGAGCTCCGCGTGTGTGAATTTGACATCTATTTAACTGG 1803
 QY 1842 CTTCAGGCTTCGCCACCTTCTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACC 1901
 DB 1804 CTTCAGGCTTCGCCACCTTCTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACC 1862
 QY 1902 TAGATCTCATGAGTGTGCAAGCAAAAGAGAGAGAGAAATAGCTGGCGGTTT 1961
 DB 1863 TAGATCTCATGAGTGTGCAAGCAAAAGAGAGAGAGAAATAGCTGGCGGTTT 1922
 QY 1962 AGTTTGGGGTTTGGCTTCTTCTTCTTATGAGACCCATTCCTATTTCTTATGCAATGT 2021
 DB 1923 AGTTTGGGGTTTGGCTTCTTCTTCTTATGAGACCCATTCCTATTTCTTATGCAATGT 1982
 QY 2022 TTCTTTTATCAGATATTTATTTAGTAAACATCACTGAATGTCTGCAAGTGACA 2081
 DB 1983 TTCTTTTATCAGATATTTATTTAGTAAACATCACTGAATGTCTGCAAGTGACA 2042
 QY 2082 TTCTTTTATCAGATATTTATTTAGTAAAGTTAAACAGGTGAGAAATCTTGAATTCACATGA 2141
 DB 2043 TTCTTTTATCAGATATTTATTTAGTAAAGTTAAACAGGTGAGAAATCTTGAATTCACATGA 2102
 QY 2142 AATGCTCTCTTCTTCCCTGCCCCAGAACTTTTATTC-ACCTTACCTGATTTCTACATATT 2200
 DB 2103 AATGCTCTCTTCTTCCCTGCCCCAGAACTTTTATTC-ACCTTACCTGATTTCTACATATT 2162
 QY 2201 CTTTAAATTTCAATCTCAGGCTCCCTCAACCCAC 2235
 DB 2163 CTTTAAATTTCAATCTCAGGCTCCCTCAACCCAC 2197
 RESULT 5
 LOCUS AR016679 2330 bp DNA PAT 05-DEC-1998
 DEFINITION Sequence 1 from patent US 5776775.
 ACCESSION AR016679
 VERSION AR016679.1 GI:3972956
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2330)
 AUTHORS Tedder, T.F. and Speert, I., O.G.
 TITLE Anti-LAM 1-3 antibody and hybridoma
 JOURNAL Patent: US 5776775-A 1 07-JUL-1998;
 FEATURES Location/Qualifiers
 source 1..2330
 BASE COUNT 661 a 522 c 487 g 660 t
 ORIGIN
 Query Match 92.4%; Score 2087.6; DB 9; Length 2330;
 Best local Similarity 98.5%; Pred. No. 0;
 Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;
 QY 44 CCCCTTGGCAAGACCTGAGACCCCTTGTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAG 103
 DB 7 CTTTGGGCAAGGACCTGAGACCCCTTGTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAG 66
 QY 104 AACTAGAGAGACCAAGCAAAAGCCATGATTTTCCATGGAATTTGCAAGCAAGCAAG 163
 DB 67 AACTAGAGAGACCAAGCAAAAGCCATGATTTTCCATGGAATTTGCAAGCAAGCAAG 126
 QY 164 GCACTTATGAAACATCTTCAAGTTGTGGGGGTGAGCAATGCTGTTGTGATTTCCGTGC 223
 DB 127 GCACTTATGAAACATCTTCAAGTTGTGGGGGTGAGCAATGCTGTTGTGATTTCCGTGC 186

QY	224	ACATCATGSAACCTTACTGCTGGACTTACCATTAATTTCTGAAAAACCAATGAACTGGCAAG	283
Db	187	ACATCATGSAACCGACTGCTGGACTTACCATTAATTTCTGAAAAACCAATGAACTGGCAAG	246
QY	284	GGTACAAGATTTCTGCCCGAGCAATTACACAGATTTTGTTGCCCTACAAAAACAAGCCGA	343
Db	247	GGTACAAGATTTCTGCCCGAGCAATTACACAGATTTTGTTGCCCTACAAAAACAAGCCGA	306
QY	344	AATTAGTATCTGGAAGAGACTTGCCTTCAGTCTGTTCTACTAGTGGATAGAGAAATCCG	403
Db	307	AATTAGTATCTGGAAGAGACTTGCCTTCAGTCTGTTCTACTAGTGGATAGAGAAATCCG	366
QY	404	GAAAGATAGAGCAATATGAGACGTGGGTGGAAACCAACAATCTTCTCACTAGAGAGCAGA	463
Db	367	GAAAGATAGAGCAATATGAGACGTGGGTGGAAACCAACAATCTTCTCACTAGAGAGCAGA	426
QY	464	GAAGTGGGAGATGGTGGAGCCCAACACAAACAAGAGAGACTGCGTGGAGATCTTA	523
Db	427	GAAGTGGGAGATGGTGGAGCCCAACACAAACAAGAGAGACTGCGTGGAGATCTTA	486
QY	524	TATCAAGAAAAACAAGATGCAAGCAATGGAAGATGAGACCTGGCCACAAATTAAGAC	583
Db	487	TATCAAGAAAAACAAGATGCAAGCAATGGAAGATGAGACCTGGCCACAAATTAAGAC	546
QY	584	AACCCCTGTGTACACAGCTTCTTGCCACAGCCTGGTCAATGCAATGGCCATGAGATGTGT	643
Db	547	AACCCCTGTGTACACAGCTTCTTGCCACAGCCTGGTCAATGCAATGGCCATGAGAAATGTGT	606
QY	644	AGAATATCATTAATATATACACCTGCACTGATGATGGGGTACTATAGGGCCCAAGTCTTA	703
Db	607	AGAATATCATTAATTAATTAACCTGCAACTGTGATGTGGGTACTATAGGGCCCAAGTCTTA	666
QY	704	GCTGTGTATCAGTGTGAGCCTTTTGAAGGCCCAAGAGCTGGTACCATGGAGTGTACTTA	763
Db	667	GTTTGTGATCAGTGTGAGCCTTTTGAAGGCCCAAGAGCTGGTACCATGGAGTGTACTTA	726
QY	764	CCCTTTGGAAACTTTCAGCTTCACTACACATGATGGTCCCTCAGCTGCTTGAAGAAACAA	823
Db	727	CCCTTTGGAAACTTTCACACTTCAACACTCACATGTGGCTTTCAGCTGCTTGAAGAAACAA	786
QY	824	CTTAATCTGGGATTTGAAGAAACACCTGTGACCAATTTGAAACCTGGTCAATCTCCAGAAC	883
Db	787	CTTAATCTGGGATTTGAAGAAACACCTGTGACCAATTTGAAACCTGGTCAATCTCCAGAAC	846
QY	884	AACCTGTCAAGTGAATCAGTGTGAGCCTTATAGCAACCAAGATTTGGGGATCATGAACTG	943
Db	847	AACCTGTCAAGTGAATCAGTGTGAGCCTTATAGCAACCAAGATTTGGGGATCATGAACTG	906
QY	944	TAGCCATCCCTGGCCAGCTTCAGCTTACCTGTGCATGTACCTTCATCTGCTCAGAAG	1003
Db	907	TAGCCATCCCTGGCCAGCTTCAGCTTACCTGTGCATGTACCTTCATCTGCTCAGAAG	966
QY	1004	AACGAGTATTTGGGAAAGAAACCAATTTGTGAATATCTGGAATGTGTCAAAATCC	1066
Db	967	AACGAGTATTTGGGAAAGAAACCAATTTGTGAATATCTGGAATGTGTCAAAATCC	1026
QY	1064	TAGTTCATATGTCAAAAAATTTGCAAAAAATTTCTCAATGATTTAAGAGAGGGATTAATTA	1123
Db	1027	TAGTTCATATGTCAAAAAATTTGCAAAAAATTTCTCAATGATTTAAGAGAGGGATTAATTA	1086
QY	1124	CCCCCTCTTCAATTCAGCTGGCAGTCAATGTACTGCATTTCTGTGGTGGCAATTAATCAT	1183
Db	1087	CCCCCTCTTCAATTCAGCTGGCAGTCAATGTACTGCATTTCTGTGGTGGCAATTAATCAT	1146
QY	1184	TTGGCTGTGCAAGAGATTTAAAAAAGGCAAGAAATCCAAGAGAGATGATGACCCATA	1243
Db	1147	TTGGCTGTGCAAGAGATTTAAAAAAGGCAAGAAATCCAAGAGAGATGATGACCCATA	1206
QY	1244	TTAATATGCCCTGTGGTGAAGAAATTTCTTGGAAATCTTAAAAATGATAGATCCTTTAAA	1303
Db	1207	TTAATATGCCCTGTGGTGAAGAAATTTCTTGGAAATCTTAAAAATGATAGATCCTTTAAA	1266

OY	1304	TCTTTCATGAAGACGTTTGtGTGTGGCACCTCCTACGCAACAACATGAAAGTGT- TTCC	1362
Db	1267	TCCTTCCATGAAGACGTTTTgGTGTGGCACCTCCTACGCAACAACATGAAAGTGTGTTTC	1326
OY	1363	TTTCAGTCATCTGGGAAGATTTCATACCGCACCAACAGTCTCCTCACCTCCCATTTTCGCC	1422
Db	1327	TTTCAGTCATCTGGGAAGATTTCATACCTGACACCAACAGTCTCCTCACCTCCCATTTTCACC	1386
OY	1423	CCTCATTTATCCCTCAACCCCCAGCCACAGGTGTTTATACAGTCAAGCTTTTGTCTTTT	1482
Db	1387	GCTCATTTATCCCTCAACCCCCAGCCACAGGTGTTTATAAGCTCAGCTTTTGTCTTTT	1446
OY	1483	CTGAGAGAAAACAAATAAGACCAT -AAGGGAAGAAGATTCATGTGGAATPATAAGATGGCT	1541
Db	1447	CTGAGAGAAAACAAATAAGACCATTAAGCGAATAAGGGAAGATTCATGTGGAATPATAAGATGGCT	1506
OY	1542	GACTTTGCTCTTTCTGTGACTCTGTGTTTCAATTTCATTCAGTGTGTAAGTATGATGACAG	1601
Db	1507	GACTTTGCTCTTTCTGTGACTCTGTGTTTCAATTTCAGTGTGTAAGTATGATGACAG	1566
OY	1602	AACACTTCAAATGAAGTGCACAAATTGATACATATPANGAATATGAGACAGTCTGTTCTGTCA	1661
Db	1567	AACACTTCAAATGAAGTGCACAAATTGATACATATGGAATATGAGACTGAGTTTCTGTCA	1626
OY	1662	GATCAAAATTCACGTCGTCCTGTGTATATCTGTGAGGTACACTCTTATAGAAAGTTCAA	1721
Db	1627	GATCAAAATTCGCGTCGTCGTCGTGTATATC -GTGAGAGTACACTCT-----ATGAGTCAA	1680
OY	1722	AAGTCTACGCTCCTCTTCTTCTTTCACATCCAGGAATPATGGGGTCGTCGCAAGTTGA	1781
Db	1681	AAGTCTACGCTCCTCTTCTTCTTCTTCTTACATCCAGGAAGTATG6GGGTCGTCGCAAGTTGA	1740
OY	1782	AAGACTCCTATTTTSCACTGTAGAGCCGTCGCGCTGTGAATTTGAGACCATCCTATTAACTGG	1841
Db	1741	AAGACTCCTATTTTSCACTGTAGAGCCGTCGCGCTGTGAATTTGAGACCATCCTATTAACTGG	1800
OY	1842	CTTCAAGGCTCCCACCTTCTTCAAGCACCTCTCTTTTCACTGTGGCTGACTTCACACC	1901
Db	1801	CTTCA -GCCCTCCACCTCTTCTTCAAGCACCTCTCTTTTCACTGTGGCTGACTTCACACC	1859
OY	1902	TAGCATCTCATGATGTGCGCAAGAAAAAGAGAGAGAGAAATATCCTGCGCGGTTTTTT	1961
Db	1860	TAGCATCTCATGATGTGCGCAAGAAAAAGAGAGAGAGAAATATACCTGCGCGTGTTTTT	1919
OY	1962	AGTTGGGGGTTTTGCTGTCTTTTATGAGACCCATTCCTATTCTTATATGATCAATGT	2021
Db	1920	AGTTGGGGGTTTTGCTGTCTTTTATGAGACCCATTCCTATTCTTATATGATCAATGT	1979
OY	2022	TTCTTTTATCAGATATTATTACTAGAAAACATCAGTAATGCTATAGCTCAGTAGTACA	2081
Db	1980	TTCTTTTATCAGATATTATTACTAGAAAACATCAGTAATGCTATAGCTCAGTAGTACA	2039
OY	2082	TCTCTTGAATGTCATATGAAAGATTAAACAGGTGAGAAATTCCTTGATTCACAATGA	2141
Db	2040	TCTCTTGAATGTCATATGAAAGATTAAACAGGTGAGAAATTCCTTGATTCACAATGA	2099
OY	2142	AATGCTCTCTCTTCCCTGCGCCCGCAGAACCTTTTATTCACATTACTAGATTCTACATATTC	2201
Db	2100	AATGCTCTCTCTTCCCTGCGCCCGCAGAACCTTTTATTCACATTACTAGATTCTACATATTC	2159
OY	2202	TTTAAATTTATCTCAGAGGCTCCTCTCAACCCGAC	2235
Db	2160	TTTAAATTTATCTCAGAGGCTCCTCTCAACCCGAC	2193
RESULT	6		
LOCUS	AR040718	2330 bp DNA	PAT
DEFINITION	Sequence 1 from patent US 5808025.		29-SEP-1999
ACCESSION	AR040718		
VERSION	AR040718.1	GI:5960081	
KEYWORDS	Unknown.		

ORGANISM	Unknown.	Unclassified.	REFERENCE	1 (bases 1 to 2330)
AUTHORS	Tedder, T. F. and Kansas, G. S.	Chimeric selections as simultaneous blocking agents for component	JOURNAL	Patent: US 5808025-A 1 15-SEP-1998;
FEATURES	source	Location/Qualifiers		
BASE COUNT	661 a	522 c	487 g	660 t
ORIGIN	/organism="unknown"			
Query Match	92.4%;	Score 2087.6;	DB 9;	Length 2330;
Best Local Similarity	98.5%;	Pred. No. 0;		
Matches 2161;	Conservative 0;	Mismatches 24;	Indels 9;	Gaps 5;
OY	44	CCCTTGGCAAGAGACCTGAGACCCCTTGTGCTAAGTCAAGAGGCTCAATGGGCTGAGAAG	103	
DB	7	CCCTTGGGCAAGAGACCTGAGACCCCTTGTGCTAAGTCAAGAGGCTCAATGGGCTGAGAAG	66	
OY	104	AACCTGAGAAGGACCAAGCAAGAACCCATGATATTTCATGGAATATGTCAGAGCACCAGAG	163	
DB	67	AACCTGAGAAGGACCAAGCAAGAACCCATGATATTTCATGGAATATGTCAGAGCACCAGAG	126	
OY	164	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAATGCTCTGTGATTTCTCTGAC	223	
DB	127	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAATGCTCTGTGATTTCTCTGAC	186	
OY	224	ACATCATGGAACTACTGCTGACTTACCATTATTCTGAAAAACCATGAACCTGGCAAG	283	
DB	187	ACATCATGGAACTACTGCTGACTTACCATTATTCTGAAAAACCATGAACCTGGCAAG	246	
OY	284	GGCTGAAGATCTCTCCCGAGACAATTACACAGATTAGTGGCATACAAACAAGCGGA	343	
DB	247	GGCTGAAGATCTCTCCCGAGACAATTACACAGATTAGTGGCATACAAACAAGCGGA	306	
OY	344	AATTGAGTATCTGGAGAAGACTCTCCCTTCAGTGGTCTTACTACTGGATGGAATCG	403	
DB	307	AATTGAGTATCTGGAGAAGACTCTCTCCCTTCAGTGGTCTTACTACTGGATGGAATCG	366	
OY	404	GAAGTATAGGAGGAATATGGACGTGGGTGGGAACAACAATCTCTCACTGAAGAAGAGA	463	
DB	367	GAAGTATAGGAGGAATATGGACGTGGGTGGGAACAACAATCTCTCACTGAAGAAGAGA	426	
OY	464	GAACCTGGGAGATGTGTGAGCCCAACAACAAGAAGAAGAGAGACTGCTGTGAATCTTA	523	
DB	427	GAACCTGGGAGATGTGTGAGCCCAACAACAAGAAGAAGAGAGACTGCTGTGAATCTTA	486	
OY	524	TATCAAGAGAACAAGAATGACGAGCAAAATGGAAGCATGACGCTGCCAACAATCTAAAGC	583	
DB	487	TATCAAGAGAACAAGAATGACGAGCAAAATGGAAGCATGACGCTGCCAACAATCTAAAGC	546	
OY	584	AGCCCTCTGTTAACACAGCTTCTTGGCAGCCCTGTCATATGCACTGGCCATGAGAAATGCT	643	
DB	547	AGCCCTCTGTTAACACAGCTTCTTGGCAGCCCTGTCATATGCACTGGCCATGAGAAATGCT	606	
OY	644	AGAAATTCATCAATATATACACACTGCAACTGTATGTGGGGTACTATGGGCCCACTGTCA	703	
DB	607	AGAAATTCATCAATATATATACACACTGCAACTGTATGTGGGGTACTATGGGCCCACTGTCA	666	
OY	704	GCTTGTGATTCAGTGTGAGCCCTTGGAGGCCCAAGAGCTGGGTACCATGAGATGTATCA	763	
DB	667	GCTTGTGATTCAGTGTGAGCCCTTGGAGGCCCAAGAGCTGGGTACCATGAGATGTATCA	726	
OY	764	CCCTTTTGGAAACTTCAGCTTCAGCTCAACAGTGTCCCTTCACCTGCTCTGAAGAAACAA	823	
DB	727	CCCTTTTGGAAACTTCAGCTTCAGCTTCAGCTTCAGCTCTCTGAAGAAACAA	786	
OY	824	CTTAACTGGGATGGAAGAACCACTGTGGACCAATTTGGAAACTGTGTCAACAAC	883	
DB	787	CTTAACTGGGATGGAAGAACCACTGTGGACCAATTTGGAAACTGTGTCAACAAC	846	

QY	884	AACCTGCAAACTGATTCGAGTGTAGGCTCTATATAGACACCAAGATTGGGGATCATATACATCG	943
Db	847	AACCTGTCAAACTGATTAAGTGTAGGCTCTATATAGACACCAAGATTGGGGATCATATACATCG	906
QY	944	TAGCATTCCCTGGCCAGCTTCACAGCTTTCCTCGATGTACCTTCATCTGCTCCAGAAAG	1003
Db	907	TAGCATTCCCTGGCCAGCTTCACAGCTTTCCTCGATGTACCTTCATCTGCTCCAGAAAG	966
QY	1004	AACGTAGTTAAATTGGGAAGAAGAAACCAATTGTGAATCATCTGGANCTGGTCAAAATCC	1063
Db	967	AACGTAGTTAAATTGGGAAGAAGAAACCAATTGTGAATCATCTGGANCTGGTCAAAATCC	1028
QY	1064	TAGTCCAAATTGTCAAAAATTGGCAAAAATTTCTCAATGATTAAGGAGCGGATTAATA	1123
Db	1027	TAGTCCAAATTGTCAAAAATTGGCAAAAATTTCTCAATGATTAAGGAGCGGATTAATA	1086
QY	1124	CCCCCTTCATTCACAGTGGCAGTCATGTGTACTGCATTCCTCGGGTTGGCATTTATCAT	1183
Db	1087	CCCCCTTCATTCACAGTGGCAGTCATGTGTACTGCATTCCTCGGGTTGGCATTTATCAT	1168
QY	1184	TTGGCTGGCAAGGAGATTAAAAAAGGCAAGAAATCCAGAGAAGATATGATGACCCATA	1243
Db	1147	TTGGCTGGCAAGGAGATTAAAAAAGGCAAGAAATCCAGAGAAGATATGATGACCCATA	1206
QY	1244	TTAAATGCCCCCTTGCTGTAAGAAATAATCTTGGAAATCTATAAATCATGAGATCTTTAAA	1303
Db	1207	TTAAATGCCCCCTTGCTGTAAGAAATAATCTTGGAAATCTATAAATCATGAGATCTTTAAA	1266
QY	1304	TCCTTCATGAAACGTTTTGTGTGTGTGGCACCCTCTAGCTCAACACATGAATGTGTG - TTCC	1362
Db	1267	TCCTTCATGAAACGTTTTGTGTGTGTGGCACCCTCTAGCTCAACACATGAATGTGTGTTC	1326
QY	1363	TTTCAGTGCATGTGGAGAGATTTCACCCGCAACAGTTCTCTGACGCTCCCATTTGGCCG	1422
Db	1327	TTTCAGTGCATGTGGAGAGATTTCACCTGACCAACAGTTCTCTGACGCTTCATTTCCACC	1386
QY	1423	CTCATTTATCCCTCAACCCCCCAGCCCAAGGTTTATACAGCTCAGCTTTTGTCTTTT	1482
Db	1387	CTCATTTATCCCTCAACCCCCCAGCCCAAGGTTTATACAGCTCAGCTTTTGTCTTTT	1446
QY	1483	CTGAGGAGAAACAATATGAACCAAT - AAGGAAAGATTCATGTGAATATTAAGATGGCT	1541
Db	1447	CTGAGGAGAAACAATATGAACCAATTAAGGAAAGATTCATGTGAATATTAAGATGGCT	1506
QY	1542	GACTTTGCTTTCTTTACACCTGTGTTTTCAGTTCAATTCAGTGTGTTACTTGATGAGACAG	1601
Db	1507	GACTTTGCTTTCTTTACACCTGTGTTTTCAGTTTTCGAATTCAGTGTGTTACTTGATGAGACAG	1566
QY	1602	ACACTTCTAAATGAATGACAAATTTGATATCATATGTGAATATGAGACTCAGTTTCTTGCA	1661
Db	1567	ACACTTCTAAATGAATGACAAATTTGATATCATATGTGAATATGAGACTCAGTTTCTTGCA	1626
QY	1662	GATCAAAATTTACGTCGTCCTGTCTGTATACGTGAGAGACTCAGCTCAATATGAAGATTGAA	1721
Db	1627	GATCAAAATTTACGTCGTCCTGTCTGTATAC - GTGAGAGACTCAGCTCT - - - - - ATGAGACTAA	1680
QY	1722	AAGTCTACGCTCTCTTTCTTTCTAATCCAGTGAAGTAATGGGCTGCTGCTCAAGTTGA	1781
Db	1681	AAGTCTACGCTCTCTCTTTCTTTCTAATCCAGTGAAGTAATGGGCTGCTGCTCAAGTTGA	1740
QY	1782	AAGAGTCCATTTTTCAGTGTAGGCTCGCGCTGTGTGAATTTGGAACCATCCTATTTAACGG	1841
Db	1741	AAGAGTCCATTTTTCAGTGTAGGCTCGCGCTGTGTGAATTTGGAACCATCCTATTTAACGG	1800
QY	1842	CTTACAGGCTTCCCAACCTCTTTCAGGCACACTCTCTTTTTCAGTTGGCTGATCTTCCACAC	1901
Db	1801	CTTCA - GCGTCCCACTTCTTCAGGCACACTCTCTTTTTCAGTTGGCTGATCTTCCACAC	1859
QY	1902	TAGCATCTCATGAGTGGCAAGCAAAAAGAGAGAGACAAATAGCTGTGCGCGGTTTTT	1961
Db	1860	TAGCATCTCATGAGTGGCAAGCAAAAAGAGAGAGACAAATAGCTGTGCGCGGTTTTT	1919

OY	1962	AGTTTGGGAGTTTGATGTGTCCTTTATATGAGACCCATTCTATTCTTATATGTAATGT	2021
Db	1920	AGTTTGGGAGTTTGATGTGTCCTTTATATGAGACCCATTCTATTCTTATATGTAATGT	1979
OY	2022	TTCCTTTATCAGATATATTATATGAAGAAACATCACTGAATAATGCTGCTGCAAGTAGCA	2081
Db	1980	TTCCTTTATCAGATATATTATATGAAGAAACATCACTGAATAATGCTGCTGCAAGTAGCA	2039
OY	2082	TCTCTTGATGTCTATATGAGAAGATTAACAAGSTGGAGAAATTCCTTGATGCACAATGA	2141
Db	2040	TCTCTTGATGTCTATATGAGAAGATTAACAAGSTGGAGAAATTCCTTGATGCACAATGA	2099
OY	2142	AATGCTCTCCCTTCCCTGCCCGAGAACCTTTATCATCTACTACTGATCTGATATATTC	2201
Db	2100	AATGCTCTCCCTTCCCTGCCCGAGAACCTTTATCATCTACTACTGATCTGATATATTC	2159
OY	2202	TTTAAATTTATCTCAGAGGCTCCCTCAACCCAC	2235
Db	2160	TTTTAATTTATCTCAGAGGCTCCCTCAACCCAC	2193
RESULT	7		
LOCUS	AR054061	2330 bp	DNA
DEFINITION	Sequence 1 from patent US 5834425.		PAT
ACCESSION	AR054061		29-SEP-1999
VERSION	AR054061.1	GI:5978923	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2330)		
AUTHORS	Tedder, T.F. and Kansas, G.S.		
TITLE	Use of chemie selectin function as simultaneous blocking agents for component selectin function		
JOURNAL	Patent: US 5834425-A 1 10-NOV-1998;		
FEATURES	Location/Qualifiers source 1..2330		
BASE COUNT	661 a 522 c 487 g 660 t		
ORIGIN	/organism="unknown"		
Query Match	92.4% Score 2087.6; DB 9; Length 2330;		
Best Local Similarity	98.5% Pred. No. 0;		
Matches 2161; Conservative	0; Mismatches 24; Indels 9; Gaps 5;		
OY	44	CCCCCTTGGCAAGGACCTGAGACCCTTGTGCTAAGTCAGAGAGGCTCAATGGCTGCAGAG	103
Db	7	CCTTTGGCAAGGACCTGAGACCCTTGTGCTAAGTCAGAGAGGCTCAATGGCTGCAGAG	66
OY	104	AACCTGAGAAAGGACCAACAAAGCCATGATATTTCCATGAAATGTGCAGAGCACCCAGAG	163
Db	67	AACCTGAGAAAGGACCAACAAAGCCATGATATTTCCATGAAATGTGCAGAGCACCCAGAG	126
OY	154	GCACTTATGGAACATCTCTCAAGTTGTGGGGGTGCAGCAATGCTCTGTGATTTCCGGC	223
Db	127	GCACTTATGGAACATCTCTCAAGTTGTGGGGGTGCAGCAATGCTCTGTGATTTCCGGC	186
OY	224	AACATCATGGAACCTACCTGCTGAGCTTACCATTTATTTGAAAAAACCATGAACTGGCAAAG	283
Db	187	AACATCATGGAACCTACCTGCTGAGCTTACCATTTATTTGAAAAAACCATGAACTGGCAAAG	246
OY	284	GGCTAGAGATTTGCGGAGACATTTACAGAGATTTAGTGGCCATCAAAAACAAGGCGA	343
Db	247	GGCTAGAGATTTGCGGAGACATTTACAGAGATTTAGTGGCCATCAAAAACAAGGCGA	306
OY	344	AATGATATCTGGAAGAGACTGCGCTTCACTGCTTCTTACTAGTGAATAGGAATCGG	403
Db	307	AATGATATCTGGAAGAGACTGCGCTTCACTGCTTCTTACTAGTGAATAGGAATCGG	366
OY	404	GAAGATGGAAGATATGAGAGCTGGGGGGAACCAACAATCTCTACGTAAGAGACGA	463
Db	367	GAAGATGGAAGATATGAGAGCTGGGGGGAACCAACAATCTCTACGTAAGAGACGA	426
OY	464	GAACCTGGGAGATGGTGAAGCCCAACACAGAGAACAAGAGAGCTGGTGAGATCTA	523
Db	427	GAACCTGGGAGATGGTGAAGCCCAACACAGAGAACAAGAGAGCTGGTGAGATCTA	486
OY	524	TATCAAGAGAAACAAGATGAGGCAAAATGGAAGATGAGAGGCTGCCACAATTAAGG	583
Db	487	TATCAAGAGAAACAAGATGAGGCAAAATGGAAGATGAGAGGCTGCCACAATTAAGG	546
OY	584	AGCCCTCTGTTACACAGCTTTTCCAGCCCTGTCTATGCAAGTGGCCATGGAATGTGT	643
Db	547	AGCCCTCTGTTACACAGCTTTTCCAGCCCTGTCTATGCAAGTGGCCATGGAATGTGT	606
OY	644	AGAAATCATCAATATATCAGACCTGCACTGATGATGGGGTACTATGGGCCCAAGTGA	703
Db	607	AGAAATCATCAATATATATACACCTGCACTGATGATGGGGTACTATGGGGCCAAGTGA	666
OY	704	GCTTGTGATTCAGTGTAGAGCTTTTGAAGGCCAGAGCTGGTATCCTGATGATCTA	763
Db	667	GCTTGTGATTCAGTGTAGAGCTTTTGAAGGCCAGAGCTGGTATCCTGATGATCTA	726
OY	764	CCCCTTTGGAAACCTTCAGCTCAGCTCAGAGCTGCTCAGCTGCTGGAAGAACAA	823
Db	727	CCCCTTTGGAAACCTTCAGCTCAGCTCAGAGCTGCTCAGCTGCTGGAAGAACAA	786
OY	824	CTTAACCTGGGATTTGAAGAAACCACTGTGGACCATTTGGAACCTGCTATCCGAAC	883
Db	787	CTTAACCTGGGATTTGAAGAAACCACTGTGGACCATTTGGAACCTGCTATCCGAAC	846
OY	884	AACCTGCAAGTATTCAGTGTAGAGCTCTATCAGACCAAGTTTGGGATCATGACTG	943
Db	847	AACCTGCAAGTATTCAGTGTAGAGCTCTATCAGACCAAGTTTGGGATCATGACTG	906
OY	944	TAGCAATCCCTGCGCAGCTTGAAGCTTATCTCTGATGATGATCTTCACTGCTGGAAG	1003
Db	907	TAGCAATCCCTGCGCAGCTTGAAGCTTATCTCTGATGATGATCTTCACTGCTGGAAG	966
OY	1004	AACCTGATTAATTTGGGAAACAAACCAATTTGTAATCATCTGGAATCTGCTCAATCC	1063
Db	967	AACCTGATTAATTTGGGAAACAAACCAATTTGTAATCATCTGGAATCTGCTCAATCC	1026
OY	1064	TACTCCATATGTCAAAATTTGAGCAAAAGTTTTCATGATTAAGAGGGGTGATTA	1123
Db	1027	TACTCCATATGTCAAAATTTGAGCAAAAGTTTTCATGATTAAGAGGGGTGATTA	1086
OY	1124	CCCCCTTCAATTCAGTGTGCAAGTATGCTGATCTCTGCTGGGTTGGCATTTATCAT	1183
Db	1087	CCCCCTTCAATTCAGTGTGCAAGTATGCTGATCTCTGCTGGGTTGGCATTTATCAT	1146
OY	1184	TTGGCTGGCAAGGATTAATAAAGGCAAAATCCAAAGAGTATGATATGACCATTA	1243
Db	1147	TTGGCTGGCAAGGATTAATAAAGGCAAAATCCAAAGAGTATGATATGACCATTA	1206
OY	1244	TTAAATCGCCCTTGTGTAAGAAATTTCTGGAATACTAAAAATCATGAGATCCTTTAA	1303
Db	1207	TTAAATCGCCCTTGTGTAAGAAATTTCTGGAATACTAAAAATCATGAGATCCTTTAA	1266
OY	1304	TCCCTTCATGAAGACCTTTGTGTGTGGCACTCTGTCAGTCAAAACATGAAGTGTG	1362
Db	1267	TCCCTTCATGAAGACCTTTGTGTGTGGCACTCTGTCAGTCAAAACATGAAGTGTG	1326
OY	1363	TTCACTGATCTGGGAAGATTTTCAACCGAACCAAGTCTCTCAGCTTCCATTTGGCC	1422
Db	1327	TTCACTGATCTGGGAAGATTTTCACTGCAACCAAGTCTCTCAGCTTCCATTTGGCC	1386

Qy	1542	GACCTTCGCTCTTCCTTGACAGCCCTGTTTTCAGTTTCAATTCAGTGCCTGACCTTGATGACAG	1601
Db	1507	GACTTTCCTCTTCTTCTTGACTCTCTGTTTTCAGTTTCAATTCAGTGCCTGACCTTGATGACAG	1566
Qy	1602	ACACTTCTAAATGAAGTGCAGAAATTTGATACATATGTGAATATGAGTCAAGTTTCTTGCA	1661
Db	1567	ACACTTCTAAATGAAGTGCAGAAATTTGATACATATGTGAATATGAGTCAAGTTTCTTGCA	1626
Qy	1662	GATCAAAATTTGGGTGCTCTTCTGTATAC-GTGGAGATGACACTG- ----ATGAAGTCAA	1721
Db	1627	GATCAAAATTTGGGTGCTCTTCTGTATAC-GTGGAGATGACACTG- ----ATGAAGTCAA	1680
Qy	1722	AAGCTACGCGTCTCTTCTTCTTCTTAACTCCAGTGAAGTAAATGGGCTCCGTCAAGTTGA	1781
Db	1681	AAGCTACGCGTCTCTTCTTCTTCTTAACTCCAGTGAAGTAAATGGGCTCCGTCAAGTTGA	1740
Qy	1782	AAGAGTCCCTATTTGCACTGTAGCCTGCGGCTGTGTAAATGGACACAATCCTATTTAACTGG	1841
Db	1741	AAGAGTCCCTATTTGCACTGTAGGCTGCGGCTGTGTAAATGGACACATCCTATTTAACTGG	1800
Qy	1842	CTTACAGGACCTCCACCACCTTTTTCAGGCACACTCTCTTCTTCAATTTGGCTGACCTCCACAC	1901
Db	1801	CTTCA-GCTGCCACACTCTTTTAAAGCACACTCTCTTTTCAATTTGGCTGACCTCCACAC	1859
Qy	1902	TAGCATCTCATGAGTGCAGAGCAAAAGAGAGAGAGAGAAATAGCCTGCGCGGTTTTTT	1961
Db	1860	TAGCATCTCATGAGTGCAGAGCAAAAGAGAGAGAGAGAGAAATAGCCTGCGCGGTTTTTT	1919
Qy	1962	AGTTTGGGGGGTTTGGCTTCCCTTTTATGAGACCATTCCTATTTCTTATATGTCAAATGT	2021
Db	1920	AGTTTGGGGGGTTTGGCTTCCCTTTTATGAGACCATTCCTATTTCTTATATGTCAAATGT	1979
Qy	2022	TTCCTTTATCAGATATTTATTTAGTAAGAAACATCAGTAAATGCTAGCTGCAGATGACA	2081
Db	1980	TTCCTTTATCAGATATTTATTTAGTAAGAAACATCAGTAAATGCTAGCTGCAGATGACA	2039
Qy	2082	TCTCTTTGATGTCAATATGGAAGGTTAAACAGGTGGAAGAAATTCCTGATTCACAATGA	2141
Db	2040	TCTCTTTGATGTCAATATGGAAGGTTAAACAGGTGGAAGAAATTCCTGATTCACAATGA	2099
Qy	2142	AATGCTCTCCTTTCCCTGCGCCAGAGACTTTTATCCATTTACCTAGATTCATCATATTC	2201
Db	2100	AATGCTCTCCTTTCCCTGCGCCAGAGACTTTTATCCATTTACCTAGATTCATCATATTC	2159
Qy	2202	TTTAAATTTTATCTCAGAGCTCCCTCAACCCAC	2235
Db	2160	TTTAAATTTTATCTCAGAGCTCCCTCAACCCAC	2193

	RESULT	8			
	LOCUS	I70140		PAT	02-APR-1998
	DEFINITION	I70140	2330 bp	DNA	
	ACCESSION	I70140	Sequence 1 from patent US 5679346.		
	VERSION	I70140.1	GI:3006275		
	KEYWORDS				
	SOURCE				
	ORGANISM				
	REFERENCE				
AUTHORS	Tedder,R.F. and Speetlin,O.G.				
TITLE	Methods of blocking adhesion with anti-lam1-3 antibody				
JOURNAL	Patent: US 5679346-A 1 21-Oct-1997;				
FEATURES	location/Qualifiers				
source	1..2330				
BASE COUNT	/organism="unknown"				
ORIGIN	661 a 522 c 487 g 660 t				
Query Match	92.4%	Score 2087.6;	DB 10;	Length 2330;	
Best Local Similarity	98.5%;	Pred. NO. 0;			

	Matches 1261:	Conservative	0:	Mismatches	24:	Indels	9:	Gaps	5:
QY	44	CCCTTTGGCAGAGACCTGAGACCCCTTGTGCTAAGTCACAGAGCGCTCAATGGCTGCAGAAAG	103						
Db	7	CCTTTGGGCAAGAGACCTGAGACCCCTTGTGCTAAGTCACAGAGCGCTCAATGGCTGCAGAAAG	66						
QY	104	AACCTGAGAGAGGACCAAGCAAGCAAGCCATGATATTTCCATGGAATATCCAGAGACCAGAG	163						
Db	67	AACCTGAGAGAGGACCAAGCAAGCAAGCCATGATATTTCCATGGAATATCCAGAGACCAGAG	126						
QY	164	GGACTTATGGAACATCTTCAGTTGTGGGGGCGAGCAATGCTCTGTGTGATTTCTGTGC	223						
Db	127	GGACTTATGGAACATCTTCAGTTGTGGGGGCGAGCAATGCTCTGTGTGATTTCTGTGC	186						
QY	224	ACATCATGGAACCTTACTGTGGACTTACCATTATTTCTGAAAAACCATGACATGSCAAAG	283						
Db	187	ACATCATGGAACCCGACTGCTGACTTACCATTATTTCTGAAAAACCATGACATGSCAAAG	246						
QY	284	GGCTGAGAGATTCTCCCGAGCAATTTACACAGATTTAGTGGCATTCACAAACAAAGCGGA	343						
Db	247	GGCTGAGAGATTCTCCCGAGCAATTTACACAGATTTAGTGGCATTCACAAACAAAGCGCGA	306						
QY	344	AATTGAGTATCTGGAGAAAGACTCTCCCTTCAGTGGTCTTACTACTGGATAGAAATCCG	403						
Db	307	AATTGAGTATCTGGAGAAAGACTCTGCTCTTCAAGTGGTCTTACTACTGGATAGAAATCCG	366						
QY	404	GAAGATAGGAGAGAAATATGGACGTGGGTGGGAACAACAATCTCTACTGAAGAAGACA	463						
Db	367	GAAGATAGGAGAGAAATATGGACGTGGGTGGGAACAACAATCTCTACTGAAGAAGACA	426						
QY	464	GAACTGGGGAGATGGTGAAGCCCAACAACAAGAAGAAAGAGAGACTGCTGTGGAATCTA	523						
Db	427	GAACTGGGGAGATGGTGAAGCCCAACAACAAGAAGAAAGAGAGACTGCTGTGGAATCTA	486						
QY	524	TATCAAGAGAAACAAGAATGACGAGCAATGGAAGCATGACGCTGCCAACAACCTAAAGGC	583						
Db	487	TATCAAGAGAAACAAGAATGACGAGCAATGGAAGCATGACGCTGCCAACAACCTAAAGGC	546						
QY	584	AGCCCTCTGTTCACACAGCTCTTGGCAGCCCTGGTCATGCACTGAGCCATGAGAAATGTGT	643						
Db	547	AGCCCTCTGTTCACACAGCTCTTGGCAGCCCTGGTCATGCACTGAGCCATGAGAAATGTGT	606						
QY	644	AGAAATTCATCAATATATCACACCTGCAACCTGTATGTGGGGTACTATTTGGGCCCAATGTCA	703						
Db	607	AGAAATTCATCAATATATATCACACCTGCAACCTGTATGTGGGGTACTATTTGGGCCCAATGTCA	666						
QY	704	GCTTGTGATTCAGTGTGAGCCCTTTGGAGGCCCAAGAGCGGGGTACCATGAGACTGTACTCA	763						
Db	667	GCTTGTGATTCAGTGTGAGCCCTTTGGAGGCCCAAGAGCGGGGTACCATGAGACTGTACTCA	726						
QY	764	CCCTTTGGAAACCTTCAGCTTACGCTCAACAGTGTCCCTTCACGCTGCTGGAAGGAACAA	823						
Db	727	CCCTTTGGGAACCTTCACCTTCAACTTCACACAGTGTGCCCTTCACGCTGCTGGAAGGAACAA	786						
QY	824	CTTAACTGGGATTTGAAGAAACCACTGTGAGCAATTTGGAAACTGTGCTATCTCCGAAGC	883						
Db	787	CTTAACTGGGATTTGAAGAAACCACTGTGAGCAATTTGGAAACTGTGCTATCTCCGAAGC	846						
QY	884	AACCGTCAAGTGATTCAGTGTGAGCCCTATACACACACAGATTTGGGGATCATGAACG	943						
Db	847	AACCGTCAAGTGATTCAGTGTGAGCCCTATACACACACAGATTTGGGGATCATGAACG	906						
QY	944	TAGCCATCCCCGCGCAGCTTCAGCTTTTACCTCTGCATGTACTCTTCATCTGCTCGCAAGG	1003						
Db	907	TAGCCATCCCCGCGCAGCTTCAGCTTTTACCTCTGCATGTACTCTTCATCTGCTCGAAGG	966						
QY	1004	AACGTAGTTAATTGGGAAGAGAAACCAATTTGTGAATCATCTGGAATCTGTCAAATCC	1063						
Db	967	AACGTAGTTAATTGGGAAGAGAAACCAATTTGTGAATCATCTGGAATCTGTCAAATCC	1026						
QY	1064	TAGTCCAAATATGCTCAAAAATTTGGACAAAAGTTTCCATAGATTAAGAGAGGTGATATTA	1123						
Db	1027	TAGTCCAAATATGCTCAAAAATTTGGACAAAAGTTTCCATAGATTAAGAGAGGTGATATTA	1086						

QY 1124 CCCCCCTTCATTCAGTGGCAGTATGTTACTGATTCCTGCGGTGGCATTTATCAT 1183
 |||||
 DB 1087 CCCCCCTTCATTCAGTGGCAGTATGTTACTGATTCCTGCGGTGGCATTTATCAT 1146
 QY 1184 TTGGCTGGCAAGAGATTAAAAAGGCAAGAAATCCAGAGAGATGATGACCCATA 1243
 |||||
 DB 1147 TTGGCTGGCAAGAGATTAAAAAGGCAAGAAATCCAGAGAGATGATGACCCATA 1206
 QY 1244 TTAATGCCCTGGTGGAAGAAATTTCTTGGATFACIAAAATCATGAGATCCCTTTAAA 1303
 |||||
 DB 1207 TTAATGCCCTGGTGGAAGAAATTTCTTGGATFACIAAAATCATGAGATCCCTTTAAA 1266
 QY 1304 TCCCTTCATGAAGGTTTGTGTGGGACACCTCTACGTCAACATGAAAGTGG-ITCC 1362
 |||||
 DB 1267 TCCCTTCATGAAGGTTTGTGTGGGACACCTCTACGTCAACATGAAAGTGGITCC 1326
 QY 1363 TTGAGTGCATGGGAAGATTTCACCCGACCAACAGTTCCTTCAGCTTCATTTCCGCC 1422
 |||||
 DB 1327 TTGAGTGCATGGGAAGATTTCACCCGACCAACAGTTCCTTCAGCTTCATTTCCGCC 1386
 QY 1423 CTCATTTATCCCTCAGCCCGACAGGCTGTTTATACAGCTCAGCTTTTGTCTTTT 1482
 |||||
 DB 1387 CTCATTTATCCCTCAGCCCGACAGGCTGTTTATACAGCTCAGCTTTTGTCTTTT 1446
 QY 1483 CTGAGGAGAAACAAATTAAGACCAT-AAAGGAAAGATTTCATGGAATATAAGATGGCT 1541
 |||||
 DB 1447 CTGAGGAGAAACAAATTAAGACCATAAAGGAAAGATTTCATGGAATATAAGATGGCT 1506
 QY 1542 GACTTGGCTCTTCTTCTGACCTCTGTTTTCAGTTCAATTTAGTGTGACTGATGACAG 1601
 |||||
 DB 1507 GACTTGGCTCTTCTTCTGACCTCTGTTTTCAGTTCAATTTAGTGTGACTGATGACAG 1566
 QY 1602 ACACCTTAAATGAAGTGAATTTGATACATATGGAATATGAGTCACTGTTTCTTGA 1661
 |||||
 DB 1567 ACACCTTAAATGAAGTGAATTTGATACATATGGAATATGAGTCACTGTTTCTTGA 1626
 QY 1662 GATCAATTTACAGTGTCTCTCTGTATCTGTGAGGATACACTCTTATAGAAAGTTCAA 1721
 |||||
 DB 1627 GATCAATTTACAGTGTCTCTCTGTATCTGTGAGGATACACTCTTATAGAAAGTTCAA 1680
 QY 1722 AAGTTCAGCT 1781
 |||||
 DB 1681 AAGTTCAGCT 1740
 QY 1782 AAGTTCAGTATTTGACACTGTAGCGCTGCGTCTGTGAATTTGACCAATCCTATTAACTGG 1841
 |||||
 DB 1741 AAGAGTCTTATTTGACACTGTAGCGCTGCGTCTGTGAATTTGACCAATCCTATTAACTGG 1800
 QY 1842 CTTCAGGCGCTCCGACCT 1901
 |||||
 DB 1801 CTTCAGGCGCTCCGACCT 1859
 QY 1902 TAGCATCTCATGATGAGTCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1961
 |||||
 DB 1860 TAGCATCTCATGATGAGTCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1919
 QY 1962 AGTTGGGGGTTTGTCTGTCTCTTTTATGAGACCAATCTCTATTCTTATAGTCAATGT 2021
 |||||
 DB 1920 AGTTGGGGGTTTGTCTGTCTCTTTTATGAGACCAATCTCTATTCTTATAGTCAATGT 1979
 QY 2022 TTCTTTTATCAGATATTTATGTAAGAAACATCAGTGAATGTGTACTGCAATGACA 2081
 |||||
 DB 1980 TTCTTTTATCAGATATTTATGTAAGAAACATCAGTGAATGTGTACTGCAATGACA 2039
 QY 2082 TCTCTTTATGTCATATGAGAGAGTAAACAGAGTGGAGAAATTCCTGATTCACAAGA 2141
 |||||
 DB 2040 TCTCTTTATGTCATATGAGAGAGTAAACAGAGTGGAGAAATTCCTGATTCACAAGA 2099
 QY 2142 AATGCTCTCTTCCCGCCCGCCAGACTTTTATCAGTCACTTACCTAGATTTACATATTC 2201
 |||||
 DB 2100 AATGCTCTCTTCCCGCCCGCCAGACTTTTATCAGTCACTTACCTAGATTTACATATTC 2159

QY 2202 TTTAATTTATCTCAGGCGCTCCCTCAACCCAC 2235
 |||||
 DB 2160 TTTAATTTATCTCAGGCGCTCCCTCAACCCAC 2193
 RESULT 9
 LOCUS HSLYAM1 2330 bp mRNA PRI 22-MAR-1995
 DEFINITION Human Lyam-1 mRNA for leukocyte adhesion molecule-1.
 X16150
 ACCESSION X16150.1 GI:34428
 VERSION cell surface protein; leukocyte adhesion protein; transmembrane protein.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2330)
 TITLE Tedder T.F.
 JOURNAL Direct Submission
 REFERENCE 2 (bases 1 to 2330)
 TITLE Tedder T.F., Isaacs C.M., Ernst T.J., Demetri G.D., Adler D.A. and Distche C.M.
 JOURNAL Isolation and chromosomal localization of cDNAs encoding a novel human lymphocyte cell surface molecule, LAM-1. Homology with the mouse lymphocyte homing receptor and other human adhesion proteins
 MEDLINE J. Exp. Med. 170 (1), 123-133 (1989)
 FEATURES 89310350
 source Location/Qualifiers
 1..2330
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="1q23-25"
 /tissue-type="tonsil"
 /clone_id="lambda gt11"
 /clone="pLam-1"
 92..1210
 /note="prepro-polypeptide (AA -28 to 344)"
 /codon_start=1
 /protein_id="CAA34275.1"
 /db_xref="GI:34429"
 /db_xref="SWISS-PROT:P14151"
 /translation="MIFPMKOSTORDLNNIFKLMGTM.LCDDFLAHGTDQWTHYS EKPMNQRRARFQRDWDYD.VATONKAELEIYEKTPERSYTWGIGIRIGETWVG TNSLTPEARNMDDGERNNKKNKEDVEIYIRNKDAGKMNDDACHKLAAICVASC QPNSCHGECVELINNYTNCNDVGYGQCFVIOCEPLAEPLGMDCTHPLGNFN FNSQCAFSCSEGTNLGIEBTCEPPGNMSSPEPTCOVIOCEPLAPDLGIMNCSHPL ASFSPTSACTFICSEGTLEIGKKTKICSSGIMSNPSPICOKLDSFSMIKRGYNPL FIPVAVMVTAFFSGIAFLIWLARLKRKRKSRSMNDPY"
 92..175
 /product="signal peptide (AA -28 to -1)"
 176..1207
 /note="propeptide (AA 1 to 344)"
 206..1207
 /product="mature leukocyte adhesion protein (AA 11 to 344)"
 2296..2301
 /note="polya attachment site"
 BASE COUNT 661 a 522 c 487 g 660 t
 ORIGIN
 Query Match 92.4%; Score 2087.6; DB 93; Length 2330;
 Best Local Similarity 98.5%; Pred No. 0;
 Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;
 QY 44 CCTTTGGCAAGACCTGAGACCTTGCTCTAAGTCAAGAGCTCAATGGCTGAGAG 103
 |||||
 DB 7 CTTTGGGCAAGACCTGAGACCTTGCTCTAAGTCAAGAGCTCAATGGCTGAGAG 66
 |||||
 QY 104 AACTAGAGAGGACCAAGAACCATGATTTTCATGGAATGTGAGAGACCCAGAG 163
 |||||

Db 67 AACTAGAGAAGCAAGCAAGCAAGCATGATATTTTCATGGAATGTGAGACACCAGAG 126
QY 164 GGACTTATGGAACATCTTCAAGTTGTGGGGTGACAATGCTCTGTTGTGATTTCCGGC 223
Db 127 GGACTTATGGAACATCTTCAAGTTGTGGGGTGACAATGCTCTGTTGTGATTTCCGGC 186
QY 224 ACATCATGGAACGACTCTGAGCTTACCATTTATTTGAAAAAACCCTGAATGGCAAG 283
Db 187 ACATCATGGAACGACTCTGAGCTTACCATTTATTTGAAAAAACCCTGAATGGCAAG 246
QY 284 GGCTAGAAAGTTGTGCCGAGACATATACAGATTTAGTTGCCATACAAAAAGCGCGA 343
Db 247 GGCTAGAAAGTTGTGCCGAGACATATACAGATTTAGTTGCCATACAAAAAGCGCGA 306
QY 344 AATTGACTATCTGAGAAAGCTCTGCCCTTCACTGTTCTTACTACTGATAGGAATCCG 403
Db 307 AATTGACTATCTGAGAAAGCTCTGCCCTTCACTGTTCTTACTACTGATAGGAATCCG 366
QY 404 GAAGATGAGGAATATGAGAGTGGGGTGGGAGCAACAAATCTCTCACTGAAGAAGGAGA 463
Db 367 GAAGATGAGGAATATGAGAGTGGGGTGGGAGCAACAAATCTCTCACTGAAGAAGGAGA 426
QY 464 GAATGGGAGATGTGAGGCCCAACAAGAAAGAAAGAGGAGCTGCTGGAGATCTA 523
Db 427 GAATGGGAGATGTGAGGCCCAACAAGAAAGAAAGAGGAGCTGCTGGAGATCTA 486
QY 524 TATCAGAGAAACAAGATGAGGCAAAATGGAACGATGAGCCTGCCAACAATGAAAGC 583
Db 487 TATCAGAGAAACAAGATGAGGCAAAATGGAACGATGAGCCTGCCAACAATGAAAGC 546
QY 584 AGCCCTGTATACACACTCTTGGCCAGCCCTGGTCACTGAGTGGCCATGGAAGAATGT 643
Db 547 AGCCCTGTATACACACTCTTGGCCAGCCCTGGTCACTGAGTGGCCATGGAAGAATGT 606
QY 644 AGAATCATCAATATACACACTGCAACTGTATGTGGGTACTATGAGGCCAGTGTCA 703
Db 607 AGAATCATCAATATATACACACTGCAACTGTATGTGGGTACTATGAGGCCAGTGTCA 666
QY 704 GCTTGTGATTCAGTGTGAGGCTTTGGAGGCCAGAGCTGGGTACATGAGACTGTACTCA 763
Db 667 GCTTGTGATTCAGTGTGAGGCTTTGGAGGCCAGAGCTGGGTACATGAGACTGTACTCA 726
QY 764 CCCCTTGGAACTTCAGCTTCAGCTTCACAGTGTGCTTACGCTGCTTAAGGAACAAA 823
Db 727 CCCCTTGGAACTTCAGCTTCAGCTTCACAGTGTGCTTACGCTGCTTAAGGAACAAA 786
QY 824 CTTAATCGGATTTGAAGAACAACCTGTGAGCAATTTGAAACGTGCTCTCAGAAC 883
Db 787 CTTAATCGGATTTGAAGAACAACCTGTGAGCAATTTGAAACGTGCTCTCAGAAC 846
QY 884 AACCTGTCAAGTATTCAGTGTGAGGCTTATCAGACACGAAATTTGGGATCATGAACTG 943
Db 847 AACCTGTCAAGTATTCAGTGTGAGGCTTATCAGACACGAAATTTGGGATCATGAACTG 906
QY 944 TAACCATCCCTGCCAGCTTCAGCTTACCTGCTGATGATCTTCACTGCTCAGAGG 1003
Db 907 TAACCATCCCTGCCAGCTTCAGCTTACCTGCTGATGATCTTCACTGCTCAGAGG 966
QY 1004 AACTGATTAATTTGGGAAAGAAAGCAATTTGTAATCATCTGGAATCTGCTCAAAATCC 1063
Db 967 AACTGATTAATTTGGGAAAGAAAGCAATTTGTAATCATCTGGAATCTGCTCAAAATCC 1026
QY 1064 TAGTCAATATGTCAAAAAATTTGACAAAAGTTTCTCAATGATTAAGAGGGTATTAATA 1123
Db 1027 TAGTCAATATGTCAAAAAATTTGACAAAAGTTTCTCAATGATTAAGAGGGTATTAATA 1086
QY 1124 CCCCCTCTTATTCAGTGGCAGTCAATGTTTACTGCAATTTCTGCGGTGGCAATTTATCAT 1183
Db 1087 CCCCCTCTTATTCAGTGGCAGTCAATGTTTACTGCAATTTCTGCGGTGGCAATTTATCAT 1146
QY 1184 TTGGCTGGCAAGAGATTTAAAAAAGGCAAGAATCCAAAGAGTATGTAATGCCCATTA 1243
Db 1147 TTGGCTGGCAAGAGATTTAAAAAAGGCAAGAATCCAAAGAGTATGTAATGCCCATTA 1206

QY 1244 TTAATGCCCTTGTGTAAGAAATATCTTGGAATACTAAAAATCATGAGATCCCTTAAA 1303
Db 1207 TTAATGCCCTTGTGTAAGAAATATCTTGGAATACTAAAAATCATGAGATCCCTTAAA 1266
QY 1304 TCCCTTCATGAAAGCTTTTGTGTGGTGGACACCTCTACGTCAACAATGAAGTGTG-7TCC 1362
Db 1267 TCCCTTCATGAAAGCTTTTGTGTGGTGGACACCTCTACGTCAACAATGAAGTGTGTTCC 1326
QY 1363 TTCAGTCAATCTGGGAAGATTTCTACCCGACCAACAGCTTCCCTTGAGCTTCCATTTGGCC 1422
Db 1327 TTCAGTCAATCTGGGAAGATTTCTACCTGACCAACAGCTTCCCTTGAGCTTCCATTTACCC 1386
QY 1423 CTCATTTATCCCTCAACCCCGACAGAGTGTATACAGCTACAGCTTTTGTCTTTT 1482
Db 1387 CTCATTTATCCCTCAACCCCGACAGAGTGTATACAGCTACAGCTTTTGTCTTTT 1446
QY 1483 CTGAGGAGAAACAATTAAGACCAT-AAAGGAAAGATTCATGTGAATATTAAGATGGCT 1541
Db 1447 CTGAGGAGAAACAATTAAGACCATTAAGGAAAGATTCATGTGAATATTAAGATGGCT 1506
QY 1542 GACTTTGCTCTTCTTCTGACTCTTGTTCAGTTTCAATTCAGTCTGACTGTATGACAG 1601
Db 1507 GACTTTGCTCTTCTTCTGACTCTTGTTCAGTTTCAATTCAGTCTGACTGTATGACAG 1566
QY 1602 ACATTTTAATGAAGTCAAAATTTGATACATATGTGAATATGAGCTACAGTTTCTTGA 1661
Db 1567 ACATTTTAATGAAGTCAAAATTTGATACATATGTGAATATGAGCTACAGTTTCTTGA 1626
QY 1662 GATCAAAATTCAGTCTGCTCTGTATACGTGAGAGTACACTGTTATGAAAGTTCAAA 1721
Db 1627 GATCAAAATTCAGTCTGCTCTGTATACGTGAGAGTACACTGTTATGAAAGTTCAAA 1680
QY 1722 AAGTCTACGCTCTCTTCTTCTTCACTCAAGTGAATGAGGCTGCTGCTCAAGTTGA 1781
Db 1681 AAGTCTACGCTCTCTTCTTCTTCACTCAAGTGAATGAGGCTGCTGCTCAAGTTGA 1740
QY 1782 AAGAGTCTATTTGCACTGTAGCTGCGCGCTGTGTAATTTGGACATCTATTTAACTGG 1841
Db 1741 AAGAGTCTATTTGCACTGTAGCTGCGCGCTGTGTAATTTGGACATCTATTTAACTGG 1800
QY 1842 CTTGAGGCTGCCCGACCTCTGTGAGCAGCCTCTTTTCAAGTGGTGACTTCCACAGC 1901
Db 1801 CTTGAGGCTGCCCGACCTCTGTGAGCAGCCTCTTTTCAAGTGGTGACTTCCACAGC 1859
QY 1902 TAGCATCTCATGAGTGTGCAAGCAAAAGAGAGAAGAGAAATAGCTGCGCGTCTTTT 1961
Db 1860 TAGCATCTCATGAGTGTGCAAGCAAAAGAGAGAAGAGAAATAGCTGCGCGTCTTTT 1919
QY 1962 AGTTGGGGGTTTGTCTTCTTTTATGAGACCATCTCATTTCTTATATGCAATGT 2021
Db 1920 AGTTGGGGGTTTGTCTTCTTTTATGAGACCATCTCATTTCTTATATGCAATGT 1979
QY 2022 TTCTTTATCAGCATATTTATTAAGAAAAATCACTGAAATGCTGAGCAAGTACA 2081
Db 1980 TTCTTTATCAGCATATTTATTAAGAAAAATCACTGAAATGCTGAGCAAGTACA 2039
QY 2082 TCTCTTGAATGTCATATGAGAAAGTAAACAGGTGAGAAATCTTGAATTCACAATGA 2141
Db 2040 TCTCTTGAATGTCATATGAGAAAGTAAACAGGTGAGAAATCTTGAATTCACAATGA 2099
QY 2142 AATGCTCTCTTCCCTGCGCCCGAGACCTTTATCCACTTACCTAGATTTCAATATTC 2201
Db 2100 AATGCTCTCTTCCCTGCGCCCGAGACCTTTATCCACTTACCTAGATTTCAATATTC 2159
QY 2202 TTTTAAATTTATCTCAGGCTCCCTCAACCCGAC 2235
Db 2160 TTTTAAATTTATCTCAGGCTCCCTCAACCCGAC 2193

RESULT 10
HSA246000
LOCUS HSA246000 1569 bp mRNA PRI 08-SEP-1999

DEFINITION	Homo sapiens mRNA for leucocyte adhesion receptor, L-selectin.
ACCESSION	AJ246000
VERSION	AJ246000.1 GI:5852071
KEYWORDS	L-selectin gene; leucocyte adhesion receptor.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Ekakoyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1569)
JOURNAL	Fieger, C.B.
TITLE	Thesis (1998) Freie Universitaet Berlin, Fachbereich Chemie
REFERENCE	2 (bases 1 to 1569)
AUTHORS	Fieger, C.B.
TITLE	Direct Submission
JOURNAL	Submitted (04-SEP-1999) Fieger C.B., Benjamin Franklin Klinikum der Freien Universitaet Berlin, Institut fuer Klinische Chemie & Pathobiochemie, Hindenburgdamm 30, 12200 Berlin, GERMANY
FEATURES	Location/Qualifiers
source	1..1569
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/tissue_type="hematopoietic (B lymphocyte)"
	/rname_lib="Raji cDNA library (Clontech HL1002a)"
	/cell_type="burkitt lymphoma"
	/cell_line="Raji"
	<1..36
5'UTR	/gene="L-selectin"
	1..1569
gene	/gene="L-selectin"
	37..1194
CDS	/gene="L-selectin"
	/function="leucocyte adhesion receptor"
	/codon_start=1
	/product="L-selectin"
	/protein_id="CAB55488.1"
	/db_xref="GI:5852072"
	/translation="MGCKRTREGEYSKAMIFPWKQSTQRODLMIPIKMGWTMLCDPL AHHOTDCTVTHYSKRPMMQKARRFCNDNTDILVLIQNKIEIYLEETTFPSRYWI GIRIKIGIITWVGTINKSLTEAEENWGDGEPNNKNKBDVEIYIKRKDAGKWNDAK HKILALCLYTAASCPQWSCSGHGECVELINNYTNCMDVGYPCQCOEYIOCEPLEDEL GTMDCIHPGLNMFSSQCAFCSEGTMLTGLEETTCGFENMSSPEPTCOVICPELS APDGMINGSHPLFASFTFACITFCSEGTGLIGKTKTICESSGIMSNSPTCQKDKD SFSMKREDYVPLPIPAVAVWTAPSLAFIIMLARLRKKKKRSMNDPY"
	37..189
sig_peptide	/gene="L-selectin"
	190..1191
mat_peptide	/gene="L-selectin"
	/product="L-selectin"
	1195..>1569
3'UTR	/gene="L-selectin"
	463 a 338 c 364 g 404 t
BASE COUNT	
ORIGIN	
Query Match	67.8%; Score 1532.2; DB 93; Length 1569;
Best Local Similarity	99.4%; Pred. No. 0;
Matches 1559; Conservative	0; Mismatches 8; Indels 2; Gaps 2;
54	AGGACCTAGACCCCTGTCGTAAGTCAAGAGCGTCATTTGGGCTGCAGAGACTAGAGAA 113
1	AGGACCTAGACCCCTGTCGTAAGTCAAGAGCGTCATTTGGGCTGCAGAGAACTAGAGAA 60
114	GGACCAAGCAAGCCATGATATTTCCATGTGAATAAGTGAAGACCCGAGAGGGACTATGG 173
61	GGACCAAGCAAGCCATGATATTTCCATGTGAATAAGTGAAGACCCGAGAGGGACTATGG 120
174	AACATCTTCAAGTTGTGGGGGTGACAACTCTCTGTGTGATTTCCATGACATCATGGA 233
121	AACATCTTCAAGTTGTGGGGGTGACAACTCTCTGTGTGATTTCCATGACATCATGGA 180
234	ACCAAGCTGGAGCTTACCATTTATTCGAAAAAACCATGAATGCGCAAAAGGCTAGAGA 293
181	ACCAAGCTGGAGCTTACCATTTATTCGAAAAAACCATGAATGCGCAAAAGGCTAGAGA 240

QY	294	TTTCGCCGACCAATTACAGAAATTAGTTGGCATACAAACAAAGCGGAAATTGAGAT	355
Db	241	TTTCGCCGACCAATTACAGAAATTAGTTGGCATACAAACAAAGCGGAAATTGAGAT	300
QY	354	CTGAGAGAAGACTCTGCCCTTCACTGCTTCTACTACCTGATAGAAATCCGGAAGATAGGA	413
Db	301	CTGAGAGAAGACTCTGCCCTTCACTGCTTCTACTACCTGATAGAAATCCGGAAGATAGGA	360
QY	414	GGATATAGGACGTGGGGGAACCAACAAATCTCTACCTGAAGAAGCAGAACTGGGGA	473
Db	361	GGATATAGGACGTGGGGGAACCAACAAATCTCTACCTGAAGAAGCAGAACTGGGGA	420
QY	474	GATGGTAGCCCAACAAGAAGAACAAGAGAGACTGCTGGAGATATATACAGAGA	533
Db	421	GATGGTAGCCCAACAAGAAGAACAAGAGAGACTGCTGGAGATATATACAGAGA	480
QY	534	AACAAAGATCGAGCAATGGAACGATGACGCTCCCAACAACTPAAAGCAGCCCTCTGT	593
Db	481	AACAAAGATCGAGCAATGGAACGATGACGCTCCCAACAACTPAAAGCAGCCCTCTGT	540
QY	594	TACACAGCTCTTGCCAGCCCTGGTCATGACAGTGGCCATGGAGAATGTAGAAATATC	653
Db	541	TACACAGCTCTTGCCAGCCCTGGTCATGACAGTGGCCATGGAGAATGTAGAAATATC	600
QY	654	AATTAATCACCTGCACCTGTGATGTGGGGTACTATGGGCCCCAGTGCAGCTTGTGATT	713
Db	601	AATTAATTAACCTGCACCTGTGATGTGGGGTACTATGGGCCCCAGTGCAGCTTGTGATT	660
QY	714	CATGTGACCTTTGGAGGCCCAAGAGCTGGGTACATAGATGACCTACTCACCCCTTTGGA	773
Db	661	CATGTGACCTTTGGAGGCCCAAGAGCTGGGTACATAGATGACCTACTCACCCCTTTGGA	720
QY	774	AACCTGACCTTACGTCACAGTGTGCTTCTACAGTGTCTGAAGAACAACTTAACGTGG	833
Db	721	AACCTGACCTTACGTCACAGTGTGCTTCTACAGTGTCTGAAGAACAACTTAACGTGG	780
QY	834	ATTGAAGAAGAACCACTGTGGACATTTTGGAACTGTGTATCTCAGAACCAACTGTCAA	893
Db	781	ATTGAAGAAGAACCACTGTGGACATTTTGGAACTGTGTATCTCAGAACCAACTGTCAA	840
QY	894	GTGATTCAGTGTGACCTCTATACAGACACAGATTTGGGGATTCATGAACCTGACCATGCC	953
Db	841	GTGATTCAGTGTGACCTCTATACAGACACAGATTTGGGGATTCATGAACCTGACCATGCC	900
QY	954	CTGGCAGCTTACGTTTACTCTGTGATGATACCTTCACTGTCTCAGAAAGAACGTAGTTA	1013
Db	901	CTGGCAGCTTACGTTTACTCTGTGATGATACCTTCACTGTCTCAGAAAGAACGTAGTTA	960
QY	1014	ATTGGGAAGAAACCACTTGTGGATCATCTGSAATCTGGTCAAAATCCTAGTCCAAATA	1077
Db	961	ATTGGGAAGAAACCACTTGTGGATCATCTGSAATCTGGTCAAAATCCTAGTCCAAATA	1020
QY	1074	TGTCAAAAATTGGACAAAGTTTCTCATGATTAAGAGAGGGTATTATTAACCCCTTTC	1133
Db	1021	TGTCAAAAATTGGACAAAGTTTCTCATGATTAAGAGAGGGTATTATTAACCCCTTTC	1080
QY	1134	ATTCCAGTGGCAGTCATGTTACTGTGCAATTTCTGTGGGTTGGSCATTTATCAATTTGGCTGCA	1193
Db	1081	ATTCCAGTGGCAGTCATGTTACTGTGCAATTTCTGTGGGTTGGSCATTTATCAATTTGGCTGCA	1140
QY	1194	AGGACATTAATAAAGCAAGCAAAATCCACAGAGAATGATGAATAGCCATATTAATGGCC	1255
Db	1141	AGGACATTAATAAAGCAAGCAAAATCCACAGAGAATGATGAATAGCCATATTAATGGCC	1200
QY	1254	CTTGGTGAAGAAAATTCTTGGATATACATAAAATCATGAGATCTTTAAATCCTTCCATG	1313
Db	1201	CTTGGTGAAGAAAATTCTTGGATATACATAAAATCATGAGATCTTTAAATCCTTCCATG	1260
QY	1314	AAACGTTTTGTGTGTGGACCTTCTACGTCGAACATGAAGTGTG-TTCTTTCAGTGCAT	1372
Db	1261	AAACGTTTTGTGTGTGGACCTTCTACGTCGAACATGAAGTGTG-TTCTTTCAGTGCAT	1320

QY	1373	CMGGGAAGATTTCTACCCGACCAACAGTTCTTTCAGCTTCCATTTCGGCCCTCATTTATTC	1432
Db	1321	CTGGGAAGATTTCTACCCGACCAACAGTTCTTTCAGCTTCCATTTCGGCCCTCATTTATTC	1380
QY	1433	CTCAACCCCGACCCACAGAGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGAGAA	1492
Db	1381	CCTCAACCCCGACCCACAGAGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGAGAA	1440
QY	1493	ACAAATTAAGACCAT-AAGGGAAGAGATTCTATGTGAATATAAAGATGGCTGACTTTGCTC	1551
Db	1441	ACAAATTAAGACCATTAAGGGAAGAGATTCTATGTGAATATAAAGATGGCTGACTTTGCTC	1500
QY	1552	TTTCTTGACTCTTGTTCACGTTTCAATTCAGCTGCTGTACTGATGACAGACACTTTAA	1611
Db	1501	TTTTCTTGACTCTTGTTCACGTTTCAATTCAGCTGCTGTACTGATGACAGACACTTTAA	1560
QY	1612	ATGAAGTGC 1620	
Db	1561	ATGAAGTGC 1569	
RESULT	11		
LOCUS	PHU52074	1510 bp	16-JAN-1997
DEFINITION	Papio hamadryas anubis L-selectin precursor mRNA, complete cds.		
ACCESSION	U52074		
VERSION	U52074.1	GI:1326148	
KEYWORDS			
SOURCE	Olive baboon.		
ORGANISM	Papio cynocephalus anubis		
REFERENCE	Euhariyola; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae; Papio.		
AUTHORS	1 (bases 1 to 1510)		
TITLE	Tsurushita, N., Fu, H. and Berg, E. L.		
JOURNAL	PCR cloning of the cDNA encoding baboon L-selectin		
MEDLINE	Gene 181 (1-2), 219-220 (1996)		
REFERENCE	97128794		
AUTHORS	2 (bases 1 to 1510)		
JOURNAL	Tsurushita, N.		
FEATURES	Direct Submission		
source	Submitted (21-MAR-1996) Naoya Tsurushita, Protein Design Labs, Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA		
	Location/Qualifiers		
	1..1510		
	/organism="Papio cynocephalus anubis"		
	/sub_species="anubis"		
	/db_xref="taxon:9555"		
	79..1197		
	/codon_start=1		
	/product="L-selectin precursor"		
	/protein_id="AAB40903.1"		
	/db_xref="GI:1326149"		
	/translation="MIEPRKQSTQRDLMNIFKLMGWTMLSCDFLANHGTDQWTHYS		
	ENPMNQAKRFRENYTDVAIONKKEIEYELTFPSYSYWIIGRKIGIWTWVG		
	TNKILTOAEKMGDEGNKKKNDCEVEIYIKRKDAGKWNDDCHPKAKLCYATSC		
	PSQSGSGHECVETIINNYTCMDVGYGPGQGFYIOCEPLERPYGLMDCTNPLGDS		
	FPSCGAFNCSRGTLTGTEIETGQPCPNMSPEPTCOYICERLSADPLIMNSHPL		
	ASFEPSNACTSCSEGEITLIGEKTTIETSSISMSNPPICTCKLDRFSMTKEGDYFL		
	FIPAVIVTAVSGAIFIIWLARLRKKKKSKSMDDPY"		
BASE COUNT	467 a 328 c 349 g 366 t		
ORIGIN			
Query Match	59.8%; Score 1351.2; DB 97; Length 1510;		
Best Local Similarity	95.6%; Pred. No. 0;		
Matches 1422; Conservative	0; Mismatches 63; Indels 3; Gaps 3;		
QY	52	CAAGACCGGAA-CCGTTGCTTAAGCAAGAGCTCAATGAGGCTGCAAGAACTAGA	110
Db	1	CAAGACCTGAGATCATTTGCTTAAGCAAGAGCTCAATGAGGCTGCAAGAACTAGA	60
QY	111	GAAGACCAAGCAAGCATGATATTTCCATGGAATGTCAAGACCAAGAGGACTTA	170

Db	61	GAAGGACCAAGCAAAAGCCATGATATTTTCACGAGAAATGTAGAGTACCCAGAGGACTTAA	120
Qy	171	TGGAACATCTTCAGATTGTGGGGGTGGACAATGCTCTGTTGTATTTCCGTGGACATCAT	230
Db	121	TGGAAACATCTTCAGATTGTGGGGGTGGACAATGCTCTGTTGTATTTCCGTGGACATCAT	180
Qy	231	GGAACTCTACTGCTGGACTTACCATTTATTTGAAAAACCATGAAGTGGCAAAAGGCTTAA	290
Db	181	GGAAACGCACTGCTGACTTACCATTTATTTGAAAAATCCCATGAAGTGGCAAAAGGCTTAA	240
Qy	291	AATATCTCCCGACAGCAATTTACACAGATTTTAGTTGCCATTAACAAACAAAGCGGAAATTTAG	350
Db	241	AATATCTCCCGACAGCAATTTACACAGATTTAGTTGCCATTAACAAACAAAGCGGAAATTTAG	300
Qy	351	TATTCGGAAGAAGACTCTGCCCTTCAGTCTGTTCTTACTACATGAGATAGAAATCCGGAAGATA	410
Db	301	TATTCGGAAGAAGACTCTGCCCTTCAGTCTTCTTACTACATGAGATAGAAATCCGGAAGATA	360
Qy	411	GGAGGAATATGAGAGCTGGGTGGGAACCAACAAATCTCTACTGAAAGACAGAAACTGG	470
Db	361	GGAGGCATATGAGAGCTGGGTGGGAACCAACAAATCTCTACTGAAAGACAGAAACTGG	420
Qy	471	GGAGATGTGTAGCCCAACACAAACAAGAGAGACTGCGTGGAGATCTATATCAAG	530
Db	421	GGAGATGTGGGAGCCCAACACAAACAAGAGAGACTGCGTGGAGATCTATATCAAG	480
Qy	531	AGAAACAAAGATGCAAGGCAATTTGAAAGATGAGAGCCCTGCCACAAACTAAAAGGAGCCCTC	590
Db	481	AGAAACAAAGATGCGGGCAATTTGAAAGATGAGAGCCCTGCCACAAACCAAGGAGCCCTC	540
Qy	591	TGTTACACAGCTTCTTGGCAGCCCTGGTCAATGCAAGTGGCCATGGAGAATGTGTAGAATC	650
Db	541	TGTTACACAGCTTCTTGGCAGCCCTGGTCAATGCAAGTGGCCATGGAGAATGTGTAGAATC	600
Qy	651	ATCAATTAATCAACCTGCACTGTGATGTGGGGTACTATGGCCCCAGTGTCACTTGTG	710
Db	601	ATCAATTAATTAACCTGCACTGTGATGTGGGGTACTATGGCCCCAGTGTCACTTGTG	660
Qy	711	ATTCAGTGTGAGCCCTTGGAGAGCCCCAGACCTGGGTACATAGGACGTGACTCACCCCTTT	770
Db	661	ATTCAGTGTGAGCCCTTGGAGAGCCCCAGACCTGGGTACATAGGACGTGACTCACCCCTTTG	720
Qy	771	GGAAACTTCACAGCTTCAGCTACAGTGTGACCTTCAGCTCTGTAAGGAACAAACTTAAT	830
Db	721	GGAGACTTCACAGCTTCAGCTACAGTGTGACCTTCAGCTCTGTAAGGAACAAACTTAAT	780
Qy	831	GGGATTTGAAGAAACCACTGTGACCAATTTGGAAACTGTCTACCTCAGAACCAACTGT	890
Db	781	GGGATTTGAAGAAACCACTGTGTGACCAATTTGGAAACTGTCTACCTCAGAACCAACTGT	840
Qy	891	CAAGATTTCAAGTGTGAGACCTCTATACAGCAACAGATTTGGGGATTCATGAAACGTAGCAT	950
Db	841	CAAGATTTCAAGTGTGAGACCTCTATACAGCAACAGATTTGGGGATTCATGAAACGTAGTAC	900
Qy	951	CCCGTGGCCACTTCAGCTTACCTGTGCAATGTAACCTTCATCTGCTCAGAAAGGAACGTAG	1010
Db	901	CCCGTGGCCACTTCAGCTTTCCTCTGCGTGTACCTTCAGCTGCTCAGAAAGGAACGTAG	960
Qy	1011	TTTAATTTGGGAAGAAAAACCATTTGTGAATCATCTGGAATCTGTGCAANTCCTAGTCCA	1070
Db	961	TTTAATTTGGGGGAAGAAAAACCATTTGTGAATCATCTGGAATCTGTGCAANTCCTAGTCCA	1020
Qy	1071	ATATCTCAAAAATTTGACAAAGTTTCTCAATGATTAAGAGAGGTGATTAATTAACCCCTTC	1130
Db	1021	ATATCTCAAAAATTTGACAGAAATTTCTCATGATTAAGAGAGGTGATTAATTAACCCCTTC	1080
Qy	1131	TTTCATTTCCAGTGGGAGATCATGTTACTGCAATCTCTGCGGTTGGCATTTATCATTTGGCGTG	1190
Db	1081	TTTCATTTCCAGTGGGAGATCATGTTACTGCAATCTCTGCGGTTGGCATTTATCATTTGGCGTG	1140
Qy	1191	GCAAGGAGATTTAAAAAAGCCAGAGAAATCCAGAGAAATGTGAATGACCATTAATTAATC	1250

Db 1141 GCAAGAGATTAAGAAAGGCAAGAAATCCAGAAAGATGATGATGACCATATTAATC 1200
 QY 1251 GCCCTGGTGAAGAAATCTTGGAATACTATAAATCAGAGATCCTTTAAATCCTCC 1310
 Db 1201 GCCGTGGTGAAGAAATCTTGGAATACTATAAATCAGAGATCCTTTAAATCCTCC 1260
 QY 1311 ATGAACGTTTGTGTGGTGGCACTCTCTACGTCAAAACATGAAGTGTG-TTCCTTCAGTG 1369
 Db 1261 ATGAACGTTTGTGTGGTGGCACTCTCTACGTCAAAACATGAAGTGTGTCTTCAGCA 1320
 QY 1370 CATCTGGGAAGATTTCTACCCGACCAAGTCTCTTACGCTTCATTTGCCCTCATTT 1429
 Db 1321 CATCTGGGAAGATTTCTACCTGACCAACAGCTCTTACGCTTCATTTGCCCTCATTT 1380
 QY 1430 ATCCCTCAACCCCGACGCGCAGGTGTTTACAGCTCAGCTTTTGTCTTTCTGAGGA 1489
 Db 1381 ATCCCTCAACCCCGACGCGCAGGTGTTTATGAGCTCAGCTTTTGTCTTTCTGAGGA 1440
 QY 1490 GAAACAAATTAAGACAT-TAAGGAAAGGATTCATGTGATATTAAGA 1536
 Db 1441 GAAACAAATTAAGACATTAAGGAAAGGATTAATGTGATATTAACAAA 1488

RESULT 12

PT073728 1119 bp mRNA PRI 05-NOV-1996
 LOCUS Pan troglodytes L-selection mRNA, complete cds.
 DEFINITION U73728
 ACCESSION U73728
 VERSION 073728.1 GI:1658019
 KEYWORDS

SOURCE

ORGANISM chimpanzee.
 SOURCE Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

REFERENCE

AUTHORS Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
 Tsunushita,N.
 TITLE Cloning of the cDNA encoding L-selection from nonhuman primates
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1119)

AUTHORS

Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
 Tsunushita,N.

TITLE Direct Submission
 JOURNAL Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
 Avenue, Mountain View, CA 94043, USA

FEATURES

source

CDS

1..1119
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 1..1119
 /codon_start=1
 /product="L-selection"
 /protein_id="AAB18248.1"
 /db_xref="GI:1658020"
 /translation="MIFPMKCOSTQRDLMNIFKLGWMTLCCDFLAHGHGIDCWYHY
 EKPMWQARRECDNDYDIAIONKAEIIEFLKRNKDGKMDACHKRLKALCYTAS
 TNSLIEAEENMGDEPNKKKKECVETIYKRNKDGKMDACHKRLKALCYTAS
 QPMSCSGECVEIINNYTNCNDYGYGPOCPYIQCRLDAPELGTDCHPLRPNES
 FSSOCARSCSEGTNLTEETCCPFGWMSSEPTCOVTCQEPISAPDGLIMNSHPL
 AFSFTSACTICSEGTLELIGKRTICSSSIWNSPSTCQKLDKSPSMIKEGDYNPL
 FIPAVAVTASGIAFIIMLARLRKKGKRSRMDPY"

BASE COUNT 332 a 236 c 277 g 274 t
 ORIGIN

Query Match 48.8%; Score 1101.4; DB 97; Length 1119;
 Best Local Similarity 99.0%; Pred. No. 5.6e-293;
 Matches 1108; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 129 ATGATATTTCATGGAATGTGAGACCCAGAGGACTTATGGAACATCTTCAAGTTG 188
 Db 1 ATGATATTTCATGGAATGTGAGACCCAGAGGACTTATGGAACATCTTCAAGTTG 60

QY 189 TGGGGGTGACAAATGCTGTGTGATTTCTGGCACATCATGAACCTACTGCTGACT 248
 Db 61 TGGGGGTGACAAATGCTGTGTGATTTCTGGCACATCATGAACCTACTGCTGACT 120
 QY 249 TACCATTATTCGAAAAAACCATGAACCTGCAAGGGCTAGAAGATTTCGCCAGACAT 308
 Db 121 TACCATTATTCGAAAAAACCATGAACCTGCAAGGGCTAGAAGATTTCGCCAGACAT 180
 QY 309 TACACGATTTAGTTCGCATACAAAACAAGGGGAATTGATATCTGAGAAAGACTCTG 368
 Db 181 TACACGATTTAGTTCGCATACAAAACAAGGGGAATTGATATCTGAGAAAGACTCTG 240
 QY 369 CCTTATAGTCGTTCTTACTACTGATAGGAATCCGAGATGAGGAATATGAGAGCTGG 428
 Db 241 CCTTATAGTCGTTCTTACTACTGATAGGAATCCGAGATGAGGAATATGAGAGCTGG 300
 QY 429 GTGGGAACCAACAAATCTCTCACTGAAGAAGAGAACTGGGGAGATGGTGAAGCCAAC 488
 Db 301 GTGGGAACCAACAAATCTCTCACTGAAGAAGAGAACTGGGGAGATGGTGAAGCCAAC 360
 QY 489 AACCAAGAAGACAGAGAGACCTGCGGAGATCTATATCAAGAAACAAAGATGACAGC 548
 Db 361 AACCAAGAAGACAGAGAGACCTGCGGAGATCTATCAAGAAACAAAGATGACAGC 420
 QY 549 AATGGAAGATGACGCGCTGCACAAACTAAGGAGAGCCCTGTTCACACAGCTTCTGC 608
 Db 421 AATGGAAGATGACGCGCTGCACAAACTAAGGAGAGCCCTGTTCACACAGCTTCTGC 480
 QY 609 CAGCCCTGTCTATGCACTGGCCATGAGAGATGTGAAGAAATCATATATCACACTGC 668
 Db 481 CAGCCCTGTCTATGCACTGGCCATGAGAGATGTGAAGAAATCATATATCACACTGC 540
 QY 669 AACTGTGATGTGGGTACTATGAGGCGCCAGTGTCAAGCTTGATGATCACTGAGGCTTG 728
 Db 541 AACTGTGATGTGGGTACTATGAGGCGCCAGTGTCAAGCTTGATGATCACTGAGGCTTG 600
 QY 729 GAGGCCCGAGACCTGGTACATGACACTGTACTACCCCTTGGAAACTGACGTTTCAGC 788
 Db 601 GAGGCCCGAGACCTGGTACATGACACTGTACTACCCCTTGGAAACTGACGTTTCAGC 660
 QY 789 TCACAGTGTGCTTCACTGCTCTGAAGAACAACTTAAGTGGATTTGAAGAAACACCC 848
 Db 661 TCACAGTGTGCTTCACTGCTCTGAAGAACAACTTAAGTGGATTTGAAGAAACACCC 720
 QY 849 TGTGACCAATTTGGAAACTGTGATCTCCAGAACCAACCTGTCAAGTATCACTGATGAG 908
 Db 721 TGTGACCAATTTGGAAACTGTGATCTCCAGAACCAACCTGTCAAGTATCACTGATGAG 780
 QY 909 CCTATATGACACGATTTGGGAGATCAATGAACTATCCCTGGCAGCTTACG 968
 Db 781 CCTATATGACACGATTTGGGAGATCAATGAACTATCCCTGGCAGCTTACG 840
 QY 969 TTTACCTGTGATGATCTTCACTGCTCAGAAAGAACTGATTAATTGGAGAAAGAAA 1028
 Db 841 TTTACCTGTGATGATCTTCACTGCTCAGAAAGAACTGATTAATTGGAGAAAGAAA 900
 QY 1029 ACCATTTGTGAATCATCTGGAATCTGGTCAAACTCTATCTCAATATGCAAAAATTGGAC 1088
 Db 901 ACCATTTGTGAATCATCTGGAATCTGGTCAAACTCTATCTCAATATGCAAAAATTGGAC 960
 QY 1089 AAAGATTCTCAATGATTAAGAGAGGTATATTAACCCCTTCATTTCCAGTGGCAGTC 1148
 Db 961 AAAGATTCTCAATGATTAAGAGAGGTATATTAACCCCTTCATTTCCAGTGGCAGTC 1020
 QY 1149 ATGTTACTGCAATCTCTGGGTGGCAATTTATVCAATTTGGCTGGCAAGAGATTAAGAAA 1208
 Db 1021 ATGTTACTGCAATCTCTGGGTGGCAATTTATVCAATTTGGCTGGCAAGAGATTAAGAAA 1080
 QY 1209 GGCAAGAAATCCAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1247
 Db 1081 GGCAAGAAATCCAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1119


```

RESULT 13
LOCUS PP073729 1119 bp mRNA PRI 05-NOV-1996
DEFINITION Pongo pygmaeus L-selectin mRNA, complete cds.
ACCESSION U73729
VERSION U73729.1 GI:1658017
KEYWORDS
SOURCE
ORGANISM
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pongo.
REFERENCE
1 (bases 1 to 1119)
AUTHORS Budman, J.I., Fu, H., Johnson, C.E., Thakur, A.B., Berg, E.L. and
Tsurushita, N.
TITLE Cloning of the cDNA encoding L-selectin from nonhuman primates
JOURNAL Unpublished
2 (bases 1 to 1119)
AUTHORS Budman, J.I., Fu, H., Johnson, C.E., Thakur, A.B., Berg, E.L. and
Tsurushita, N.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
Avenue, Mountain View, CA 94043, USA
FEATURES
source
1..1119
/organism="Pongo pygmaeus"
/db_xref="taxon:9600"
1..1119
/codon_start=1
/product="L-selectin"
/protein_id="AAB18247.1"
/db_xref="GI:1658018"
/translation="MIPRKCSSTORDLCNIFKMGWIMLCCDFLAHSTDCVTHYS
EKPMWQRARRCRENYTDVAIQNKAELEYELKLPESRYWIGIRIGITWVW
TNKSLTEAEAMNDEPNKKNKEDCEVEYIKRNDAGKMDACHKRLKAAICLYASC
OPWSCSGHECEVEIINNYCNCDEYVYGCOCFVIOCELEAPBELGTMDCTPLGNS
FSSOCAPNCSSEGTNLGIEETTCGPFGMSNPEPCOVYIOCEPLSAPDGLNCSHPL
ASFSTACTFICSEGTLEICKKTKICSSGMSNPSPCQKLDKFSNIRKGDVNL
ETPVAVWYTAESGLAFITILARLKKKKSKKSMDDP1"
BASE COUNT 336 a 233 c 273 g 277 t
ORIGIN
Query Match 48.0%; Score 1085.4; DB 97; Length 1119;
Blast Local Similarity 98.1%; Pred. No. 1.5e-286;
Matches 1098; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 129 ATGATATTTTCATGTAATGTCTGAGACACCCAGAGGACTTATGAAACATCTTCAAGTTG 188
DB 1 ATGATATTTTCATGTAATGTCTGAGACACCCAGAGGACTTATGAAACATCTTCAAGTTA 60
QY 189 TGGGGGTGACAAATGCTGTGTGTGATTTCTGGCACATCAGTAAGACCTACTGCGACT 248
DB 61 TGGGGGTGACAAATGCTGTGTGTGATTTCTGGCACATCAGTAAGACCTACTGCGACT 120
QY 249 TACCATTATTCGAAAAACCCATGAGGCAAGGGCTAGAGAGATTCTGCCGAGACAAT 308
DB 121 TACCATTATTCGAAAAACCCATGAGGCTAGAGAGATTCTGCCGAGACAAT 180
QY 309 TACACAGATTAGTCCATACAAACCAAGGCGGAATGAGTATCTGAGAGACTCTG 368
DB 181 TACACAGATTAGTCCATACAAACCAAGGCGGAATGAGTATCTGAGAGACTCTG 240
QY 369 CCCTTCAGTCGTTCTTACTACTGATAGAGAAATCCGAAAGATAGAGAGAAATATGAGCTGG 428
DB 241 CCCTTCAGTCGTTCTTACTACTGATAGAGAAATCCGAAAGATAGAGAGAAATATGAGCTGG 300
QY 429 GTGGGAACCAACAATCTCTCACTGAAGAAGCAGAGAAGGGGAGATGGTGGGCCCAAC 488
DB 301 GTGGGAACCAACAATCTCTCACTGAAGAAGCAGAGAAGGGGAGATGGTGGGCCCAAC 360
QY 489 AACCAAGAGAACAGAGAGACTGCTGAGAGATATATCAAGAGAAACAAGATGAGAGC 548
DB 361 AACCAAGAGAACAGAGAGACTGCTGAGAGATATATCAAGAGAAACAAGATGAGAGC 420

```

```

QY 549 AATGGAACGATGACGCTGCCAACAACATAAGGACACCCCTCTGTACAGACTTCTTGC 608
DB 421 AATGGAACGATGACGCTGCCAACAACATAAGGACACCCCTCTGTACAGACTTCTTGC 480
QY 609 CAGCCCTGATCATGACAGTGGCCATGAGAAATGATAGAAATCATATCAATATACACCTGC 668
DB 481 CAGCCCTGATCATGACAGTGGCCATGAGAAATGATAGAAATCATATATATACACCTGC 540
QY 669 AACTGTGATGTGGGGTACTATGAGGCCCAAGTGCAGCTGTGATTCAGTGTGAGCCCTTTC 728
DB 541 AACTGTGATGTGGGGTACTATGAGGCCCAAGTGCAGCTGTGATTCAGTGTGAGCCCTTTC 600
QY 729 GAGGCCCAAGAGCTGGGTACCATGAGACTGATCTACCCCTTTGGAACCTCAGCTTACG 788
DB 601 GAGGCCCAAGAGCTGGGTACCATGAGACTGATCTACCCCTTTGGAACCTCAGCTTACG 660
QY 789 TCAAGTGTGCTTTCAGCTGCTGCTGAGAAACAACCTTAATCTGGGATTTGAAGAACACC 848
DB 661 TCAAGTGTGCTTTCAGCTGCTGCTGAGAAACAACCTTAATCTGGAATTTGAAGAACACC 720
QY 849 TGTGACACATTTGGAACCTGCTATCTCAGAACCAACCTGTCAAGTATTCAGTGTGAG 908
DB 721 TGTGACACATTTGGAACCTGCTATCTCAGAACCAACCTGTCAAGTATTCAGTGTGAG 780
QY 909 CCTCTATACACACCAAGATTTGGGATCATGATGATGATGATGATGATGATGATGATGATG 968
DB 781 CCTCTATACACACCAAGATTTGGGATCATGATGATGATGATGATGATGATGATGATGATG 840
QY 969 TTATACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
DB 841 TTATACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 1029 ACCATTTGTGAATCATCTGGAATCTGCTCAATCTAGTCAATATGCTCAAAATTTGAC 1088
DB 901 ACCATTTGTGAATCATCTGGAATCTGCTCAATCTAGTCAATATGCTCAAAATTTGAC 960
QY 1089 AAAAGTTTCAATGATTAAGAGAGGATGATTAATACCCCTCTTCAATTCAGTGGCAGTC 1148
DB 961 AAAAGTTTCAATGATTAAGAGAGGATGATTAATACCCCTCTTCAATTCAGTGGCAGTC 1020
QY 1149 ATGTTACTGATCTCTGCTGGTGGCATTTATCATTTGGCTGGCAAGAGATTAATAAAA 1208
DB 1021 ATGTTACTGATCTCTGCTGGTGGCATTTATCATTTGGCTGGCAAGAGATTAATAAAA 1080
QY 1209 GGCAGAAATCAAGAGAAATGATGAATGACCATATTAA 1247
DB 1081 GGCAGAAATCAAGAGAAATGATGAATGACCATATTAA 1119
RESULT 14
LOCUS MMU73730 1119 bp mRNA PRI 05-NOV-1996
DEFINITION Macaca mulatta L-selectin mRNA, complete cds.
ACCESSION U73730
VERSION U73730.1 GI:1658015
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecoidea; Macaca.
REFERENCE
1 (bases 1 to 1119)
AUTHORS Budman, J.I., Fu, H., Johnson, C.E., Thakur, A.B., Berg, E.L. and
Tsurushita, N.
TITLE Cloning of the cDNA encoding L-selectin from nonhuman primates
JOURNAL Unpublished
2 (bases 1 to 1119)
AUTHORS Budman, J.I., Fu, H., Johnson, C.E., Thakur, A.B., Berg, E.L. and
Tsurushita, N.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
Avenue, Mountain View, CA 94043, USA

```

FEATURES
Source Location/Qualifiers
1..1119
/organism="Macaca mulatta"
/db_xref="taxon:9544"
1..1119
/codon_start=1
/product="L-selectin"
/protein_id="AB18246.1"
/db_xref="GI:1658016"
/translation="MIFPRKCSSTORDLNIFLMGWMICDPLAHNGTDCMTYHS
ENPMNOKARRCRENYDLVALIONKALEIYELEKTLPEPSYIWIIRKIGITWVG
TKSLTQEAENNDGEPNNKKNKEDCEVEITIKRKAGKWNDDACKPKAALCYTASC
QPMSCGHECEVEIINNYTCNCDVGYGQCFVIGCELEPKLGTMDCTHPLGFS
FSSQCAFNCSEGTNLGIEETTCGPGNMSSEPTCOVIOCEPLAPDLGIMNCSHPL
ASFSSSACTFSCSEGTLEIGERKTLICESSGIWSNPNPCOKLDRFSMIKEDYNPL
FIPVAVMTAFSGIAFIILWLRRLKRGKSKSMDDPY"

BASE COUNT 332 a 239 c 275 g 273 t
ORIGIN

Query Match 46.8%; Score 1056.6; DB 97; Length 1119;
Best Local Similarity 96.5%; Pred. No. 1.3e-280;
Matches 1080; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

129 ATGATATTTCCATGAAATGTCAGACACCCAGAGGACTTATGAACATCTTCAAGTTG 188
1 ATGATATTTCCAGAAATGTCCAGTACCCAGAGGACTTATGAACATCTTCAAGTTG 60
189 TGGGGGTGACATGCTGCTGTTGATTTCTGCGCACATCATGGAACCTTACTGAGCT 248
61 TGGGGGTGACAAVGTCTGTTGTGATTTCTGCGCACATCATGGAACCGACTGCTGAGCT 120
249 TACCATTTATTTGAAAAACCCATGACATGCGCAAAAGGCTAGAAATTTGCGCGAGCAAT 308
121 TACCATTTATTTGAAATCCATGAACTGGCAAAAGGCTAGAAATTTGCGCGAGCAAT 180
309 TACACAGATTAGTGGCCATPACAAAACAAAGCGGAAATAGATATCTGAGAGAGCTGTG 368
181 TACACAGATTAGTGGCCATPACAAAACAAAGCGGAAATAGATATCTGAGAGAGCTGTG 240
369 CCCTTCAGTCCTTCTTACTAGTGTAGAGATCCGGAATATAGAGAGATATGAGAGCTGG 428
241 CCCTTCAGTCCTTCTTACTAGTGTAGAGATCCGGAATATAGAGAGATATGAGAGCTGG 300
429 GTGGGAACCAACAATCTCTCACTGAAGAAGCAGAGACATGGGAGATGTTGAGCCCAAC 488
301 GTGGGAACCAACAATCTCTCACTGAAGAAGCAGAGACATGGGAGATGTTGAGCCCAAC 360
489 AACAGAGACAAAGAGAGAGTGGCTGAGATCTATATCAAGAGAAACAAGATGACAGC 548
361 AACAGAGACAAAGAGAGAGTGGCTGAGATCTATCAAGAGAAACAAGATGAGCGGC 420
549 AATGGAAG 608
421 AATGGAAG 480
609 CAGCCCTGTGATGAGAGTGGCCATGAGAGATGTAGAAATCATCAATATATACACCTGC 668
481 CAGCCCTGTGATGAGAGTGGCCATGAGAGATGTAGAAATCATCAATATATACACCTGC 540
669 AACTGTGATGAGAGTGGCCATGAGAGATGTAGAAATCATCAATATATACACCTGTTG 728
541 AACTGTGATGAGAGTGGCCATGAGAGATGTAGAAATCATCAATATATACACCTGTTG 600
729 GAGGGCCCAAGACTGGTACCATGAGAGTGTATCAACCCCTTTGAAACTTCAGCTTACG 788
601 GAGGGCCCAAGACTGGTACCATGAGAGTGTATCAACCCCTTTGAAACTTCAGCTTACG 660
789 TCACAGTGTGCTTACAGTGTCTGAGAGAACAACTTAAGTGGATTGAGAGAACCCAC 848
661 TCACAGTGTGCTTACAGTGTCTGAGAGAACAACTTAAGTGGATTGAGAGAACCCACT 720
849 TGTGACCATTTTGAAGTGTCTGAGAGAACCAACTGTCAAGTATTCAGTGTGAG 908

|||||
Db 721 TGTGACCATTTTGAAGATGTCATCTCCAGAACCAACCTGTCAAGTATGATGAGTGTGAG 780
Qy 909 CCTCTATCAGACACCATATTTGGGATCATGACTGTAGACATCCCTGGCAGCTTACAC 968
Db 781 CCTCTATCAGACACCATATTTGGGATCATGACTGTAGACATCCCTGGCAGCTTACAC 840
Qy 969 TTTACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
Db 841 TTTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 1029 ACCATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1088
Db 901 ACCATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 1089 AAAAGTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1148
Db 961 AGAAGTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 1149 ATGTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1208
Db 1021 ATGTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1209 GGCAGAAATCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1247
Db 1081 GGCAGAAATCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1119
RESULT 15
LOCUS OC026535 1680 bp mRNA MAM 03-JUN-1995
DEFINITION Oryctolagus cuniculus L-selectin precursor, mRNA, complete cds.
ACCESSION U26535
VERSION U26535.1 GI:847787
KEYWORDS
SOURCE
ORGANISM
Oryctolagus cuniculus
domestic rabbit.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
1 (bases 1 to 1680)
Qian,J. and Marks,R.M.
TITLE cDNA for rabbit L-selectin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1680)
Qian,J.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1995) Jin Qian, Internal Medicine, University of
Michigan, Kresge I, Rm, 4570, Ann Arbor, MI 48109, USA
FEATURES
source
1..1680
/organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
/clone_id="CDNA library in lambda ZAPII, provided by
R.Wiggins."
/tissue_type="kidney, cortex"
/dev_stage="adult"
155..268
153..1285
/codon_start=1
/product="L-selectin precursor"
/protein_id="AA67896.1"
/db_xref="GI:847788"
/translation="MIFPRKCSSTORDLNIFLMGWMICDPLAHNGTDCMTYHS
EKPMNWRARFCRENTDLVALIONKGEIYELEKTLPEPSYIWIIRKIGITWVG
TKNSLTAEAENNDGEPNNKKNKEDCEVEITIKRKAGKWNDDACKPKAALCYTASC
HPSCSGHECEVEIINNYTCNCDVGYGQCFVIGCELEPKLGTMDCTHPLGFS
FSSQCAFNCSEGTNLGIEETTCGPGNMSSEPTCOVIOCEPLAPDLGIMNCSHPL
ASFSSSACTFSCSEGTLEIGERKTLICESSGIWSNPNPCOKLDRFSMIKEDYNPL
FIPVAVMTAFSGIAFIILWLRRLKRGKSKSMDDPY"
mat_peptide
269..1282
BASE COUNT 472 a 384 c 418 g 406 t

ORIGIN

Query Match 45.9%; Score 1037; DB 7; Length 1680;
Best Local Similarity 82.6%; Pred. No. 3,6e-275;
Matches 1334; Conservative 0; Mismatches 260; Indels 21; Gaps 12;

QY 26 CCTGACGACAGACACATCCCTTTGGCAG---GACCTGAGACCCCTGTCTAAGTCAG 82
DB 51 CCTGACGACAGACAGACATCCCTTTGGCAGAGATCCAGGATCCCTGGGCTATGTGAG 110
QY 83 AGGCTCAATGGGCTGAGAGAACTAGAGAGACCAGGAAAGCCATGATATTTCCATG 142
DB 111 AGGCTGAA--GACTGCGAAGAGACTAGAGAGGGCCAGAGAAA--CCATGATATTTCCATG 168
QY 143 GAAATGTGAGAGAGCCAGAGGAGGACTTATGAAATCTTCAAGTGTGGGGGTGAGCAAT 202
DB 169 GAATGCGCAGAGCCCTCAGAGGGGATTTGTGAAGCTTCAAGTGTGGGTGAGCAAC 228
QY 203 GCTCTGTGTGATTTTCTGGACATCATGAGACCTACTGCTGACCTTACATTTATCTGA 262
DB 229 ACTCTGCTGATTTCTGCGCATATCATGAGAACCACTGTGGACCTTACCATTTATCTGA 288
QY 263 AAAACCCATGAACTGGGAAAGGGCTAGAAAGATTCTGGCCGAGACATTTACAGATTTAGT 322
DB 289 AAAACCCATGAACTGGGAAAGGGCTGAAAGTTCTGCCGAGAAACTACAGGATTTAGT 348
QY 323 TGGCATACAAACAGAGCGGAAATTGAGTATCTGAGAGAGACTCTGCCCTTCACTGCTTC 382
DB 349 CGCCATACAAACAGAGGAGAAATCGAGTATCTGAGAGAAAGCTGGCCCTTACGCCCTC 408
QY 383 TTACTACTGATAGGAATCCGGAAGATAGAGAGAAATGTGACGTGGGTGGAAACCAAA 442
DB 409 TTACTACTGATAGGAATCCGGAAGATAGAGAAACATATGACATGGGTGGGAGCCAA 468
QY 443 ATCTACATGAGAGAGAGAACTGGGAGATGGGAGAGCCCAACAAAGAGAGAA 502
DB 469 ATCTACATGAGAGAGAGAACTGGGAGATGGGAGAGCCCAACAAAGAGAGAA 528
QY 503 GAGAGACTGGCTGAGATCTATATCAAGAGAAACAAAGATGAGAGCAATGAGACATGA 562
DB 529 GAGAGACTGGCTGAGATCTATATCAAGAGAGCTCAGAGACTCGGGAATGGAATGTA 588
QY 563 CGGCTGCGCAAACTAAAGGACCCCTCTGTACACAGCTTCTTGGCAGCCCTGGTATG 622
DB 589 CTCTTGGCAAAAGGAGAGAGCCCTCTGTACACAGCTTCTCTGCATCTGTGGTATG 648
QY 623 CAGTGGCATGAGAGAAATGTGTAGAAATCATCAATATCACACCTGCAACTGTATGGG 682
DB 649 CAGTGGCATGAGAGAAATGTGTAGAAATCATCAATATTAACCTGCAAGCTGTATGGG 708
QY 683 GTACTATGGGCCCCAGTGTGAGTTGAGTGTGAGCTTTGGAGGCCCCAGAGCT 742
DB 709 GTACTATGGGCCCCAGTGTGAGTTGAGTGTGAGCTTTGGAGGCCCCGAGAGCT 768
QY 743 GGGTACCATGAGATGTACTACCCCTTTGAAACTTCAAGTCAAGTGTGAGCTT 802
DB 769 GGGGACCATGAGCTGTACCTCTTGGAGAGTTCAAGTTCAAGTGTGAGCTT 828
QY 803 CAGCTGCTGAGAGAGAACTTAAGTGGATTTGAAGAAACCAACCTGTGGACATTTGG 862
DB 829 CAGCTGCTGAGAGAGAACTTAAGTGGATTTGAAGAAACCACTGTGGACCACTTTGG 888
QY 863 AAATGCTATCTCCAGAAACCACTGTCAAGTGTGAGTGTGAGCTTATCAGCAGC 922
DB 889 AAATGCTATCTCCAGAAACCACTGTCAAGTGTGAGTGTGAGCTTATCAGCAGC 948
QY 923 AGATTTGGGATCATGACTGTAGCCATCCCTGGCCAGCTTCAAGCTTACCTGTGAG 982
DB 949 TGAATGAGGAGACCATGATGTAGTATCTCGGCTGTCTTGGCTTACCTGTAGTG 1008
QY 983 TACCTATCTGTGAGAGAGAACTAGTTAATTGGAGAGAGAAACCACTTTGTGAATC 1042

DB 1009 CACCTTACGCTGCTCAGAGAGAGCCGAGTTAATCGGATGAGAAAAAACTGTTGTGATC 1068
QY 1043 ATCTGGAATCTGGTCAAAATCCTAGTCCATATGTCAAAAATTTGACAAAAGTTCTCAAT 1102
DB 1069 ATCTGGAATCTGGTCCAGTCTCTACACCAAAATGTCAAAAAGTGGACGAAAGCTTCTAT 1128
QY 1103 GATTAAAGAGGATATATTAACCCCTCTTCAATCCAGTGGCAGTACTGTACTGATTT 1162
DB 1129 GATCAAAAGGGGTGACTATTAACCCCTCTTCAATCCAGTGGCAGTACTGTACTGATTT 1188
QY 1163 CTCGAGGTTGGCAATTTATCAATTTGGCTGCGAGAGATTTAAAAAGCAAGAAATCCAA 1222
DB 1189 CTCTGGTGTGGCTGATCATTTTGGCTGCGAGAGCCAGCTCAAAAAGGAAAGAAATCTCA 1248
QY 1223 GAGAGATGATGATGACCCATATTAATCGCCCTTGTGAAAGAAATTTCTGGAATACTA 1282
DB 1249 GAAAGCAAGAGATGA--CATATTAATCCACCTCTGTGAAAGAAATTTCTGGAATAGTA 1306
QY 1283 AA--ATTCATGATATCCCTTTAAATCCCTTCATGAAACGTTTGTGTGGTGGACCTCTAC 1341
DB 1307 AAGAGTCAATTAATCCCTTCAAA--TTCCATGAAAGAAATTTGTGTGTGTCTCTGT 1363
QY 1342 GTCAACATGAAATGTGCTTC--CTTCAAGTGCATCTGGAGAGATTTCTACCCGACCAACAGT 1400
DB 1364 ACCAAGATGACGTGTCTCTTCAAGTGCATCTGGAGAGATTTCTACGTGGCCACAGC 1423
QY 1401 TCTTACGCTTC--CATTTGCCCTCATTTATCCCTCAACCCCGACCCAGAGGTGTTT 1458
DB 1424 TCTTTCGCTCGAGCTTTTGTCTTCCTGCTCATCTC--CGAGCCGACCTCACAATGATTT 1482
QY 1459 ATACAGTCAAGCTTTT---GTCTTTCTGAGAGAGAAACAAATTAAGCATTAAGG-AA 1513
DB 1483 AGATAGCTCAGTCTTTTATTTATTTTGTGTGAGAAACCAAGATCTTTCAGGGAAA 1542
QY 1514 AGATTCATGTGGAATTAAGATGAGCTGACTTGTCTTCTTGTGACTTGTGTTTCAGT 1573
DB 1543 AGGATTAACCTGGAGATTAAGATGTCTTATGTGCTCTTCTTGTGTTGTTCAAT 1602
QY 1574 TTCATTCAGTGTCTGATGATGACA--GACACTTCTAAATGAAGTGCAAAATTTG 1627
DB 1603 TTCATTCAGTGTGCTGCTGACAGCATTAACACTTGGAAATACAGTGAATTTG 1657

Search completed: October 13, 2001, 01:41:07
Job time: 8562 sec

```

FT Modified-site 232..234
FT /note="potential N-glycosylation site"
FT Modified-site 246..248
FT /note="potential N-glycosylation site"
FT Region 259..317
FT /label="Complement_Binding_Repeat_2"
FT Modified-site 271..273
FT /note="potential N-glycosylation site"
FT Modified-site 311..313
FT /note="potential N-glycosylation site"
FT Domain 333..355
FT /label="Transmembrane_Domain"
FT /note="stop transfer sequence"
FT Domain 356..372
FT /label="Cytoplasmic_Domain"
XX
XX US5216131-A.
XX
XX 01-JUN-1993.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 31-OCT-1991; 91US-0786149.
XX
XX (GETH ) GENENTECH INC.
XX
XX Lasky LA, Rosen SD, Slinger MS, Stachel SE, Yednock TA;
XX
XX WPI: 1993-188586/23.
XX
XX N-PSDB; AA043154.
XX
XX Human and murine lymphocyte homing receptors to treat graft
XX rejection and inflammation - comprise carbohydrate binding,
XX epidermal growth factor and complement binding domains
XX
XX Claim 1; Fig 1 and Fig 3; 32pp; English.
XX
XX A human peripheral blood lymphocyte cDNA library in lambda gt10 was
XX screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone
XX (1.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was
XX isolated and sequenced. The ORF codes for 372 amino acids with a mol.
XX wt. of approximately 42,200. Comparison of the HULHR amino acid
XX sequence with the murine LHR sequence (AAR37961) showed a high degree
XX of amino acid conservation in each of the LHR domains, e.g. 96% in
XX the transmembrane domain and 83% in the carbohydrate binding domain.
XX The LHRs could be used to compete with the normal binding of
XX CC lymphocytes to lymphoid tissue to treat inflammation or graft
XX rejection. They could also be used to control lymphoma metastasis
XX and to treat conditions involving lymphocyte accumulation.
XX
XX SQ Sequence 372 AA:

```

```

OY 241 CGPFGNMSPEPTCOVYIQCEPLSAPDLGIMNCSHPLASFSFTSACTFTCSGETELLGKKR 300
DB 241 cgpfgnmspeptcqvlyqceplsapdlgimncshplastsfstsactftcsegtellgkxx 300
OY 301 TIESSGIMSNPPIQOKLDKSPSMKEGDYNPLFPVAVMTATPSGLAFITWLARLKK 360
DB 301 tieessgimwnpspplcqkldksfsmikegdynplfpvavmvtatpsglafitwlarlkk 360
OY 361 GKRSKRSMDPY 372
DB 361 gkkskrsmndpy 372
XX
XX RESULT 2
XX AAR38908
XX ID AAR38908 standard; Protein; 372 AA.
XX
XX AC AAR38908;
XX
XX DT 11-JAN-1994 (first entry)
XX
XX DE HULHR.
XX
XX KW Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;
XX LHR; endothelium; lymphoid tissue; signal; domain; complement binding;
XX carbohydrate binding; epidermal growth factor-like; egf; intracellular;
XX transmembrane binding; cytoplasmic; ligand binding partner protein;
XX TMD; LBPP.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FH Location/Qualifiers
XX FT 20..32
XX FT /note="Signal peptide"
XX FT 39..372
XX FT /note="Mature protein"
XX FT 39..155
XX FT /note="Lectin domain"
XX FT 160..193
XX FT /note="egf domain"
XX FT 197..317
XX FT /note="Complement factor binding domain"
XX FT 333..355
XX FT /note="Transmembrane binding domain"
XX FT 356..372
XX FT /note="Cytoplasmic domain"
XX
XX PN US522538-A.
XX
XX PD 06-JUL-1993.
XX
XX PE 23-FEB-1989; 89US-0315015.
XX
XX PR 23-FEB-1989; 89US-0315015.
XX 22-NOV-1989; 89US-0440625.
XX 16-DEC-1991; 91US-0808122.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Capon DJ, Lasky LA;
XX
XX WPI: 1993-226664/28.
XX N-PSDB; AA044243.
XX
XX PT New lymphocyte homing receptor immunoglobulin fusion
XX PT polypeptide(s) - used to inhibit binding of lymphocytes in
XX PT therapeutic and diagnostic uses
XX
XX PS Disclosure; Fig 1; 44pp; English.
XX
XX CC The sequences given in AAR38908-09 represent human and murine lymphocyte
XX cell surface glycoprotein (LHR) respectively. These proteins mediate

```

CC the binding of lymphocytes to the endothelium of lymphoid tissue. LHR
 CC is a glycoprotein which contains a signal domain, a carbohydrate
 CC binding domain, an epidermal growth factor-like (egf) domain, at least
 CC one complement binding domain repeat, a transmembrane binding domain
 CC (TMD) and a charged intracellular or cytoplasmic domain. The murine
 CC and human amino acid sequences show a high degree of overall homology
 CC (83%), however degrees of homology between the various domains is
 CC variable. These proteins may be fused to a ligand binding partner
 CC protein (LBP) which causes an increase in the half life of the LHR.
 CC The fusions may be used therapeutically to compete with the normal
 CC binding of lymphocytes to lymphoid tissue. They may be used in organ
 CC or graft rejection and for the treatment of inflammation.

SO Sequence 372 AA:

Query Match 100.0%; Score 2116; DB 14; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5,4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCGSTQRDLNIFKMGWTMLCCDFLAHGYCWTYHSEKPMNQARPCRDN 60
 DB 1 mlfpmkcgstqrdlnifkmgwtmccdflahgytcwtyhsekpmmwqrarrfcrdn 60
 QY 61 YTDLVAIONKAEIEYLEKTLPEFSRYWIGIRKIGIMTWGINKSLTEBAEMWGDEPN 120
 DB 61 ytdlvalionkaeieylektlpfsrywigirkgimtwginkslteeaenwgdepn 120
 QY 121 NKNKEDCEIYIKRNKDAGKWNDDACHKALKALCYTASCQPSGSGHCEVEIINNHTC 180
 DB 121 nknkedceiyikrnkdagkwnddachkalkalcytascqpscsgghceveilinnhtc 180
 QY 181 NCDVYGYGQCQLVIOCEPLEABELCTMDCTHPFGNFSFGSCAFSGSEGTNLGTIEET 240
 DB 181 ncdvygygqcqlviocepleabelctmdcthpfgnfsgscsfsgsegtnlgtieett 240
 QY 241 CGPFGMSSPEPTCOYIOCEPLSAPDLGIMNCHPLASFSTACFTISEGTELGGKK 300
 DB 241 cgpfgmsspeptcoyioceplsapdlgimnchplasfstaftisegtellgkxk 300
 QY 301 TICESGIMNSPFIQKLDKSFMSKEGDPNLFIPVAVMVAFSGLAFITILARLKK 360
 DB 301 ticesgimnsfpikldksfmskegdpnlfpvavmvafsglafitilarrlkk 360
 QY 361 GKSKRSKNDPY 372
 DB 361 gkskrskndpy 372

RESULT 3

AA76506 standard; Protein; 372 AA.

AA76506;

01-DEC-1995 (first entry)

Human LHR.

Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;

LHR; ligand binding partner; immunoglobulin; constant region;

antibody engineering; immunomodulator.

Homo sapiens.

Location/Qualifiers

/label= Sig-peptide

/note= "hydrophobic domain, may act as signal for insertion into the endoplasmic

reticulum lumen"

39..372

label= Mat-protein

FT Domain 39..374
 FT /note= "putative extracellular domain"
 FT Modified-site 60..62
 FT /label= N-glycosylation-site
 FT Modified-site 104..106
 FT /label= N-glycosylation-site
 FT Modified-site 177..179
 FT /label= N-glycosylation-site
 FT Modified-site 216..218
 FT /label= N-glycosylation-site
 FT Modified-site 232..234
 FT /label= N-glycosylation-site
 FT Modified-site 246..248
 FT /label= N-glycosylation-site
 FT Modified-site 271..273
 FT /label= N-glycosylation-site
 FT Modified-site 311..313
 FT /label= N-glycosylation-site
 FT Domain 335..357
 FT /note= "putative stop transfer or membrane anchor domain"
 FT Region 358..372
 FT /note= "putative intracellular region"

PN US5428130-A.
 PD 27-JUN-1995.
 PF 23-FEB-1989; 89US-0315015.
 XX

PR 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.
 PR 16-DEC-1991; 91US-0808122.
 PR 08-DEC-1992; 92US-0986931.
 XX

PA (GETH) GENENTECH INC.

PI Capon DJ, Lasky LA;

XX WPI: 1995-240086/31.

DR N-PSDB; AAQ92802.

XX New hybrid ligand binding partner molecules - fused to immunoglobulin

PT constant region sequences to increase stability and in vivo plasma

PT half-life

PS Disclosure; Fig. 1a-1c; 40pp; English.

XX A murine Mel 14 antigen cDNA clone was used to screen a lambda gt10

CC cDNA library derived from human peripheral blood lymphocyte mRNA

CC obtd. from primary cells. A cDNA clone encoding LHR was isolated.

XX Sequence 372 AA:

Query Match 100.0%; Score 2116; DB 16; Length 372;

Best Local Similarity 100.0%; Pred. No. 5,4e-141;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCGSTQRDLNIFKMGWTMLCCDFLAHGYCWTYHSEKPMNQARPCRDN 60
 DB 1 mlfpmkcgstqrdlnifkmgwtmccdflahgytcwtyhsekpmmwqrarrfcrdn 60
 QY 61 YTDLVAIONKAEIEYLEKTLPEFSRYWIGIRKIGIMTWGINKSLTEBAEMWGDEPN 120
 DB 61 ytdlvalionkaeieylektlpfsrywigirkgimtwginkslteeaenwgdepn 120
 QY 121 NKNKEDCEIYIKRNKDAGKWNDDACHKALKALCYTASCQPSGSGHCEVEIINNHTC 180
 DB 121 nknkedceiyikrnkdagkwnddachkalkalcytascqpscsgghceveilinnhtc 180
 QY 181 NCDVYGYGQCQLVIOCEPLEABELCTMDCTHPFGNFSFGSCAFSGSEGTNLGTIEET 240
 DB 181 ncdvygygqcqlviocepleabelctmdcthpfgnfsgscsfsgsegtnlgtieett 240


```

Db 181 ncdvgyypgcqlviqceplaeapeltgltndcthpfnfsgsfscsfsegntltgiet 240
QY 241 CGPGNMSPEPTCOVIOCEPLSAPDGLIMNCSPHPLASFSTSACTPICSEGTLEIGKKR 300
Db 241 cspignwsspeptcqvliqceplsapdglimncshplastsfcticsactficsgltelgk 300
QY 301 TICSSSGIWSNPSPICOKLDFSMIKEGDYNPFLIPVAVMTAFSGLAFTIWLARLKK 360
Db 301 ticessglwnspplcqkldksfsmikegdynpflfpvaavmtafsglatilwlarrlkk 360
QY 361 GKSKRSKSNMPY 372
Db 361 gkkskrsmndpy 372

RESULT 4
AAR83050
ID AAR83050 standard; Protein; 372 AA.
AC AAR83050;
XX
XX 31-JAN-1996 (first entry)
DE Human LHR.
XX
XX Lymphocyte cell surface glycoprotein; LHR; transmembrane receptor;
KW immunoglobulin; IgG; constant region; receptor-mediated disease;
KW vector; plasma-life.
XX
XX Homo sapiens.
OS

FH Key Location/Qualifiers
FT Peptide 20..32
FT 1/label= Sig_peptide
FT 39..155
FT 1/label= Carbohydrate_binding_domain
FT 160..193
FT 1/label= Epidermal_growth_factor_domain
FT 197..317
FT 1/label= Complement_factor_binding_domain
FT 333..355
FT 1/label= Transmembrane_binding_domain
FT 356..372
FT 1/label= Cytoplasmic_domain
FT 1/label= Cytoplasmic_domain
FT 1/label= potential stop transfer sequence*
FT 60..62
FT 1/label= N-glycosylation_site
FT 104..106
FT 1/label= N-glycosylation_site
FT 177..179
FT 1/label= N-glycosylation_site
FT 216..218
FT 1/label= N-glycosylation_site
FT 232..234
FT 1/label= N-glycosylation_site
FT 248..248
FT 1/label= N-glycosylation_site
FT 271..273
FT 1/label= N-glycosylation_site
FT 311..313
FT 1/label= N-glycosylation_site
FT 311..313
FT 1/label= N-glycosylation_site
PV US5455165-A.
XX
XX 03-OCT-1995.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185669.

```

```

XX (GETH ) GENENTECH INC.
XX Capon DJ, Lasky LA;
XX
XX MPI: 1995-350776/45.
XX DR N-PSDB; AAT05869.
XX
XX Expression vector encoding fusion protein to increase plasma life -
XX PT comprises receptor ligand binding site and Ig constant region, for
XX PT treatment of receptor mediated disease
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used
XX CC to screen an oligo-dT primed lambda gt10 cDNA library derived from
XX CC human peripheral blood lymphocyte mRNA obtd. from primary cells. A
XX CC 2.2 kb clone (sequence given in AAT05869) was isolated that encoded the
XX CC human LHR protein (AAR83050). LHR-196 hybrids were constructed for use
XX CC in the targeting of therapeutic moieties to lymphoid tissue.
XX
XX SQ Sequence 372 AA;

```

```

Query Match 100.0%; Score 2116; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 5,4e-141;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPWKCSTORDLWNIKFLMGWTM/CDDFLAHNGTYCWTYHSEKPMNQRARPCRON 60
Db 1 mifpwkcstqrdlwnikflmgwtm/ccdfflahngtycwtlyhsekpmnqrarrfcrdn 60
QY 61 YTDVLAIONKAEIELEKTLPPSNSTYWGIRKIGTWVGVTKSLTEAEKMGDEPN 120
Db 61 ytdvlaionkaeielektlppsnstywgirkiigtwtvgtkkslteaeamgdgpn 120
QY 121 NKKNKEDCEVEIYIKRNKAGKWDACHKLAALCYASQCPWSCSGHGCVEIINHTC 180
Db 121 nknkedceveiyikrnkagkwndachkkaalcycascpwscsghgcveiinhtc 180
QY 181 NCDVGYPGCOLVIQCEPLAEAPELGTMDCTHPGPNFSSQCAFSCSEGTNLGIEET 240
Db 181 ncdvgyypgcqlviqceplaeapeltgltndcthpfnfsgsfscsfsegntltgiet 240
QY 241 CGPGNMSPEPTCOVIOCEPLSAPDGLIMNCSPHPLASFSTSACTPICSEGTLEIGKKR 300
Db 241 cspignwsspeptcqvliqceplsapdglimncshplastsfcticsactficsgltelgk 300
QY 301 TICSSSGIWSNPSPICOKLDFSMIKEGDYNPFLIPVAVMTAFSGLAFTIWLARLKK 360
Db 301 ticessglwnspplcqkldksfsmikegdynpflfpvaavmtafsglatilwlarrlkk 360
QY 361 GKSKRSKSNMPY 372
Db 361 gkkskrsmndpy 372

RESULT 5
AAR8106
ID AAR8106 standard; Protein; 372 AA.
AC AAR8106;
XX
XX 31-OCT-1996 (first entry)
DE Human lymphocyte cell surface glycoprotein (HuLHR).
XX
XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
XX KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
XX KW immunomodulator; cell adhesion; graft rejection; inflammation;
XX KW metastasis.
XX
XX Homo sapiens.
OS

```

```

XX Key Location/Qualifiers
FH Region 1..38
FT /label= Signal region.
FT Domain 39..155
FT /label= Lectin domain.
FT Domain 160..193
FT /label= EGF domain.
FT Binding-site 197..258
FT /label= Complement binding repeat 1.
FT Binding-site 259..317
FT /label= Complement binding repeat 2.
FT Domain 333..355
FT /label= Transmembrane domain.
FT Domain 356..372
FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
PN
PD 07-MAY-1996.
PE
PE 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
PR 23-FEB-1989; 89US-0315015.
PR 16-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
PR -21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
PA
XX Capon DJ, Lasky LA;
XX WPI; 1996-238773/24.
DR N-PSDB; AAR8106.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
PT binding site of a receptor fused to ig constant region - useful for
PT diagnosis and treatment e.g. of inflammation
XX
XX Example 2; Figure 1; 41pp; English.
PS
XX A hybrid immunoglobulin chain comprising the ligand binding site of
CC a single transmembrane receptor without an active transmembrane
CC region; fused at its C-terminus with the N-terminus of an
CC immunoglobulin constant region. The receptor is not a member of the
CC immunoglobulin super family, nor a multiple subunit polypeptide
CC encoded by discrete genes. The hybrid immunoglobulin chain combines
CC the adhesion/targeting of a ligand binding partner (LRP) with the
CC effector functions of immunoglobulin and can bind to and/or activate
CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particular cells.
CC Typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection, inflammation, metastasis of lymphoma etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC facilitates recovery, improves aqueous solubility and removes
CC potentially immunogenic epitopes.
XX
XX Sequence 372 AA;

```

Query Match 100.0%; Score 2116; DB 17; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5, 4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTFPMKCGSTORDIWMIFKLMGWTMLCCDFLAHHGYCWTYHVSSEKPMNQARRECRDN 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 mlfpmkcgstgrdlwnlfkmgwtmlccdflahhgytswtyhvssekpmnqarrrfcrdn 60
QY 61 YTDLVAIQNAELEYLEKTLPFGRSRYWIGIRKIGIWTWVGTRKSLTEPAENMGDQEPN 120

```

```

Db 61 ytdlvaliqnkealeylekltlpfgrsrywigrlrkgilwtwgtlkslleesengddgepn 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 NKKNKEDCEVEIYIKRNKDAGKWNPDACHKALKALCYTASCPMWSGSGHEVEIINHTC 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 nknkedcevelyikrnkdagkwndachkalkaalcytascgpmwscsgnhevevllnnhtc 180
QY 181 NCDVGYGPGQOLVIOCEPLAPLGTMDCHPRGNGSFSSQCAFSCSEGNLTGIEFTT 240
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ncdvgygpgqolvioceplapeltgmdchprgngsfssqcafscsegnltgieftt 240
QY 241 CGPFGNNSPEPTQVIOCEPLAPDLGIMNCSHPLASFSTSACTFICSEGTGICKK 300
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 cgpfgnnspeptqvioceplapdlgimncshplasfstsactficsegteligkkk 300
QY 301 TICSSGSIWNSPFCQKLDKFSMIKEGDNPLFIPAVWVTAFGSLAFTIIMLARLKK 360
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 ticessgslwvnsplfcqkldksfmikegdyndplfipavwvtafsglafllwlarlkk 360
QY 361 GKSKRSMDPY 372
   ||||||||||||
Db 361 gkkskrsmndpy 372

RESULT 6
AAW37781
ID AAW37781 standard; Protein: 372 AA.
XX
XX AAW37781;
AC
AC 17-AUG-1998 (first entry)
XX
XX Homo sapiens lymphocyte homing receptor (LHR).
DE
XX Lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
XX treatment; inflammatory disorders; rheumatoid arthritis;
KW autoimmune diseases; lymphoma metastasis; control; lymphocyte;
KW accumulation.
XX
XX Homo sapiens.
OS
XX
XX Location/Qualifiers
FH Key 20..33
FT Peptide /note= "potential signal sequence"
FT Region /note= "potential N-linked glycosylation site"
FT Region 60..62
FT Region /note= "potential N-linked glycosylation site"
FT Region 104..106
FT Region /note= "potential N-linked glycosylation site"
FT Region 177..179
FT Region /note= "potential N-linked glycosylation site"
FT Region 216..218
FT Region /note= "potential N-linked glycosylation site"
FT Region 232..234
FT Region /note= "potential N-linked glycosylation site"
FT Region 246..248
FT Region /note= "potential N-linked glycosylation site"
FT Region 271..273
FT Region /note= "potential N-linked glycosylation site"
FT Region 311..313
FT Region /note= "potential N-linked glycosylation site"
FT Region 335..357
FT Domain /note= "potential N-linked glycosylation site"
FT /note= "membrane anchoring domain/stop transfer"
XX
XX US5714147-A.
PN
PN 03-FEB-1998.
PD
PD 23-FEB-1989; 89US-0315015.
PE
PE 23-NOV-1989; 89US-0440625.
PR 23-FEB-1989; 89US-0315015.
PR 19-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.

```

PR 21-JAN-1994; 94US-0185670.
 XX 26-MAY-1995; 95US-0451848.
 PA (GETH) GENENTECH INC.
 XX
 PI Capon DJ, Lasky LA;
 XX
 DR WPI; 1998-129805/12.
 DR N-PSDB; AAV19012.
 XX

PT Prevention of lymphocyte attachment to endothelial cells - using
 PT chimeric molecule comprising lymphocyte homing receptor and
 PT immunoglobulin constant region
 PT
 XX
 PS
 XX

Disclosure; Fig 1; 43pp; English.

CC The sequence is that of a human lymphocyte homing receptor
 CC (LHR) which may be used in the construction of a chimeric molecule
 CC comprising an LHR fused at its C terminus to the N terminus of an
 CC immunoglobulin constant region. This can be used for the prevention
 CC of lymphocyte attachment to endothelial cells. Such a method may
 CC be used for preventing organ or graft rejection, for treating
 CC inflammatory disorders, e.g. rheumatoid arthritis or other
 CC autoimmune diseases, for controlling lymphoma metastasis and
 CC for treating conditions in which there is an accumulation of
 CC lymphocytes.
 CC
 XX
 SO Sequence 372 AA;

Query Match 100.0%; Score 2116; DB 19; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5,4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCSQSTQRDLMNIFKLMGWTMLCCDFLAHHGYCWTYHSEKPMNQRRRCRDN 60
 DB 1 mifpmkcsqstqrdlmnifkmgwtmccdflahghgycwtyskpmnqrarricrdn 60
 QY 61 YTDVAIQNKAEIEYLEKTLPEFSRYWIGIRKIGIWTWGTNKSITTEAENMGDEPN 120
 DB 61 ytdvaliqnkaeylektpfarsywigirkiigltwgtvgnksltteaenmgdgn 120
 QY 121 NKNKEDCVELYIKRNKDAGKNDACHTKLAALCTTASQCPWSCSGHGECVEIINNHTC 180
 DB 121 nknkedcvelyikrnkdagkndachtklaalcyytasqpcwscgshgcevelinnh 180
 QY 181 NCDVGYGPOCQVLYICEPLAPELCTMDCTHHPGNFSFSSQCAFSCSGTNLTGTEET 240
 DB 181 ncdvgygpcqvlvigeplapeltmdcthpfnfsfssqafscsgtnltgteeet 240
 QY 241 CGPFGNWSPEPTCOVYICEPLSAPDLGIMNCSHPLASFSTACTFTICSEGTGLGKKK 300
 DB 241 cgpfgnwspeptcovyiceplsapdlgimncshplasfstsactfticsegtelgk 300
 QY 301 TICSSGIMNSPICOIKDKSFSMIKEGDYNPLFIPVAVMTAFSGLAFTIWLARLKK 360
 DB 301 ticssgimnspicokldksfsmikegdynplfipvavmtafsglaftiwlarrlkk 360
 QY 361 GKKSRSKSNMPPY 372
 DB 361 gkksrksnmdpy 372

RESULT 7

AAW73264
 ID AAW73264 standard; Protein; 372 AA.

XX AC AAW73264;

XX DT 02-FEB-1999 (first entry)

XX DE Human lymphocyte homing receptor.

KW Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein;
 KW lymphocyte binding; endothelium; graft rejection; inflammation; therapy;
 KW arthritis; autoimmune disease; lymphoma metastasis;
 KW lymphocyte accumulation; human.

OS Homo sapiens.

PN US5840844-A.

PD 24-NOV-1998.

PF 10-AUG-1995; 95US-0513278.

PR 23-FEB-1989; 89US-0315015.

PR 31-OCT-1991; 91US-0786149.

PR 06-MAY-1993; 93US-0059029.

PR 10-AUG-1995; 95US-0513278.

PA (GETH) GENENTECH INC.

DR WPI; 1999-034122/03.

DR N-PSDB; AAV08321.

PT Lymphocyte homing receptor polypeptides - useful for inhibiting

PT lymphocyte binding to lymphoid endothelium

PS Claim 1; Fig 1; 33pp; English.

This sequence is the human lymphocyte homing receptor (LHR) of the
 invention. LHR is a lymphocyte cell-surface glycoprotein that mediates
 the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble
 LHR polypeptides, lacking signal peptide (amino acids 1-38),
 transmembrane domain (amino acids 333-355) and cytoplasmic domain (amino
 acids 356-372), can be used therapeutically to compete with the normal
 binding of lymphocytes to lymphoid tissue and are especially useful for
 organ or graft rejection treatment protocols, for treating inflammations
 such as arthritis and other autoimmune diseases, for control of lymphoma
 metastasis and for treating conditions involving lymphocyte accumulation.
 LHR polypeptides can also be used in assays for LHR, anti-LHR antibodies
 or competitive inhibitors of LHR activity, and for purifying anti-LHR
 antibodies, and as immunogens for raising anti-LHR antibodies.

Sequence 372 AA;

Query Match 100.0%; Score 2116; DB 20; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5,4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCSQSTQRDLMNIFKLMGWTMLCCDFLAHHGYCWTYHSEKPMNQRRRCRDN 60
 DB 1 mifpmkcsqstqrdlmnifkmgwtmccdflahghgycwtyskpmnqrarricrdn 60
 QY 61 YTDVAIQNKAEIEYLEKTLPEFSRYWIGIRKIGIWTWGTNKSITTEAENMGDEPN 120
 DB 61 ytdvaliqnkaeylektpfarsywigirkiigltwgtvgnksltteaenmgdgn 120
 QY 121 NKNKEDCVELYIKRNKDAGKNDACHTKLAALCTTASQCPWSCSGHGECVEIINNHTC 180
 DB 121 nknkedcvelyikrnkdagkndachtklaalcyytasqpcwscgshgcevelinnh 180
 QY 181 NCDVGYGPOCQVLYICEPLAPELCTMDCTHHPGNFSFSSQCAFSCSGTNLTGTEET 240
 DB 181 ncdvgygpcqvlvigeplapeltmdcthpfnfsfssqafscsgtnltgteeet 240
 QY 241 CGPFGNWSPEPTCOVYICEPLSAPDLGIMNCSHPLASFSTACTFTICSEGTGLGKKK 300
 DB 241 cgpfgnwspeptcovyiceplsapdlgimncshplasfstsactfticsegtelgk 300
 QY 301 TICSSGIMNSPICOIKDKSFSMIKEGDYNPLFIPVAVMTAFSGLAFTIWLARLKK 360

```
|||||
Db 301 ltsessgiwspncpqlkldksfsmklegdynplflpvawvmtasglafliwlarlk 360
Qy 361 GKSKRSMDPY 372
   |||||||
Db 361 gkkskrsmndpy 372

RESULT 8
AAR98122
ID AAR98122 standard; Protein; 371 AA.
AC AAR98122;
XX
XX 01-NOV-1996 (first entry)
DX
DE Human lymphocyte cell surface glycoprotein (HULHR) variant.
KM Immunoglobulin; transmembrane receptor; adhesion; targeting;
KM diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KM immunomodulator; cell adhesion; graft rejection; inflammation;
KM metastasis.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 1..37
FH Domain /label= Signal region.
FH Domain /label= Lectin domain.
FH Domain 159..192
FH Domain /label= EGF domain.
FH Binding-site 136..257
FH Binding-site /label= Complement binding repeat 1.
FH Binding-site 258..316
FH Domain /label= Complement binding repeat 2.
FH Domain 332..354
FH Domain /label= Transmembrane domain.
FH Domain 355..371
FH Domain /label= Cytoplasmic domain.
XX
PN USS514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Laskey LA;
XX WPI; 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX Disclosure; Page 19; 41pp; English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
XX a single transmembrane receptor without an active transmembrane
XX region; fused at its C-terminus with the N-terminus of an
XX immunoglobulin constant region. The receptor is not a member of the
XX immunoglobulin super family, nor a multiple subunit polypeptide
XX encoded by discrete genes. The hybrid immunoglobulin chain combines
XX the adhesion/targeting of a ligand binding partner (LBP) with the
XX effector functions of immunoglobulin and can bind to and/or activate
```

```
CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particular cells.
CC Typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC facilitates recovery, improves aqueous solubility and removes
CC potentially immunogenic epitopes. Variants of the human lymphocyte
CC cell surface glycoprotein described in AAR98106 are given in
CC AAR98109-R98135. This variant contains an Ile288Val substitution.
XX
XX Sequence 371 AA:
SQ
Query Match 99.7%; Score 2110; DB 17; Length 371;
Best Local Similarity 99.7%; Pred. No. 1,4e-140;
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 IFPWKCOSTORDLWNTFRKLGWMTMLCCDFLAHGGTYCWTHYSEKPMNQPARRFCDNY 61
Db 1 ifpwkcqstgrdlwnlfkllgwmtlccdflahnglycwyhysekpmnqparrrfcdny 60
Qy 62 TDLVAIQNKAEIEYLEKTLPRSRSYWIGIRKIGIWTWGTNKSLEEAENMGDGEPPN 121
Db 61 tdlvalqnkaleylektlprsfrywylrklgilcwtwgtcnksleeeenmgdgeppn 120
Qy 122 KKNKEDCEVEIYIRKKNKAGKNDACHKRLKALCYTASCPWMSGHGECEVEIINHTCN 181
Db 121 knkedceveiyirknkagkndachkrlkaalcytascqpwmsgygeceveiinhtcn 180
Qy 182 CDVGYYGPGCOLYIQCEPLAPBLGTMDCTHPRGNEFSFSCAFCSGEGNLGIEETTC 241
Db 181 cdvgyygpgcolyiqceplapblgtmdcthprgnfssqcfscsegnlgtieettc 240
Qy 242 GPGGNMSPEPTCOVIOCEPLSAPDGLIMNCSPHLASFSTACTPFCSGTETLGKKKT 301
Db 241 gpggnmspeptcovioceplsapdglimncshplasfstactpfcsgtettlgkkkt 300
Qy 302 ICESSGIWSNPSPICQKLDKSFMSKIRGDNPLFIPVAVWVTFSSGLAFTIWLARRLKG 361
Db 301 ltsessgiwspncpqlkldksfsmklegdynplflpvawvmtasglafliwlarlk 360
Qy 362 KSKRSMDPY 372
Db 361 kkskrsmndpy 371

RESULT 9
AAR98115
ID AAR98115 standard; Protein; 371 AA.
XX
XX AAR98115;
XX
XX 01-NOV-1996 (first entry)
DX
DE Human lymphocyte cell surface glycoprotein (HULHR) variant.
XX
XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
XX diagnosis; therapy; drug delivery; antiviral; neuromodulator;
XX immunomodulator; cell adhesion; graft rejection; inflammation;
XX metastasis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..37
XX Domain /label= Signal region.
XX Domain 38..154
XX Domain /label= Lectin domain.
XX Domain 159..192
XX Domain /label= EGF domain.
```

```

FT .Binding-site 196..257
FT /label= Complement binding repeat 1.
FT Binding-site 258..316
FT /label= Complement binding repeat 2.
FT Domain 332..354
FT /label= Transmembrane domain.
FT Domain 355..371
FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI; 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX Disclosure; Page 19; 41pp; English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
XX a single transmembrane receptor without an active transmembrane
XX region; fused at its C-terminus with the N-terminus of an
XX immunoglobulin constant region. The receptor is not a member of the
XX immunoglobulin super family, nor a multiple subunit polypeptide
XX encoded by discrete genes. The hybrid immunoglobulin chain combines
XX the adhesion/targeting of a ligand binding partner (LBP) with the
XX effector functions of immunoglobulin and can bind to and/or activate
XX more than one ligand. It can be used diagnostically for the in
XX vitro assay of LBP and their targets; or therapeutically to deliver
XX LBP such as toxins, enzymes, growth factors to particular cells.
XX Typical applications are as antiviral, neuromodulating and
XX immunomodulating agents, or as modulators of cell adhesion (e.g. in
XX treating graft rejection; inflammation; metastasis of lymphoma etc.)
XX The immunoglobulin component increases plasma half life and
XX facilitates purification while deletion of the transmembrane region
XX potentially improves recovery, improves aqueous solubility and removes
XX potentially immunogenic epitopes. Variants of the human lymphocyte
XX cell surface glycoprotein described in AAR98106 are given in
XX AAR98109-R98135. This variant contains an Ile174Leu substitution.
XX
XX Sequence 371 AA:
SQ

```

```

Query Match 99.7%; Score 2109; Db 17; Length 371;
Best Local Similarity 99.7%; Pred. No. 1.7e-140;
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 2 IFPMKCOSTORDLMNIFKIMGWTMLCCDFLAHGGTYCWTYHSEKPMWQRAARECRDNY 61
OY 1 ifpwkcgstqrdlwnlfiikwgtmlccdfiahgtycwtlyhsekpmwqrartrfcrdny 60
Db
OY 62 TDVATLONKAELEYEKLTPFSRSYYNIGIRKIGIMTWGNGNKSUTBEAEWNGGGEPRN 121
OY 61 tdvtaiqnaaeleyekltipstsywlgtrkigtwgngnkslteaeawngdgeppn 120
Db
OY 122 KKNKEDCEVEITYKRNKDKGNWDACHKILKALCYTASQCPSCSGHGEVIEINNHTCN 181
OY 121 knkedceveiykrnkdkgwnwdachklkaalcytasqpscsghgeveielnnhcn 180
Db
PS

```

```

OY 182 CDVGYGPOCOLVIOCEPLEAPELGTMDCTHPRGNFSSFOCAFSCSEGTNLGIEETTC 241
OY 181 cdvgygppgcqlviqcepleapelgmdcthpignfsfgcafsesqetnltlgieettc 240
Db
OY 242 GPRGNMSSPEPTCOVIQCEPLSAPDGLINCSHPLASFSFTSACFTICSEGTILGKKRT 301
OY 241 gprgnwsspeptcqv iqceplsapdglimcshplastsftsficticsegtelgkkt 300
Db
OY 302 ICSSSGIWSNPSPICOKLCKFSMTKEGDPNPLFTFVAVMVTAFTSLATITLRLKKG 361
OY 301 icessgiwsspiscqklckfstmkedgpnplftfvavmvtaftslatitlrlkkg 360
Db
OY 362 KKSRSMDNDPY 372
OY 361 kksrsmndpy 371
Db
RESULT 10
AAR98124
ID AAR98124 standard; Protein; 371 AA.
XX
XX AAR98124;
XX
XX 01-NOV-1996 (first entry)
XX
XX Human Lymphocyte cell surface glycoprotein (HULHR) variant.
XX
XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
XX diagnosis; therapy; drug delivery; antiviral; neuromodulator;
XX immunomodulator; cell adhesion; graft rejection; inflammation;
XX metastasis.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
XX FT Region 1..37
XX FT /label= Signal region.
XX FT Domain 38..154
XX FT /label= Lectin domain.
XX FT Domain 159..192
XX FT /label= EGF domain.
XX FT Binding-site 196..257
XX FT /label= Complement binding repeat 1.
XX FT Binding-site 258..316
XX FT /label= Complement binding repeat 2.
XX FT Domain 332..354
XX FT /label= Transmembrane domain.
XX FT Domain 355..371
XX FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI; 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX Disclosure; Page 19; 41pp; English.
XX

```

XX A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes. Variants of the human lymphocyte
 CC cell surface glycoprotein described in AAR98106 are given in
 CC AAR98109-R98135. This variant contains an Ile302Leu substitution.
 CC
 SQ Sequence 371 AA:

Query Match 99.7%; Score 2109; DB 17; Length 371;
 Best Local Similarity 99.7%; Pred. No. 1.7e-140;

Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 IFPPKQSTQRLDMLNIFKMGWMTLCCDFLAHHGTYCWTYHYSEKPMNQRRRCRDNY 61
 DB 1 ifpwkcsgtqrdlwnlfkmgwmtlccdflahhgytcwtyhysekpmnqrrrrcndy 60
 OY 62 TDLVAIQNKAETLEYEKLTPFSRSYYWIGIRKIGIWTWVGINKSLTEAEKNGDEPN 121
 DB 61 tdlvaliqnkaeyleyektlpfsrsyywigirkigiwtwvginkslteeenvgdepm 120
 OY 122 KKKKECCVEIYIKRNKDGKNDACHKIKALCYTASQPMSCSGHGECVEIINNHTCN 181
 DB 121 kkkkedcveiyikrnkdgkndachkikaalcycasqpmwscsghgvevllnnhtcn 180
 OY 182 CDVGYGPOCQOLVIOCEPLAEPGLGTMDCTHPRGNFSFSSQAFSCSEGNLTGIEETTC 241
 DB 181 cdvgygppocqlviqceplaeplgmdcthpfnfsgsfscsegnltgiettc 240
 OY 242 GPPGNMSSPEPTCQVIOCEPLSAPDLGINNCSPHLASFSTSACTPCTCSEGTGKTKT 301
 DB 241 gppgnmsspeptcqviqceplsapdlgimncshplasfsttsactficesgtelgkkt 300
 OY 302 ICSSSGIWSNPSPICQKLDKSFNMEGQYNPFIYVAVWVTFSGLAFTIWLARLKG 361
 DB 301 lcsssglwnspspicqkldksfsmikegdynpfiyvaavwvtafsglafliwlarllkg 360
 OY 362 KKSRSRMNDPY 372
 DB 361 kkskrsmndpy 371

RESULT 11
 AAR24026
 ID AAR24026 standard; Protein: 372 AA.
 XX
 AC AAR24026;
 XX
 DT 22-NOV-1992 (first entry)
 XX
 DE Sequence of human lymphocyte cell surface glycoprotein
 DE (HULHR).
 XX
 KW Lymphocyte cell surface glycoprotein; ligand binding protein.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide 20..38
 FT /label= signal
 FT Modified-site 60..62
 FT /label= potential N-linked glycosylation site
 FT Modified-site 104..106
 FT /label= see above
 FT Modified-site 177..179
 FT /label= see above
 FT Modified-site 216..218
 FT /label= see above
 FT Modified-site 232..234
 FT /label= see above
 FT Modified-site 271..273
 FT /label= see above
 FT Modified-site 311..313
 FT /label= see above
 FT Region 333..355
 FT /label= stop transfer sequence

XX US5116964-A.
 XX
 PD 26-MAY-1992.
 XX
 PF 22-NOV-1989; 89US-0440625.
 XX
 PR 23-FEB-1989; 89US-0315015.
 PR 22-NOV-1989; 89US-0440625.
 XX

XX (GETH) GENENTECH INC.
 XX

PI Capon DJ, Lasky LA;
 XX

DR WPI: 1992-199589/24.
 XX

XX N-PSDB; AAQ24987.
 XX

PT Nucleic acid encoding polypeptide fusions - comprising ligand
 PT binding partner protein and immunoglobulin chain, for use in
 PT diagnosis and therapy
 XX

PS Disclosure; Fig 1-1 - 1-3; 43pp: English.
 XX

CC LHR mediates the binding of lymphocytes to the endothelium of
 CC lymphoid tissue. Full length cDNA clones and DNA encoding the human
 CC and the murine LHR (HULHR and MLHR, respectively) have been
 CC identified and isolated (see AAQ24987 and AAQ24988). LHR is a
 CC glycoprotein which contains the following protein domains: a signal
 CC sequence, a carbohydrate binding domain, and epidermal growth
 CC factor-like (egf) domain, at least one and preferably two complement
 CC binding domain repeat, a transmembrane binding domain (TRD), and a
 CC charged intracellular or cytoplasmic domain. LHR is used as the
 CC ligand-binding partner in fusion polypeptides with an immunoglobulin,
 CC for use in diagnosis and therapy.
 XX

SQ Sequence 372 AA:

Query Match 99.7%; Score 2109; DB 13; Length 372;
 Best Local Similarity 99.7%; Pred. No. 1.7e-140;
 Matches 371; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MIFPPKQSTQRLDMLNIFKMGWMTLCCDFLAHHGTYCWTYHYSEKPMNQRRRCRDNY 60
 DB 1 mifpwkcsgtqrdlwnlfkmgwmtlccdflahhgytcwtyhysekpmnqrrrrcndy 60
 OY 61 YTDLVAIQNKAETLEYEKLTPFSRSYYWIGIRKIGIWTWVGINKSLTEAEKNGDEPN 120
 DB 61 ytdlvaliqnkaeyleyektlpfsrsyywigirkigiwtwvginkslteeenvgdepm 120
 OY 121 NKKKEDCVEIYIKRNKDGKNDACHKIKALCYTASQPMSCSGHGECVEIINNHTCN 180
 DB 121 nkkkedcveiyikrnkdgkndachkikaalcycasqpmwscsghgvevllnnhtc 180

```

OY 181 NCDVGYGPOCOLVIOCEPLAEPELGTMDCTHPFGNFSSSCAPSCSEGNLNGIEETT 240
DB 181 ncdvgygppcqlviqcepleapepeltmdcthpfgnfsfsqcaiscsegnllygieett 240
OY 241 GPFQWMSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTCSGTELGKKT 300
DB 241 gpfqwnsspeptcqvioceplsapdlgimncshplastsactftcsgetelgkkt 300
OY 301 TICSSGIMWNSPPTCOKLDSFSGMIRKGDYNPFIPIVAVWVTAFSGLAFITWLARRLKK 360
DB 301 ticesgimwnspptcqlkdsfsgmirkedynpfiipavwvtafsglafitwlarrlkk 360
OY 361 GKSKRSNMNDPY 372
DB 361 gksksrsmndpy 372

RESULT 12
AAR98110
ID AAR98110 standard; Protein: 371 AA.
AC AAR98110;
XX
DT 01-NOV-1996 (first entry)
XX
DE Human lymphocyte cell surface glycoprotein (HULHR) variant.
XX
KM Immunoglobulin: transmembrane receptor; adhesion; targeting;
KM diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KM immunomodulator; cell adhesion; graft rejection; inflammation;
KM metastasis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..37
FT /label= Signal region.
FT Domain 38..154
FT /label= Lectin domain.
FT Domain 159..192
FT /label= EGF domain.
FT Binding-site 196..257
FT /label= Complement binding repeat 1.
FT Binding-site 258..316
FT /label= Complement binding repeat 2.
FT Domain 332..354
FT /label= Transmembrane domain.
FT Domain 355..371
FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI, 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX

```

```

PS Disclosure; Page 19; 41pp; English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
CC a single transmembrane receptor without an active transmembrane
CC region; fused at its C-terminus with the N-terminus of an
CC immunoglobulin constant region. The receptor is not a member of the
CC immunoglobulin super family, nor a multiple subunit polypeptide
CC encoded by discrete genes. The hybrid immunoglobulin chain combines
CC the adhesion/targeting of a ligand binding partner (LBP) with the
CC effector functions of immunoglobulin and can bind to and/or activate
CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particular cells.
CC Typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC facilitates recovery. Improves aqueous solubility and removes
CC potentially immunogenic epitopes. Variants of the human lymphocyte
CC cell surface glycoprotein described in AAR98106 are given in
CC AAR98109-R98135. This variant contains an Ala71Ser substitution.
XX
XX SQ Sequence 371 AA:
XX
XX Query Match 99.6%; Score 2108; DB 17; Length 371;
XX Best Local Similarity 99.7%; Pred. No. 2e-140;
XX Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 IPPWKOQSTQRPDLMMNIFKMGWMLCCDFIAHHGYCTHYHSEKPMWQARRFCNDY 61
DB 1 ifpwkcgstqrdlwnifkfwgwmccdfiahghyctwyhsekpmwqarrfcndy 60
OY 62 TDVAIQNKAELEYLEKTLPEFSRSYTWIGIRKIGITWVTGNTKSLTEAENMGDGEPN 121
DB 61 tdlvaigqkseeleyektlpefsrswytwigirkiigitwvtnkslteaenmgdgsppn 120
OY 122 KKNKEDCWEIYIKRNKDKGKNDACHTKALCYTASCPWSCSGHGEVEIINHTCN 181
DB 121 knkedcweilykrnkdkgkndachtkaalcytascpwsccghgeveiinhtcn 180
OY 182 CDVGYGPOCOLVIOCEPLAEPELGTMDCTHPFGNFSSSCAPSCSEGNLNGIEETT 241
DB 181 cdvgygppcqlviqcepleapepeltmdcthpfgnfsfsqcaiscsegnllygieett 240
OY 242 GPFQWMSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTCSGTELGKKT 301
DB 241 gpfqwnsspeptcqvioceplsapdlgimncshplastsactftcsgetelgkkt 300
OY 302 ICESGIMWNSPPTCOKLDSFSGMIRKGDYNPFIPIVAVWVTAFSGLAFITWLARRLKK 361
DB 301 icesgimwnspptcqlkdsfsgmirkedynpfiipavwvtafsglafitwlarrlkk 360
OY 362 KSKRSNMNDPY 372
DB 361 kksksrsmndpy 371

RESULT 13
AAR98113
ID AAR98113 standard; Protein: 371 AA.
AC AAR98113;
XX
XX 01-NOV-1996 (first entry)
XX
XX Human lymphocyte cell surface glycoprotein (HULHR) variant.
XX
XX Immunoglobulin: transmembrane receptor; adhesion; targeting;
XX diagnosis; therapy; drug delivery; antiviral; neuromodulator;
XX immunomodulator; cell adhesion; graft rejection; inflammation;
XX metastasis.
XX

```


OS	XX	Homo sapiens.
XX	XX	Key
XX	XX	Region
XX	XX	Location/Qualifiers
XX	XX	1..37
XX	XX	/label- Signal region.
XX	XX	38..154
XX	XX	/label- Lectin domain.
XX	XX	159..192
XX	XX	/label- EGF domain.
XX	XX	196..257
XX	XX	/label- Complement binding repeat 1.
XX	XX	258..316
XX	XX	/label- Complement binding repeat 2.
XX	XX	332..354
XX	XX	/label- Transmembrane domain.
XX	XX	355..371
XX	XX	/label- Cytoplasmic domain.
XX	XX	US5514582-A.
XX	XX	07-MAY-1996.
XX	XX	23-FEB-1989;
XX	XX	89US-0315015.
XX	XX	22-NOV-1989;
XX	XX	89US-0440625.
XX	XX	23-FEB-1989;
XX	XX	89US-0315015.
XX	XX	16-DEC-1991;
XX	XX	91US-0808122.
XX	XX	08-DEC-1992;
XX	XX	92US-0986931.
XX	XX	21-JAN-1994;
XX	XX	94US-0185670.
XX	XX	(GETH) GENENTECH INC.
XX	XX	Capon DJ, Lasky LA;
XX	XX	WPI: 1996-238773/24.
XX	XX	Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX	XX	binding site of a receptor fused to Ig constant region - useful for
XX	XX	diagnosis and treatment e.g. of inflammation
XX	XX	Disclosure: Page 19; 41pp; English.
XX	XX	A hybrid immunoglobulin chain comprising the ligand binding site of
XX	XX	a single transmembrane receptor without an active transmembrane
XX	XX	region; fused at its C-terminus with the N-terminus of an
XX	XX	immunoglobulin constant region. The receptor is not a member of the
XX	XX	immunoglobulin super family, nor a multiple subunit polypeptide
XX	XX	encoded by discrete genes. The hybrid immunoglobulin chain combines
XX	XX	the adhesion/targeting of a ligand binding partner (LBP) with the
XX	XX	effector functions of immunoglobulin and can bind to and/or activate
XX	XX	more than one ligand. It can be used diagnostically for the in
XX	XX	vitro assay of LBP and their targets, or therapeutically to deliver
XX	XX	LBP such as toxins, enzymes, growth factors to particular cells.
XX	XX	Typical applications are as antiviral, neuromodulating and
XX	XX	immunomodulating agents, or as modulators of cell adhesion (e.g. in
XX	XX	treating graft rejection; inflammation; metastasis of lymphoma etc.)
XX	XX	The immunoglobulin component increases plasma half life and
XX	XX	facilitates purification while deletion of the transmembrane region
XX	XX	facilitates recovery, improves aqueous solubility and removes
XX	XX	potentially immunogenic epitopes. Variants of the human lymphocyte
XX	XX	cell surface glycoprotein described in AAR8106 are given in
XX	XX	AAR98109-R98135. This variant contains a Leu150Val substitution.
XX	XX	Sequence 371 AA;
XX	XX	Query Match 99.6%; Score 2108; DB 17; Length 371;
XX	XX	Best Local Similarity 99.7%; Pred. No. 2e-140;
XX	XX	Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db	1	ifpwkcgstqrdlwniflwtwlmccdfiahngltycwtlyhysckpmwqrrarrfcidny	60
Qy	62	TDLVAIQKAAEEYLEKTLPPFSRSYVWIGIRKIGITWWTGNTKSLTEAEANMGDEPN	121
Db	61	tdlvaIQKAAEylekTLppfsrsywigIRkIGITwtwGntKslTeaenwgdgepn	120
Qy	122	KKNKEDCEYIITKRKKDAGKNNDACCHKLAKALCYTASQCPWSSGSGECEVEIINHTCN	181
Db	121	kknkEdceYiItkrKkDagknNdAcChkLkAlCyTasqCpWssgSGeCeVeIiNhTcn	180
Qy	182	CDVGYTGGOCOLVIOCEPLEAPELGTMDCTHPFCNFSSQCAPSCSGEATNLGIEETTC	241
Db	181	cdvgytggocolviocePlEaPeLgTMDcThpFcNfSSqCaPscSGeATnlGieETtc	240
Qy	242	GPFGMSPEPTTCOVIOCEPLSAPDLGIMNCNHPLASFSFTSACTPICSGETELIGKKT	301
Db	241	gpfgmspepttcoviocePlsApDLgImNcNhpLasfsFTsactPicsGeTeLiGkkt	300
Qy	302	ICESGIMSNSPISPCIKDKDSFSMKESDYNPFLTPAAVWWTASGLAFITWLARRLKG	361
Db	301	icesgImsnspIspIcQkIdksfsmIkegdyNpflTpAaVwWtAsGlAfItWlArRlkg	360
Qy	362	KKSKRSMNDPY 372	
Db	361	kkskrsmndpy 371	
RESULT 14			
AAR98119			
ID	AAR98119 standard; Protein: 371 AA.		
AC	AAR98119;		
XX			
DT	01-NOV-1996 (first entry)		
XX			
DE	Human lymphocyte cell surface glycoprotein (HULHR) variant.		
XX			
KW	Immunoglobulin; transmembrane receptor; adhesion; targeting;		
KW	diagnosis; therapy; drug delivery; antiviral; neuromodulator;		
KW	immunomodulator; cell adhesion; graft rejection; inflammation;		
KW	metastasis.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	Region		
FT	Location/Qualifiers		
FT	1..37		
FT	/label= Signal region.		
FT	38..154		
FT	/label= Lectin domain.		
FT	159..192		
FT	Domain		
FT	/label= EGF domain.		
FT	Blinding-site		
FT	196..257		
FT	/label= Complement binding repeat 1.		
FT	258..316		
FT	/label= Complement binding repeat 2.		
FT	332..354		
FT	Domain		
FT	/label= Transmembrane domain.		
FT	355..371		
FT	Domain		
FT	/label= Cytoplasmic domain.		
XX			
PN	US5514582-A.		
XX			
XX	07-MAY-1996.		
XX			
PE	23-FEB-1989;		
XX	89US-0315015.		
PR	22-NOV-1989;		
PR	89US-0440625.		
PR	23-FEB-1989;		
PR	89US-0315015.		
PR	16-DEC-1991;		
PR	91US-0808122.		
PR	08-DEC-1992;		
PR	92US-0986931.		
PR	21-JAN-1994;		
XX	94US-0185670.		
PA	(GETH) GENENTECH INC.		

XX Capon DJ, Lasky LA;
 PI
 XX WPI: 1996-238773/24.
 DR
 PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
 binding site of a receptor fused to Ig constant region - useful for
 PT diagnosis and treatment e.g. of inflammation
 XX
 PS Disclosure: Page 19; 41pp; English.
 XX
 CC A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection, inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes. Variants of the human lymphocyte
 CC cell surface glycoprotein described in AAR98106 are given in
 CC AAR98109-R98135. This variant contains a Ser226Thr substitution.
 XX
 SQ Sequence 371 AA;
 Query Match 99.6%; Score 2108; DB 17; Length 371;
 Best Local Similarity 99.7%; Pred. No. 2e-140;
 Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 0;
 QY 2 IFPMKQSTQRODLMNIFKLMGWTMLCCDFLAHGTGWTYHSEKPMNORARFCRDNY 61
 Db 1 ifpmkqstqrdlnwlfkmgwtmccdfiahgtgwtcyhsekpmmwgrartrfcrdny 60
 QY 62 TDLVAIQNAELEYEKLTPFSRSYWIIRKIGIMTWGTLKEBAENMGDEPN 121
 Db 61 tdlvaIQNAELEYEKLTPFSRSYWIIRKIGIMTWGTLKEBAENMGDEPN 120
 QY 122 KKKKECVETLYIKRNDAKWNDAKCHIKALCTYASQPMSCSHGCEVETLNNHTCN 181
 Db 121 kkkkecvetlyikrnDAKWNDAKCHIKALCTYASQPMSCSHGCEVETLNNHTCN 180
 QY 182 CDVGYYPQCOLVIOCEPEAELELTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETTC 241
 Db 181 cdvgyypqcolvIQCEPEAELELTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETTC 240
 QY 242 GPPGNMSSPEPPCOVYQCEPPLSNAPDLGIMNGCHPLASFSFTACTFTTCSEGLIGKKT 301
 Db 241 gppgnmsspeppCOVYQCEPPLSNAPDLGIMNGCHPLASFSFTACTFTTCSEGLIGKKT 300
 QY 302 ICESSGIMNPSPICOKLDKFSMKEGDYNPLFIPIVAVMAFAGLAFITLARLKKG 361
 Db 301 iceSSGIMNPSPICOKLDKFSMKEGDYNPLFIPIVAVMAFAGLAFITLARLKKG 360
 QY 362 KSKRSMDNPDY 372
 Db 361 kskrsmndpy 371

RESULT 15
 AAR22802
 ID AAR22802 standard; Protein; 372 AA.
 XX
 AC AAR22802;

XX 01-SEP-1992 (first entry)
 DT
 XX Human lymphocyte homing receptor.
 DE
 XX HuLHR: LHR: binding; endothelium; immunogens; graft; organ;
 KW rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 20..32
 FT /note="potential signal sequence"
 FT Modified-site 60..62
 FT /note="N-glycosylation site"
 FT Modified-site 104..106
 FT /note="N-glycosylation site"
 FT Modified-site 177..179
 FT /note="N-glycosylation site"
 FT Modified-site 216..218
 FT /note="N-glycosylation site"
 FT Modified-site 232..234
 FT /note="N-glycosylation site"
 FT Modified-site 271..273
 FT /note="N-glycosylation site"
 FT Modified-site 311..313
 FT /note="N-glycosylation site"
 FT Region 335..357
 FT /note="stop transfer or membrane anchoring domain"
 XX
 PN US5098833-A.
 PD 24-MAR-1992.
 XX
 PF 23-FEB-1989; 89US-0315015.
 XX
 PR 23-FEB-1989; 89US-0315015.
 XX
 PA (REGC) UNIV OF CALIFORNIA.
 PI Lasky LA, Rosen SD, Stachel SE, Slinger MS, Yednock TA;
 DR N-PSDB; AAQ23623.
 DR
 PT New DNA encoding at least one domain of lymphocyte homing
 PT receptor - useful for treating graft rejection, inflammation,
 PT etc.
 XX
 PS Disclosure: Fig 1; 32pp; English.
 XX
 CC The protein sequence was deduced from the DNA sequence obt'd. by
 CC screening an oligo dr primed lambda gt10 cDNA library derived from
 CC human peripheral blood lymphocyte mRNA obt'd. from primary cells,
 CC with a 2.2 kb EcoRI insert of the murine Mel 14 antigen cDNA clone.
 CC The protein contains regions encoding a carbohydrate binding domain,
 CC an EGF-like domain, a complement binding domain and a transmembrane
 CC domain. The protein contains 26 cysteine residues. Cells transformed
 CC by the hLHR DNA are used to produce LHR (which mediates binding of
 CC lymphocytes to the endothelium of lymphoid tissue). LHR or its
 CC variants are useful as reagents for assaying LHR or anti-LHR anti-
 CC bodies, to purify the antibodies, as immunogens, and therapeutically
 CC to compete with normal binding of lymphocytes (to prevent graft/organ
 CC rejection; to treat inflammation (such as rheumatoid arthritis or
 CC other autoimmune diseases); for control of lymphocyte metastasis,
 CC and to treat conditions associated with accumulation of lymphocytes).
 CC Derivs. and variants of LHR may be produced having modified
 CC properties, e.g. increased activity, longer plasma half-life,
 CC reduced side effects and better ag. solubility.
 CC See also AAR22803.
 XX
 SQ Sequence 372 AA;

```

Query Match          99.6%: Score 2108: DB 13: Length 372;
Best Local Similarity 99.5%: Pred. No. 2e-140: 1;
Matches 370: Conservative 1: Mismatches 1: Indels 0: Gaps 0;

QY 1 MPPWKCOSTORDLWNIFFKLMGWTMLCCDFLAHGYCWTYHYSEKPMNQARARPCRDN 60
    |||||||
Db 1 mlfpwkcgstqrdlwnlffkxlgwtmccdfllahgytcwtyhysekpnmqarrrfcrdn 60
    |||||||

QY 61 YTDLVAIQNKAEIEYLEKTLPSRSYTWIGIRKIGIWTWVGINKSLTEBAENMGDEPN 120
    |||||||
Db 61 ytdlvaigknaeylelktlpsrsytwigirkgiwtwvgnkslteeaenwgdegn 120
    |||||||

QY 121 NKKNKEDCVETIYIKRNMDAGKNDACCHKLKAALCYTASQCPWSCSGHGEVETINNHTC 180
    |||||||
Db 121 nknkqdcveiyikrnmckndackkndachklkaalcylascqpwscsghgeveellnhct 180
    |||||||

QY 181 NCDVGYGPOCQLVIOCEPLEAPELGTMCTHPFGNPFSSQCAFSCSEGTNLGIEETP 240
    |||||||
Db 181 ncdvgyygpqcdlviocepleapeigtmcthpfnfssqcafscsegtnlgleett 240
    |||||||

QY 241 CGPFGMNSPEPTCQVYIQCEPLSAPDLGIMNCSHPLASFSTACTFTICSEGTELIGKK 300
    |||||||
Db 241 cgpfgmnspeptcqvliqceplsapdlgimncshplasfstsactficsgtellignkk 300
    |||||||

QY 301 TICSSGIMNSPSPICQKLDKSFMSIKEDYNPLFTPVAVMTAFSGLAFIIMLARLKK 360
    |||||||
Db 301 ticssgimnspspicqkldksfmsikedyndplftpvavmtafsglafilwarrlkk 360
    |||||||

QY 361 GKKSRSMDPY 372
    |||||||
Db 361 gkksrsmndpy 372
    |||||||

```

Search completed: October 13, 2001, 02:53:58
 Job time: 4315 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:43:42 ; Search time 25.01 Seconds
(without alignments)
306.262 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116
Sequence: 1 MIFPWKCQSTQRDLNIFKL.....WLNRRKKKKSKRSMNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgnl_7/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgnl_7/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgnl_7/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgnl_7/ptodata/1/1aa/PCRTUS_COMB.pep:*
- 6: /cgnl_7/ptodata/1/1aa/Backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	372	2	US-08-513-278-2
2	2116	100.0	372	6	5514582-2
3	2076	98.1	385	1	US-08-340-539A-2
4	2076	98.1	385	2	US-08-461-592B-2
5	1651	78.0	372	2	US-08-513-278-4
6	1651	78.0	372	6	5514582-4
7	905	42.8	830	1	US-08-110-158-4
8	899	42.5	830	5	PCR-US91-05059-2
9	889	42.0	830	6	5378464-2
10	862	40.7	610	1	US-08-365-470-3
11	862	40.7	610	3	US-09-209-668-19
12	862	40.7	610	6	5217870-2
13	814.5	38.5	484	2	US-08-252-493C-9
14	814.5	38.5	484	3	US-09-276-197-9
15	666	31.5	117	1	US-08-274-661B-38
16	587	27.7	119	1	US-08-340-539A-14
17	572	27.0	119	1	US-08-340-539A-12
18	569	26.9	119	1	US-08-340-539A-13
19	565	26.7	117	6	5514582-7
20	487	23.0	126	6	5514582-31
21	467	22.1	119	1	US-08-340-539A-18
22	457	21.6	119	1	US-08-340-539A-17
23	452	21.4	119	1	US-08-340-539A-16
24	451	21.3	119	1	US-08-340-539A-19
25	450	21.3	120	1	US-08-274-661B-37
26	445	21.0	117	1	US-08-274-661B-39
27	431	20.4	120	1	US-08-274-661B-36

28	437	20.2	119	1	US-08-340-539A-15	Sequence 15, Appl
29	337	15.9	574	6	5378464-3	Patent No. 5378464
30	237	11.2	67	3	US-08-840-062-8	Sequence 8, Appl
31	199	9.4	36	1	US-08-340-539A-22	Sequence 22, Appl
32	189.5	9.0	1019	1	US-08-296-014A-4	Sequence 4, Appl
33	189.5	9.0	1019	2	US-08-596-405-4	Sequence 4, Appl
34	189.5	9.0	1019	2	US-08-877-620-4	Sequence 4, Appl
35	189.5	9.0	1083	1	US-08-296-014A-2	Sequence 2, Appl
36	189.5	9.0	1083	2	US-08-596-405-2	Sequence 2, Appl
37	189.5	9.0	1083	3	US-08-877-620-2	Sequence 2, Appl
38	181.5	8.6	240	3	US-08-824-692-23	Sequence 23, Appl
39	177	8.4	36	1	US-08-340-539A-20	Sequence 20, Appl
40	175.5	8.3	216	3	US-08-824-692-24	Sequence 24, Appl
41	172	8.1	1466	6	5256642-6	Patent No. 5256642
42	172	8.1	1466	6	5472939-6	Patent No. 5472939
43	172	8.1	1537	6	5256642-5	Patent No. 5256642
44	172	8.1	1537	6	5472939-5	Patent No. 5472939
45	172	8.1	1847	6	5256642-10	Patent No. 5256642

ALIGNMENTS

RESULT 1
Sequence 2, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 565D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9816
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-513-278-2

Query Match 100.0%; Score 2116; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2,9e-185;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEPCKCOSTORDLNNIRKMGWMLCCDFLAHGTCTWTHYSEKPNMWRARFCDN 60
DB 1 MIEPCKCOSTORDLNNIRKMGWMLCCDFLAHGTCTWTHYSEKPNMWRARFCDN 60
QY 61 YTDVAIONKAEIEYLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSLEAEENMGDGEPN 120
DB 61 YTDVAIONKAEIEYLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSLEAEENMGDGEPN 120
QY 121 NKKNEDEVEIYIKRNKAGKWDACHKLAALCYTASCPMCSGHECEVEIINNHTC 180
DB 121 NKKNEDEVEIYIKRNKAGKWDACHKLAALCYTASCPMCSGHECEVEIINNHTC 180
QY 181 NCDVGYGPOCQVIOCEPLAEPLAGTMDCTHPGNFSFSCAFSCSEGTNLGIEET 240
DB 181 NCDVGYGPOCQVIOCEPLAEPLAGTMDCTHPGNFSFSCAFSCSEGTNLGIEET 240
QY 241 CGPFGNMSPEPTCOVIOCEPLAPDLGINCSHPLASFSTACTFICSEGTLLGKK 300
DB 241 CGPFGNMSPEPTCOVIOCEPLAPDLGINCSHPLASFSTACTFICSEGTLLGKK 300
QY 301 TICSSGSIWNSPPIQCKLDRSFMKEGDYNPLFIPVAVMTAFSGLAFTIWLRLKK 360
DB 301 TICSSGSIWNSPPIQCKLDRSFMKEGDYNPLFIPVAVMTAFSGLAFTIWLRLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372

RESULT 2
5514582-2
; Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
; IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/185,670
; PRIORITY APPLICATION DATA:
; FILING DATE: 21-JAN-1994
; APPLICATION NUMBER: 986,931
; FILING DATE: 08-DEC-1992
; APPLICATION NUMBER: 808,122
; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440,625
; FILING DATE: 22-NOV-1989
; APPLICATION NUMBER: 315,015
; FILING DATE: 23-FEB-1989
; SEQ ID NO: 2:
; LENGTH: 372
5514582-2

Query Match 100.0%; Score 2116; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 2,9e-185;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEPCKCOSTORDLNNIRKMGWMLCCDFLAHGTCTWTHYSEKPNMWRARFCDN 60
DB 1 MIEPCKCOSTORDLNNIRKMGWMLCCDFLAHGTCTWTHYSEKPNMWRARFCDN 60
QY 61 YTDVAIONKAEIEYLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSLEAEENMGDGEPN 120
DB 61 YTDVAIONKAEIEYLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSLEAEENMGDGEPN 120
QY 121 NKKNEDEVEIYIKRNKAGKWDACHKLAALCYTASCPMCSGHECEVEIINNHTC 180
DB 121 NKKNEDEVEIYIKRNKAGKWDACHKLAALCYTASCPMCSGHECEVEIINNHTC 180

DB 121 NKKNEDEVEIYIKRNKAGKWDACHKLAALCYTASCPMCSGHECEVEIINNHTC 180
QY 181 NCDVGYGPOCQVIOCEPLAEPLAGTMDCTHPGNFSFSCAFSCSEGTNLGIEET 240
DB 181 NCDVGYGPOCQVIOCEPLAEPLAGTMDCTHPGNFSFSCAFSCSEGTNLGIEET 240
QY 241 CGPFGNMSPEPTCOVIOCEPLAPDLGINCSHPLASFSTACTFICSEGTLLGKK 300
DB 241 CGPFGNMSPEPTCOVIOCEPLAPDLGINCSHPLASFSTACTFICSEGTLLGKK 300
QY 301 TICSSGSIWNSPPIQCKLDRSFMKEGDYNPLFIPVAVMTAFSGLAFTIWLRLKK 360
DB 301 TICSSGSIWNSPPIQCKLDRSFMKEGDYNPLFIPVAVMTAFSGLAFTIWLRLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372

RESULT 3
US-08-340-539A-2
; Sequence 2, Application US/08340539A
; Patent No. 5808025
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539A
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gunnison, Jane
; REGISTRATION NUMBER: 38,479
; REFERENCE/DOCKET NUMBER: CG-104 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-340-539A-2

Query Match 98.1%; Score 2076; DB 1; Length 385;
Best Local Similarity 98.1%; Pred. No. 1,3e-181;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIEPCKCOSTORDLNNIRKMGWMLCCDFLAHGTCTWTHYSEKPNMWRARFCDN 60
DB 14 MIEPCKCOSTORDLNNIRKMGWMLCCDFLAHGTCTWTHYSEKPNMWRARFCDN 73
QY 61 YTDVAIONKAEIEYLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSLEAEENMGDGEPN 120

```

Db      74 YTDLVAIQNAEIEYLEKTLPEFSRSYYWIGIRKIGTWGINKSLTEAENKGDSEPN 133
      121 NKKNKEDCEVEIYIKRNKADKWNDDACHKLKALCYTASQPMSCSGHGEVEIINNHTC 180
      134 NKKNKEDCEVEIYIKRNKADKWNDDACHKLKALCYTASQPMSCSGHGEVEIINNHTC 193
Qy      181 NCVGVYGGPQCQVYIOCEPLAEPLGTMDCTHPLGNFNFSQCAFSCSEGTNLGIEETT 240
      194 NCVGVYGGPQCQVYIOCEPLAEPLGTMDCTHPLGNFNFSQCAFSCSEGTNLGIEETT 253
Qy      241 CGPFGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPFCSEGTLLGKKK 300
      254 CEFPGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPFCSEGTLLGKKK 313
Qy      301 TICSSGIMNSPPIQCKLDKSFSMIKEGDYNPFIPIVAVWTAFSGLAFIIMLARLKK 360
      314 TICSSGIMNSPPIQCKLDKSFSMIKEGDYNPFIPIVAVWTAFSGLAFIIMLARLKK 373
Db      361 GKSKSRMNDPY 372
      374 GKSKSRMNDPY 385
Qy      361 GKSKSRMNDPY 372
      374 GKSKSRMNDPY 385
Db      361 GKSKSRMNDPY 372
      374 GKSKSRMNDPY 385

RESULT 4
US-08-461-592B-2
; Sequence 2, Application US/08461592B
; Patent No. 5834423
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welngarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,592B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/340,539
; FILING DATE: 16-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CG-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-592B-2
```

```

Query Match      98.1%; Score 2076; DB 2; Length 385;
Best Local Similarity 98.1%; Pred. No. 1.3e-181;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 MIFPKWCOSTORDLMNIFKLMGWTMLCCDFLAHHGTGWTYHYSEKPMNQRRARFCRDN 60
      14 MIFPKWCOSTORDLMNIFKLMGWTMLCCDFLAHHGTGWTYHYSEKPMNQRRARFCRDN 73
Db      61 YTDLVAIQNAEIEYLEKTLPEFSRSYYWIGIRKIGTWGINKSLTEAENKGDSEPN 120
      74 YTDLVAIQNAEIEYLEKTLPEFSRSYYWIGIRKIGTWGINKSLTEAENKGDSEPN 133
Qy      121 NKKNKEDCEVEIYIKRNKADKWNDDACHKLKALCYTASQPMSCSGHGEVEIINNHTC 180
      134 NKKNKEDCEVEIYIKRNKADKWNDDACHKLKALCYTASQPMSCSGHGEVEIINNHTC 193
Qy      181 NCVGVYGGPQCQVYIOCEPLAEPLGTMDCTHPLGNFNFSQCAFSCSEGTNLGIEETT 240
      194 NCVGVYGGPQCQVYIOCEPLAEPLGTMDCTHPLGNFNFSQCAFSCSEGTNLGIEETT 253
Qy      241 CGPFGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPFCSEGTLLGKKK 300
      254 CEFPGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPFCSEGTLLGKKK 313
Qy      301 TICSSGIMNSPPIQCKLDKSFSMIKEGDYNPFIPIVAVWTAFSGLAFIIMLARLKK 360
      314 TICSSGIMNSPPIQCKLDKSFSMIKEGDYNPFIPIVAVWTAFSGLAFIIMLARLKK 373
Db      361 GKSKSRMNDPY 372
      374 GKSKSRMNDPY 385

RESULT 5
US-08-513-278-4
; Sequence 4, Application US/08513278
; Patent No. 5840844
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNICK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,278
; FILING DATE: 10-AUG-1995
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 06-MAY-1993
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, GINGER R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 565D1C1
```


Query Match	78.0%;	Score 1651;	DB 6;	Length 372;
Best Local Similarity	76.1%;	Pred. No. 7.6e-143;		
Matches 283; Conservative	32;	Mismatches 57;	Indels 0;	Gaps 0;

```

1  RESULT 7
2  - US-08-110-158-4
3  ; Sequence 4, Application US/08110158
4  ; Patent No. 5605821
5  ;
6  ; GENERAL INFORMATION:
7  ;
8  ; APPLICANT: McEever, Rodger P.
9  ;
10 ; APPLICANT: Pan, Junliang
11 ;
12 ; TITLE OF INVENTION: Expression Control Sequences of the
13 ; TITLE OF INVENTION: P-Selectin Gene
14 ;
15 ; NUMBER OF SEQUENCES: 17
16 ;
17 ; CORRESPONDENCE ADDRESS:
18 ;
19 ; ADDRESSEE: Patricia L. Pabst
20 ; STREET: 1100 Peachtree Street, Suite 2800
21 ; CITY: Atlanta
22 ;
23 ; STATE: GA
24 ;
25 ; COUNTRY: USA
26 ;
27 ; ZIP: 30309-4530
28 ;
29 ; COMPUTER READABLE FORM:
30 ;
31 ; MEDIUM TYPE: Floppy disk
32 ;
33 ; COMPUTER: IBM PC compatible
34 ;
35 ; OPERATING SYSTEM: PC-DOS/MS-DOS
36 ;
37 ; SOFTWARE: Patent In Release #1.0, Version #1.25
38 ;
39 ; CURRENT APPLICATION DATA:
40 ;
41 ; APPLICATION NUMBER: US/08/110,158
42 ;
43 ; FILING DATE: 19930820
44 ;
45 ; CLASSIFICATION: D24
46 ;
47 ; PRIOR APPLICATION DATA:
48 ;
49 ; APPLICATION NUMBER: US 07/320,408
50 ;
51 ; FILING DATE: 08-MAR-1989
52 ;
53 ; ATTORNEY/AGENT INFORMATION:
54 ;
55 ; NAME: Pabst, Patricia L.
56 ;
57 ; REGISTRATION NUMBER: 31,284
58 ;
59 ; TELECOMMUNICATION INFORMATION:
60 ;
61 ; TELEPHONE: (404)-815-6508
62 ;
63 ; TELEFAX: (404)-815-6555
64 ;
65 ; INFORMATION FOR SEQ ID NO: 4:
66 ;
67 ; SEQUENCE CHARACTERISTICS:
68 ;
69 ; LENGTH: 830 amino acids
70 ;
71 ; TYPE: amino acid
72 ;
73 ; STRANDEDNESS: single
74 ;
75 ; TOPOLOGY: linear
76 ;
77 ; MOLECULE TYPE: peptide
78 ;
79 ; US-08-110-158-4

```


NAME/KEY: Disulfide-bond
LOCATION: 510..554
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 523..536
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 540..567
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 572..616
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 585..616
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 602..629
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 642..686
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 655..668
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 672..699
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 704..748
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 717..730
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 734..761
FEATURE:
NAME/KEY: Binding-site
LOCATION: 98
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 180
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 212
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 219
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 411
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 460
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 518

OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 665
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 716
OTHER INFORMATION: /note= "Potential asparagine-linked
OTHER INFORMATION: glycosylation site"
FEATURE:

Query Match 42.5%; Score 899; DB 5; Length 830;
Best Local Similarity 50.3%; Pred. No. 8, 7e-74;
Matches 156; Conservative 48; Mismatches 106; Indels 0; Gaps 0;

QY 8 OSTORDLWNIFKLMGWTMLCCDFLAHHGTYCTVHYHSEKPMQRRARRRCDNTDVAI 67
DB 11 QRFQRYVFGISQLCFSLISLTLNOKVEAAMTYHSTKAYSWNISRKYCONRYTDVAI 70
QY 68 QNKAIEYLEKTLPPFSRSYWIIGIRKIGIWTWGTNKSILTEAEAMWGDEPNKKNKED 127
DB 71 QNKNEIDYLNKVLPLYSSYWIIGIRKNNKTWTWGTGKALTEAENWADNEPNKKRNED 130
QY 128 CVELIYIKRNDAGKNDADCHKLKALCYTASCOFWSGSGHGEVCEIINNHTCNCVGY 187
DB 131 CVELIYIKSPAPGKNDKMLCKKAKALCYTASCOFWSGSGHGEVCEIINNHTCNCVGY 190
QY 188 GPQCULVIOCEPLEAPETLGTMDCTHPFGNFSFSCAFSCSGTMLGIEETGSPGNW 247
DB 191 GPBCEYVRECELELPQEVLMNCSHPLGNFSNOSCRRHCTDGVGNPCKLECLASSIW 250
QY 248 SDEPTQVIOCEPLSAPDLGIMNCSHPLASFTSACTFTICEGTLEIGKKTICSSG 307
DB 251 TNKPPQCLAAQCPPLKIPRGNMICIMSAKARQWQSSCSFSEEFALVGEVQCTASG 310
QY 308 TMSNPSTIQ 317
DB 311 VMTAPAPVCK 320

RESULT 9
5378464-2
PATENT No. 5378464
APPLICANT: MCEVER, RODGER P.
TITLE OF INVENTION: MODULATION OF INFLAMMATORY RESPONSES
BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140
NUMBER OF SEQUENCES: 32
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-07/320,408
FILING DATE: 08-MAR-1989
SEQ ID NO: 2
LENGTH: 830
5378464-2

Query Match 42.0%; Score 889; DB 6; Length 830;
Best Local Similarity 50.0%; Pred. No. 7, 1e-73;
Matches 155; Conservative 48; Mismatches 107; Indels 0; Gaps 0;

QY 8 OSTORDLWNIFKLMGWTMLCCDFLAHHGTYCTVHYHSEKPMQRRARRRCDNTDVAI 67
DB 11 QRFQRYVFGISQLCFSLISLTLNOKVEAAMTYHSTKAYSWNISRKYCONRYTDVAI 70
QY 68 QNKAIEYLEKTLPPFSRSYWIIGIRKIGIWTWGTNKSILTEAEAMWGDEPNKKNKED 127
DB 71 QNKNEIDYLNKVLPLYSSYWIIGIRKNNKTWTWGTGKALTEAENWADNEPNKKRNED 130
QY 128 CVELIYIKRNDAGKNDADCHKLKALCYTASCOFWSGSGHGEVCEIINNHTCNCVGY 187
DB 131 CVELIYIKSPAPGKNDKMLCKKAKALCYTASCOFWSGSGHGEVCEIINNHTCNCVGY 190

```

QY 188 GGGCCLVTCGCELEAPELGTMDCTHPGNGFSSGCAAFSGSEGNLNLGIEETGCGPGNM 247
DB 191 GPECYVEACGELELPQVLYLNNCSHPJLGNFSFNSQCSFHTDGTQVWGPSKLECLASGIW 256
QY 248 SSPEPTCCVIOICEPLASBDLGMNCSHPLASFSPTSACTFICSEGTELIGKKKTCISSG 307
DB 251 TNKPQCLAAQCGPLKPIERBNMTCILMSAKRPQMGSSCSFSCGEGFALVGEVYQCTASG 310
QY 308 IWSNPSPIQ 317
DB 311 VWTAPAPVCK 320

RESULT 10
US-08-365-470-3
; Sequence 3, Application US/08365470
; Patent No. 5632991
; GENERAL INFORMATION:
; APPLICANT: Gimborne, Jr., Michael A.
; TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
; THEREOF
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,470
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,510
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/850,802
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0627.1350003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-365-470-3

Query Match 40.7%; Score 862; DB 1; Length 610;
Best Local Similarity 52.0%; Pred. No. 1.4e-70;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps

QY 39 WYIHSEKPMWQARRRCRDNRYTDVLAIQKAEIETLEKTPPSRSYIWIIGRIKIGIW 98
DB 22 WSYNSTEAMTYDEASACQQRTHLVAIONKEIEYLNSTLSTSPSYWIGIRKVNWM 81
QY 99 TWVGNKSLTEAEENWGDEPNKKNKEDCEYIIRKNKDAGKKNDDACGKRLAALCYTA 158
DB 82 VWVGNQKRLTEAKNMAGGEPRNNONKDBCEYIIRKKEKDVGMKNDRCSSKKLALCYTA 141
QY 159 SCQPMWSGHGECVEIINNHCTNCNDVGYYGQCOLVTCGCELEAPELGTMDCTHPGNGFS 218

```

[illegible]

```

RESULT 12
5217870-2
: Patent No. 5217870
: APPLICANT: HESSION, CATHERINE A.; LOEB, ROY R.; GOELZ, SUSAN E
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
: NUMBER OF SEQUENCES: 4
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/345,151
: FILING DATE: 28-APR-1989
: SEQ ID NO:2:
: LENGTH: 610
5217870-2
Query Match 40.7%; Score 862; DB 6; Length 610;

```

```

RESULT 12
5217870-2
: Patent No. 5217870
: APPLICANT: HESSION, CATHERINE A.; LOEB, ROY R.; GOELZ, SUSAN E
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
: NUMBER OF SEQUENCES: 4
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/345,151
: FILING DATE: 28-APR-1989
: SEQ ID NO:2:
: LENGTH: 610
5217870-2
Query Match 40.7%; Score 862; DB 6; Length 610;

```

Query Match	38.5%;	Score 814.5;	DB 2;	Length 484;
Best Local Similarity	36.1%;	Pred. No. 2.2e-66;		
Matches 159;	Conservative 55;	Mismatches 109;	Indels 117;	Gaps 7;

```

39 WTYHYSEKPMNWQRRRCFRDNITDVLVAIQNAEIEYLEKTLPEFSRSTYYWIGIRIGGIW 98
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
23 WSYASASTEMTFDDASAYCQQRTHLVAIQNAEIEYLNSTFNYSASTYYWIGIRKINGTW 82

```

99 TWVGINKSLTEEAENMGDGEPPNNKKNKEDCEVEIYIKRNDAGKWNDACHKLKALCYTA 15
 100 ||::|| ||::|| ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 83 TWIGTKKLLTPAATNMAPGEPPNNKQSNEDCEVEIYIKRDKDSGKWNDERCSKKKLLALCYTA 14

139 SCQFMSCGSGHGECEVEIINNNICLVGVGIISVQCQLVLYDEEAEAEISIMDCI
 143 ACTPTSCGSHGECIEFIINNSTCCYPGFRIGCEQVEEDALENPVNGVVTCPQSLPWNT

203 TCAFECKEGFELIGPEHLQCTSSGSGWDGKKPTCKAVTCDTVGHQPQNDVSCNHSIGFEFA 260

263 YKSTCHFTCAEGFGLGPAQIETAGGGWQAPVCAKAVKCPAVSDPKNGLVKFTHTSPG 322

323 EFTYKSCAFSCCEEGELRGSALACTSQGQWTVQEVPSQVQCCSLLEVPREIMNSCSGE 38
331 YNP_LF-----IPVAVMVT----- 34

441 FMTSASFLMLLKRRLKRAK 460

Patent No. 6040428
GENERAL INFORMATION:
APPLICANT: Rollins, Scott

TITLE OF INVENTION: PORCINE E-SELECTIN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESS: 8-4b, 714-1

CITY: New Haven
STATE: Connecticut
COUNTRY: USA

COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/253,403

REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:

TELEFAX: (203) 772-3655
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 484 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA to mRNA
 DESCRIPTION: predicted amino acid sequence of
 DESCRIPTION: Porcine E-selectin
 US-09-276-197-9

Query Match 38.5%; Score 814.5; DB 3; Length 484;
 Best Local Similarity 36.1%; Pred. No. 2.2e-66;
 Matches 159; Conservative 55; Mismatches 109; Indels 117; Gaps 7;

QY 39 WTYHYSEKPMNMQRRRCRDNYTDVAIONKAEIYELEKTLPPSRSYWIGIRKIGIW 98
 DB 23 WSYASSTETMTFPDDASAYCQQRTHLVAIONHAEIETLNSTFNYSASYWIGIRKIGIW 82
 QY 99 TWGNTKSLTEAEENWGDGEPNNKKNKEDCEYIYIKRNKDGKWNDDACHKLAALCYTA 158
 DB 83 TWIGTKKALPPEATNMAPGEPNNKQSNEDCEYIYIKRDKSGKWNDRCSKKLALCYTA 142
 QY 159 SCQPMSCSGHGEVEITNNHTCNDVGYVGPQCLVQCEPLEPELGTMDC----- 211
 DB 143 ACPTSCSGHGEIETINSSTCOCYPPGFRIGQCEQVVECDALNPVGVVTCPSDLPWMT 202
 QY 212 -----HP-----FCNFS 218
 DB 203 TCAPECKEFGELIGPEHLOCTSSGSMGDKKPTCAVTCDVYGHQNDVDVSCNHSIEFA 262
 QY 219 FSSQCAFCSEGNLNGIEETTCGPGCNWSSPEPTQVIOCEPLADLGMNCSH-PLA 277
 DB 263 YKSTCHFTCAEFGIQAIECTAAGQWTOQAAPVCAKAVCPAASQPKNGLVKPTHSPGT 322
 QY 278 SFPTSACTICSEGTFLIKKKTICSSSISWNPSPICQ-----KLKDSFMIEGD 330
 DB 323 EFTYKSSCAFCSEFELRSGAQLACTSGQWTOEVPSCVVOCSLSLEVPREINMSCSG 382
 QY 331 YNPLF-----IPVAVMVT----- 344
 DB 383 --PVFGAVCTFACPEGMLNGSVALTCGATGHSGLPTECAPAESKIPPLAMGLAAGVS 440
 QY 345 -FSGLAFTIWLARRLKKKK 363
 DB 441 FMTSASFLLWLKRLKRRAK 460

RESULT 15
 US-08-274-661B-38
 ; Sequence 38, Application US/08274661B
 ; Patent No. 5593882
 ; GENERAL INFORMATION:
 ; APPLICANT: Erbe, David V.
 ; APPLICANT: Lasky, Laurence A.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Selectin Variants
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/274,661B
 FILING DATE: 13-Jul-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/956701
 FILING DATE: 10/01/1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Dregler, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: 761P1C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-3216
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-274-661B-38

Query Match 31.5%; Score 666; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2e-53;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 WTYHYSEKPMNMQRRRCRDNYTDVAIONKAEIYELEKTLPPSRSYWIGIRKIGIW 98
 DB 1 WTYHYSEKPMNMQRRRCRDNYTDVAIONKAEIYELEKTLPPSRSYWIGIRKIGIW 60
 QY 99 TWGNTKSLTEAEENWGDGEPNNKKNKEDCEYIYIKRNKDGKWNDDACHKLAALC 155
 DB 61 TWGNTKSLTEAEENWGDGEPNNKKNKEDCEYIYIKRNKDGKWNDDACHKLAALC 117

Search completed: October 13, 2001, 02:55:41
 Job time: 719 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:48:44 ; Search time 164.14 Seconds

(Without alignments)
502.786 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116
Sequence: 1 MIFPMKQSTQRDLMNIFKL.....WLARLKKGKSKSMNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_Main:*

1: /cgnl_7/ptodata/1/paa/US06_COMB.pep:*
2: /cgnl_7/ptodata/1/paa/US07_COMB.pep:*
3: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
4: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
5: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
6: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
7: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
8: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
9: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
10: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
11: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
12: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
13: /cgnl_7/ptodata/1/paa/US08_COMB.pep:*
14: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
15: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
16: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
17: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
18: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
19: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
20: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
21: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
22: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*
23: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2116	100.0	372	15	US-09-119-209-2
2	2076	98.1	385	1	PCT-US92-03970-2
3	2076	98.1	385	1	PCT-US94-00909-2
4	2076	98.1	385	7	US-08-008-459-2
5	2076	98.1	385	7	US-08-340-539-2
6	2076	98.1	385	8	US-08-410-569-2
7	1883	89.0	1078	23	US-60-212-659-523
8	1879	88.8	1078	23	US-60-207-315-428
9	1879	88.8	1078	23	US-60-230-435-1751
10	1651	76.0	372	15	US-09-119-209-4

11	905	42.8	830	1	PCT-US94-09395-4
12	905	42.8	830	8	US-08-449-6878-4
13	898	42.4	700	23	US-60-207-315-467
14	862	40.7	610	1	PCT-US99-28965-19
15	862	40.7	610	10	US-08-657-753-2
16	862	40.7	610	11	US-08-770-435-3
17	862	40.7	610	14	US-09-009-490A-89
18	862	40.7	610	16	US-09-266-091A-2
19	862	40.7	610	16	US-09-266-091A-2
20	862	40.7	610	22	US-09-802-640-36
21	666	31.5	119	23	US-60-160-189-8687
22	666	31.5	119	23	US-60-169-867-5823
23	645	30.5	119	23	US-60-160-203-5003
24	645	30.5	119	23	US-60-169-840-6716
25	586	27.7	116	23	US-60-160-189-10011
26	586	27.7	116	23	US-60-160-203-6200
27	586	27.7	116	23	US-60-169-840-9326
28	586	27.7	116	23	US-60-169-867-7998
29	452.5	21.4	129	23	US-60-196-718-4236
30	451.5	21.3	128	23	US-60-195-053-1909
31	451.5	21.3	129	23	US-60-195-053-1908
32	451.5	21.3	138	23	US-60-196-718-4238
33	447.5	21.1	132	23	US-60-196-718-4237
34	416	19.7	112	23	US-60-160-203-3503
35	415.5	19.6	130	23	US-60-196-174-903
36	415	19.6	134	23	US-60-192-739-3226
37	403	19.0	104	23	US-60-160-189-5792
38	389	18.4	115	23	US-60-196-718-3944
39	388	18.3	68	23	US-60-163-123-1859
40	388	18.3	68	23	US-60-163-123-4179
41	283.5	13.4	355	1	PCT-US01-01332-615
42	266	12.6	309	1	PCT-US01-01332-615
43	254	12.0	75	23	US-60-188-162-5010
44	248	11.7	135	23	US-60-196-718-4486
45	247.5	11.7	1124	23	US-60-191-637-1341

ALIGNMENTS

RESULT 1
US-09-119-209-2
Sequence 2, Application US/09119209
GENERAL INFORMATION:
APPLICANT: LASRY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNICK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,209
FILING DATE: 20-Jul-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513278
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 6-MAY-1993

Sequence 4, Appl1
Sequence 4, Appl1
Sequence 467, App
Sequence 19, Appl
Sequence 2, Appl1
Sequence 89, Appl1
Sequence 2, Appl1
Sequence 8687, App
Sequence 5823, App
Sequence 5003, App
Sequence 6716, App
Sequence 10011, A
Sequence 6200, App
Sequence 9326, App
Sequence 7998, App
Sequence 4236, App
Sequence 1909, App
Sequence 1908, App
Sequence 4238, App
Sequence 4237, App
Sequence 3503, App
Sequence 903, App
Sequence 3226, App
Sequence 5792, App
Sequence 3944, App
Sequence 1859, App
Sequence 4179, App
Sequence 1145, App
Sequence 615, App
Sequence 5010, App
Sequence 4486, App
Sequence 1341, App

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0565DLC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-119-209-2

Query Match 100.0%; Score 2116; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 7.6e-177;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGTTCWTHYSEKPMNQARARFCRDN 60
DB 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGTTCWTHYSEKPMNQARARFCRDN 60
QY 61 YTDVAIONKAEIEVLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITFEAENMGDEPN 120
DB 61 YTDVAIONKAEIEVLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITFEAENMGDEPN 120
QY 121 NKKNKEDCEIYIKRNKDGKNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 121 NKKNKEDCEIYIKRNKDGKNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
QY 181 NCDVGYGPOCVIQCPELEAPELGTMDCTHPRGNSFSSQCAFSCSGTNLGIEETT 240
DB 181 NCDVGYGPOCVIQCPELEAPELGTMDCTHPRGNSFSSQCAFSCSGTNLGIEETT 240
QY 241 CGPFGNWSPEPTQVIOCEPLASAPDLGIMNCSHPLASFSFTSACFTICSEGTLLIGKK 300
DB 241 CGPFGNWSPEPTQVIOCEPLASAPDLGIMNCSHPLASFSFTSACFTICSEGTLLIGKK 300
QY 301 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 360
DB 301 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 360
QY 361 GKSKSRMNDPY 372
DB 361 GKSKSRMNDPY 372

RESULT 2
PCT-US92-03970-2

Sequence 2, Application PC/TUS9203970
GENERAL INFORMATION:
APPLICANT: Dana-Farber Cancer Institute, Inc.
TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
NUMBER OF INVENTIONS: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03970
FILING DATE: 19920513
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: DFCI-152Bq9
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
TELEX: 940675
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
PCT-US92-03970-2

Query Match 98.1%; Score 2076; DB 1; Length 385;
Best Local Similarity 98.1%; Pred. No. 2.6e-173;

Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGTTCWTHYSEKPMNQARARFCRDN 60
DB 14 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGTTCWTHYSEKPMNQARARFCRDN 73
QY 61 YTDVAIONKAEIEVLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITFEAENMGDEPN 120
DB 74 YTDVAIONKAEIEVLEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITFEAENMGDEPN 133
QY 121 NKKNKEDCEIYIKRNKDGKNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 134 NKKNKEDCEIYIKRNKDGKNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 193
QY 181 NCDVGYGPOCVIQCPELEAPELGTMDCTHPRGNSFSSQCAFSCSGTNLGIEETT 240
DB 194 NCDVGYGPOCVIQCPELEAPELGTMDCTHPRGNSFSSQCAFSCSGTNLGIEETT 253
QY 241 CGPFGNWSPEPTQVIOCEPLASAPDLGIMNCSHPLASFSFTSACFTICSEGTLLIGKK 300
DB 254 CGPFGNWSPEPTQVIOCEPLASAPDLGIMNCSHPLASFSFTSACFTICSEGTLLIGKK 313
QY 301 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 360
DB 314 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 373
QY 361 GKSKSRMNDPY 372
DB 374 GKSKSRMNDPY 385

RESULT 3
PCT-US94-00909-2

Sequence 2, Application PC/TUS9400909
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING
NUMBER OF INVENTIONS: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00909
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/962,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730,503
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-00909-2

```

Query Match 98.1%; Score 2076; DB 1; Length 385;

Best Local Similarity 98.1%; Pred. No. 2.6e-173; Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MIFPMKCGSTORDLNMIFKLMGWTMLCCDFLAHNGTYCWTYHSEKPMNQARARPCRDN 60
DB 14 MIFPMKCGSTORDLNMIFKLMGWTMLCCDFLAHNGTYCWTYHSEKPMNQARARPCRDN 73
QY 61 YTDLVAIQNKAIEYLELEKTLPSRSYYWIGIRKIGIWTWGTNKSITJEEAENMGDEPN 120
DB 74 YTDLVAIQNKAIEYLELEKTLPSRSYYWIGIRKIGIWTWGTNKSITJEEAENMGDEPN 133
QY 121 NKKNKEDCEVIYIKRNKDAGKWDNDACHKALKALCYTASQPMSCSGHGCVEIINNHTC 180
DB 134 NKKNKEDCEVIYIKRNKDAGKWDNDACHKALKALCYTASQPMSCSGHGCVEIINNHTC 193
QY 181 NCDVGYGPOCOVIOCEPLEAPDLGTMDCIHPFGNFSFSCAFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCOVIOCEPLEAPDLGTMDCIHPFGNFSFSCAFSCSEGTNLGIEETT 253
QY 241 CGPFGMSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTICSEGTNLGIEETT 300
DB 254 CGPFGMSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFTICSEGTNLGIEETT 313
QY 301 TICSEGGINSNPSPICOKLDKSFMSIKEDGYNLFIPVAVMTAFSGSLATIMLARLKK 360
DB 314 TICSEGGINSNPSPICOKLDKSFMSIKEDGYNLFIPVAVMTAFSGSLATIMLARLKK 373
QY 361 GKSKRSMDPY 372
DB 374 GKSKRSMDPY 385

```

RESULT 4

```

; US-08-008-459-2
; Sequence 2, Application US/08008459
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,459
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730,503
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-318XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; TELEX: 940675
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-008-459-2

```

Query Match 98.1%; Score 2076; DB 4; Length 385;

Best Local Similarity 98.1%; Pred. No. 2.6e-173; Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MIFPMKCGSTORDLNMIFKLMGWTMLCCDFLAHNGTYCWTYHSEKPMNQARARPCRDN 60
DB 14 MIFPMKCGSTORDLNMIFKLMGWTMLCCDFLAHNGTYCWTYHSEKPMNQARARPCRDN 73
QY 61 YTDLVAIQNKAIEYLELEKTLPSRSYYWIGIRKIGIWTWGTNKSITJEEAENMGDEPN 120
DB 74 YTDLVAIQNKAIEYLELEKTLPSRSYYWIGIRKIGIWTWGTNKSITJEEAENMGDEPN 133
QY 121 NKKNKEDCEVIYIKRNKDAGKWDNDACHKALKALCYTASQPMSCSGHGCVEIINNHTC 180
DB 134 NKKNKEDCEVIYIKRNKDAGKWDNDACHKALKALCYTASQPMSCSGHGCVEIINNHTC 193
QY 181 NCDVGYGPOCOVIOCEPLEAPDLGTMDCIHPFGNFSFSCAFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCOVIOCEPLEAPDLGTMDCIHPFGNFSFSCAFSCSEGTNLGIEETT 253

```

QY 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSPHPLASFSTACTFICSGTELLIGKK 300
DB 254 CEPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSPHPLASFSTACTFICSGTELLIGKK 313
QY 301 TICSSGIMSNPSPIQOKLDRFSMIKEDYNPLFIPVAVWTAFFSGIAFIIMLARLKK 360
DB 314 TICSSGIMSNPSPIQOKLDRFSMIKEDYNPLFIPVAVWTAFFSGIAFIIMLARLKK 373
QY 361 GKSKSRMNDPY 372
DB 374 GKSKSRMNDPY 385

RESULT 5
US-08-340-539-2
; Sequence 2, Application US/08340539
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730,503
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-318XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2280
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids

QY 1 MIFPMKQSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTYHSKPMNMOBARRECCDN 60
DB 14 MIFPMKQSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTYHSKPMNMOBARRECCDN 73
QY 61 YTDLVAIQKAEILEYLEKTLFPRSRYWYIGIRKIGIWTWGTNKSLTDEANMWDGEPN 120
DB 74 YTDLVAIQKAEILEYLEKTLFPRSRYWYIGIRKIGIWTWGTNKSLTDEANMWDGEPN 133
QY 121 NKNKEDCEYIYIKRKDKGKNNDACHKLAALCYTASCCPWSGSGEVEIINNHTC 180
DB 134 NKNKEDCEYIYIKRKDKGKNNDACHKLAALCYTASCCPWSGSGEVEIINNHTC 193
QY 181 NCDVGYGPOCOLVIOCEPLSAPDLGIMNCSPHPLASFSTACTFICSGTELLIGKK 240
DB 194 NCDVGYGPOCOLVIOCEPLSAPDLGIMNCSPHPLASFSTACTFICSGTELLIGKK 253
QY 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSPHPLASFSTACTFICSGTELLIGKK 300
DB 254 CEPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSPHPLASFSTACTFICSGTELLIGKK 313
QY 301 TICSSGIMSNPSPIQOKLDRFSMIKEDYNPLFIPVAVWTAFFSGIAFIIMLARLKK 360
DB 314 TICSSGIMSNPSPIQOKLDRFSMIKEDYNPLFIPVAVWTAFFSGIAFIIMLARLKK 373
QY 361 GKSKSRMNDPY 372
DB 374 GKSKSRMNDPY 385

Query Match 98.1%; Score 2076; DB 7; Length 385;
Best Local Similarity 98.1%; Pred. No. 2,6e-173;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-340-539-2

RESULT 6
US-08-410-569-2
; Sequence 2, Application US/08410569
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: LEUKOCYTE ADHESION MOLECULE-1 (LAM-1)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,569
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCG-152EX

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
TELEX: 940675
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-410-569-2

Query Match 98.1%; Score 2076; DB 8; Length 385;
Best Local Similarity 98.1%; Pred. No. 2,6e-173;

Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MIFPMKCGSTORDLMIIFKLGWMTLCDEPLAHGTYCWTYHYSEKPMNQARARFCRDN 60
DB 14 MIFPMKCGSTORDLMIIFKLGWMTLCDEPLAHGTYCWTYHYSEKPMNQARARFCRDN 73
OY 61 YTDLVAIQNKAEIYLEKTLPEFSRSYYWIGIRKIGIWTWVGNKSLTEEAENMGDEPN 120
DB 74 YTDLVAIQNKAEIYLEKTLPEFSRSYYWIGIRKIGIWTWVGNKSLTEEAENMGDEPN 133
OY 121 NKKNKEDCEIYIKRKNKDGKWDACCHKLKAALCYTASQCPMSSGSGHGCVELINNHTC 180
DB 134 NKKNKEDCEIYIKRKNKDGKWDACCHKLKAALCYTASQCPMSSGSGHGCVELINNHTC 193
OY 181 NCDVGYGQCOQVIOCEPLEAELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETT 240
DB 194 NCDVGYGQCOQVIOCEPLEAELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETT 253
OY 241 CGEFGMWSSEPTQVIOCEPLSAPDLGIMNCSPPLASFSTACIFICEGTGLGKKK 300
DB 254 CGEFGMWSSEPTQVIOCEPLSAPDLGIMNCSPPLASFSTACIFICEGTGLGKKK 313
OY 301 TICSEGIINSNPSPICOKLDKSFSAIKEGDYNLFIPVAVMTAFSGLAFTIILARLKK 360
DB 314 TICSEGIINSNPSPICOKLDKSFSAIKEGDYNLFIPVAVMTAFSGLAFTIILARLKK 373
OY 361 GKSKRSMDPY 372
DB 374 GKSKRSMDPY 385

RESULT 7

US-60-212-659-523
Sequence 523, Application US/60212659

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: C1000674
CURRENT APPLICATION NUMBER: US/60/212,659
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 879
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 523
LENGTH: 1078
TYPE: PRT
ORGANISM: HUMAN
US-60-212-659-523

Query Match 89.0%; Score 1883; DB 23; Length 1078;
Best Local Similarity 97.4%; Pred. No. 7,8e-156;

Matches 336; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 22 GWTMLCCDFLAHNGTYCWTYHYSEKPMNQARARFCRDNTDVAIQNKAEIYLEKTL 81
DB 604 GYFLPSKDFLAHNGTYCWTYHYSEKPMNQARARFCRDNTDVAIQNKAEIYLEKTL 663

OY 82 FSRSYWIGIRKIGIWTWVGNKSLTEEAENMGDEPNKKKNEKDCVEIYIKRNDAGK 141
DB 664 FSRSYWIGIRKIGIWTWVGNKSLTEEAENMGDEPNKKKNEKDCVEIYIKRNDAGK 723
OY 142 WNDACCHKLKAALCYTASCPMSSGSGHGCVEIINNHTCNDVGYGQCOQVIOCEPLE 201
DB 724 WNDACCHKLKAALCYTASCPMSSGSGHGCVEIINNHTCNDVGYGQCOQVIOCEPLE 783
OY 202 APELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEETGCPFGMWSSEPTQVIOCEP 261
DB 784 APELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEETGCPFGMWSSEPTQVIOCEP 843
OY 262 LSAPDLGIMNCSPPLASFSTACTFICSEGTNLGIEETGCKKTCSSGIWNSPPTCOKLDK 321
DB 844 LSAPDLGIMNCSPPLASFSTACTFICSEGTNLGIEETGCKKTCSSGIWNSPPTCOKLDK 903
OY 322 SFSMIKEDYNPLFIPIVAVMTAFSGLAFTIILARLKKKKSKR 366
DB 904 SFSMIKEDYNPLFIPIVAVMTAFSGLAFTIILARLKKKKSKR 948

RESULT 8

US-60-207-315-428
Sequence 428, Application US/60207315

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: C1000601
CURRENT APPLICATION NUMBER: US/60/207,315
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 528
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 428
LENGTH: 1078
TYPE: PRT
ORGANISM: HUMAN
US-60-207-315-428

Query Match 88.8%; Score 1879; DB 23; Length 1078;
Best Local Similarity 97.1%; Pred. No. 1,7e-155;

Matches 335; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 22 GWTMLCCDFLAHNGTYCWTYHYSEKPMNQARARFCRDNTDVAIQNKAEIYLEKTL 81
DB 604 GYFLPSKDFLAHNGTYCWTYHYSEKPMNQARARFCRDNTDVAIQNKAEIYLEKTL 663
OY 82 FSRSYWIGIRKIGIWTWVGNKSLTEEAENMGDEPNKKKNEKDCVEIYIKRNDAGK 141
DB 664 FSRSYWIGIRKIGIWTWVGNKSLTEEAENMGDEPNKKKNEKDCVEIYIKRNDAGK 723
OY 142 WNDACCHKLKAALCYTASCPMSSGSGHGCVEIINNHTCNDVGYGQCOQVIOCEPLE 201
DB 724 WNDACCHKLKAALCYTASCPMSSGSGHGCVEIINNHTCNDVGYGQCOQVIOCEPLE 783
OY 202 APELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEETGCPFGMWSSEPTQVIOCEP 261
DB 784 APELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEETGCPFGMWSSEPTQVIOCEP 843
OY 262 LSAPDLGIMNCSPPLASFSTACTFICSEGTNLGIEETGCKKTCSSGIWNSPPTCOKLDK 321
DB 844 LSAPDLGIMNCSPPLASFSTACTFICSEGTNLGIEETGCKKTCSSGIWNSPPTCOKLDK 903
OY 322 SFSMIKEDYNPLFIPIVAVMTAFSGLAFTIILARLKKKKSKR 366
DB 904 SFSMIKEDYNPLFIPIVAVMTAFSGLAFTIILARLKKKKSKR 948

RESULT 9

US-60-230-435-1751

```
; Sequence 1751, Application US/60230435
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: US$ THEREOF
; FILE REFERENCE: CL000768
; CURRENT APPLICATION NUMBER: US/60/230,435
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 2991
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1751
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: HUMAN
; US-60-230-435-1751

Query Match      88.8%; Score 1879; DB 23; Length 1078;
Best Local Similarity 97.1%; Pred. No. 1.7e-155;
Matches 335; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 22 GWMMLCCDFLAHGTCTWTHYSEKPMNQRARFCNDNTDLVAIONKAEIYELKTLR 81
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 604 GYFLPSKDFLAHGTCTWTHYSEKPMNQRARFCNDNTDLVAIONKAEIYELKTLR 663

QY 82 FSRSYWIGIRKIGITWVGTNKSLEEAENMGDEPNKKKEDCEVEIYIRKNDAGK 141
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 664 FSRSYWIGIRKIGITWVGTNKSLEEAENMGDEPNKKKEDCEVEIYIRKNDAGK 723

QY 142 WNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTCNDGVYGPQCQLVIOCEPLE 201
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 724 WNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTCNDGVYGPQCQLVIOCEPLE 783

QY 202 APELGTMDCTHPRGNSFSSQCAFSCSEGNLTGIEBETCGPRGNMSPPTQVIOCEP 261
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 784 APELGTMDCTHPRGNSFSSQCAFSCSEGNLTGIEBETCGPRGNMSPPTQVIOCEP 843

QY 262 LSAADGIMNCSHPLASFSTSACTFICSEGTLLKKTICSSGSIWNSPFCOKLKD 321
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 844 LSAADGIMNCSHPLASFSTSACTFICSEGTLLKKTICSSGSIWNSPFCOKLKD 903

QY 322 SFSMIKESGYNPLFIYAVAVMTAFSLAFTIWLARLKKGKSKR 366
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 904 SFSMIKESGYNPLFIYAVAVMTAFSLAFTIWLARLKKGKSKR 948

RESULT 10
US-09-119-209-4
; Sequence 4, Application US/09119209
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNOCK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,209
; FILING DATE: 20-Jul-1998
```

```
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513278
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 6-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0565D1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-119-209-4
```

```
Query Match      78.0%; Score 1651; DB 15; Length 372;
Best Local Similarity 76.1%; Pred. No. 4.9e-136;
Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;
```

```
QY 1 MPEPMKOSTQDQIDNINIFLMGWTMLCCDFLAHGTCTWTHYSEKPMNQRARFCNDN 60
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MPEPMKOSTQDQIDNINIFLMGWTMLCCDFLAHGTCTWTHYSEKPMNQRARFCNDN 60

QY 61 YNDVAIONKAEIYELKTLRPFSSRYWIGIRKIGITWVGTNKSLEEAENMGDEPN 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 YNDVAIONKAEIYELKTLRPFSSRYWIGIRKIGITWVGTNKSLEEAENMGDEPN 120

QY 121 NKKKEDCEVEIYIRKNDAGKNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 NKKKEDCEVEIYIRKNDAGKNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180

QY 181 NCDVYGPQCQLVIOCEPLEAPELGTMDCTHPRGNSFSSQCAFSCSEGNLTGIEBET 240
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 NCDVYGPQCQLVIOCEPLEAPELGTMDCTHPRGNSFSSQCAFSCSEGNLTGIEBET 240

QY 241 CGPFGNMSPEPTQVIOCEPLSAADGIMNCSHPLASFSTSACTFICSEGTLLKKTIC 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 CGPFGNMSPEPTQVIOCEPLSAADGIMNCSHPLASFSTSACTFICSEGTLLKKTIC 300

QY 301 TICSSGSIWNSPFCOKLKDSSFSMIKESGYNPLFIYAVAVMTAFSLAFTIWLARLKK 360
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 TICSSGSIWNSPFCOKLKDSSFSMIKESGYNPLFIYAVAVMTAFSLAFTIWLARLKK 360

QY 361 GKSKRSYNDPY 372
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 GKSKRSYNDPY 372
```

```
RESULT 11
PCT-US94-09395-4
; Sequence 4, Application PC/TUS9409395
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: Expression Control Sequences of the P-Selectin Gene
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patra L. Rabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: GA
```

```

; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09395
; FILING DATE: 19-AUG-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 830 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US94-09395-4

Query Match          42.8%; Score 905; DB 1; Length 830;
Best Local Similarity 50.6%; Pred. No. 3,8e-70;
Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0;

QY 8 OSTQDRLMNIFFKLMGTMCLCCDFLAHHGTCWYHYSEKPMNORARRCRDNYTDLVAI 67
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 ORQDRAVFGISQLCSFALSISLSELTNOEVAMTYHSTKAYSNMISKYQCNRTYDVAI 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 ONKAEIYELEKTLPEFSRSYWGIRKIGIMTWGYNKSLTEEAEMNGDEPNKKKKED 127
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 QNNNEIDYLNKVLPIYSSTYWGIRKNNKTWTWGTAKALTNEAEMNADNEPNKKRNED 130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 CVELIYIKRNKDGKWDNDACHKLKALCYTASCPMSSGSGHGEVLEIINNHTCNDVGY 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131 CVELIYIKSPAPGKWNDEHCLKKHALCYTASQDMSCSKQGELEIIGNYTCSCYPGFY 190
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 188 GPCCQVLYQCEPLAEPLGMDCTHPPGNFSSQCAFSCSEGTNLGIEETTCGPGGNW 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 191 GPCEVYREGCELELPQHYLMNCSHPLGNFSQCSFHCITDGYQVNGPSKLECLASGIW 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 248 SSPEPTQVLYQCEPLASAPDLGIMNCSHPLASFSTSACTFICSEGTLEIGKKKTTICSSG 307
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 251 TNKPPQCLAAQCPLKIPERGNMICHSAKAFQHOSSCSFCEGFLVGPVVOCTASG 310
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 308 IWSNPSPIQ 317
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 311 VWTAPAPVCK 320
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-08-449-687B-4
; Sequence 4, Application US/08449687B
; GENERAL INFORMATION:
; APPLICANT: McEever, Rodger P.
; APPLICANT: Pan, Junliang
; TITLE OF INVENTION: Expression Control Sequences of the
; TITLE OF INVENTION: P-Selection Gene
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,687B
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,158
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA: US 07/320,408
; APPLICATION NUMBER: 08-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 830 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-449-687B-4

Query Match          42.8%; Score 905; DB 8; Length 830;
Best Local Similarity 50.6%; Pred. No. 3,8e-70;
Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0;

QY 8 OSTQDRLMNIFFKLMGTMCLCCDFLAHHGTCWYHYSEKPMNORARRCRDNYTDLVAI 67
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 ORQDRAVFGISQLCSFALSISLSELTNOEVAMTYHSTKAYSNMISKYQCNRTYDVAI 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 ONKAEIYELEKTLPEFSRSYWGIRKIGIMTWGYNKSLTEEAEMNGDEPNKKKKED 127
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 QNNNEIDYLNKVLPIYSSTYWGIRKNNKTWTWGTAKALTNEAEMNADNEPNKKRNED 130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 CVELIYIKRNKDGKWDNDACHKLKALCYTASCPMSSGSGHGEVLEIINNHTCNDVGY 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131 CVELIYIKSPAPGKWNDEHCLKKHALCYTASQDMSCSKQGELEIIGNYTCSCYPGFY 190
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 188 GPCCQVLYQCEPLAEPLGMDCTHPPGNFSSQCAFSCSEGTNLGIEETTCGPGGNW 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 191 GPCEVYREGCELELPQHYLMNCSHPLGNFSQCSFHCITDGYQVNGPSKLECLASGIW 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 248 SSPEPTQVLYQCEPLASAPDLGIMNCSHPLASFSTSACTFICSEGTLEIGKKKTTICSSG 307
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 251 TNKPPQCLAAQCPLKIPERGNMICHSAKAFQHOSSCSFCEGFLVGPVVOCTASG 310
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 308 IWSNPSPIQ 317
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 311 VWTAPAPVCK 320
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-60-207-315-467
; Sequence 467, Application US/60207315
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USFS THEREOF
; FILE REFERENCE: CLO00601
; CURRENT APPLICATION NUMBER: US/60/207,315
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 528
; SOFTWARE: FastSeq for Windows Version 4.0
```


SEQ ID NO 467
LENGTH: 700
TYPE: PRT
ORGANISM: HUMAN
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(700)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-207-315-467

Query Match 42.4%; Score 898; DB 23; Length 700;
Best Local Similarity 54.1%; Pred. No. 1.3e-69;
Matches 151; Conservative 41; Mismatches 87; Indels 0; Gaps 0;

QY 39 WYHYSEKPMNQARARFCRDNTDLVAIONKAEIEYLEKTLPEFSRYWIGIRKIGIW 98
DB 34 WYHYSTKAVSMWISKYCONRTDVLAIQNKKEIDYLNKLVLYSSYWIIGIRKNNKTW 93
QY 99 TWGTVNKSILTEEAENWGDEPNKKKEDCEVEIYIKRNKDGAKWMDACHKRLKALCYTA 158
DB 94 TWGTVNKSILTEEAENWGDEPNKKKEDCEVEIYIKRNKDGAKWMDACHKRLKALCYTA 153
QY 159 SCQPMSCSGHGECEVETINNHTCNCVDVYGPQCQVLYIOCEPLAPDLGIMNCSHPLAS 218
DB 154 SCQDMSCSKQGECELETIGHYTSCYGPFGYCEVEYREGCELETLPQHVLMNCSHPLGNS 213
QY 219 FSSQCAFSCSEGTNLGIEETTCGPRGNMSSPEPTCOVYIOCEPLAPDLGIMNCSHPLAS 278
DB 214 FNSQCFHCTDGTQVQPSKLECLASGIWTKPKPCLAAQCPKLIPKGNMTCILHSARA 273
QY 279 FFSFTSACFTICSEGTLEIKKTKTICSSGSIWNSPFIQ 317
DB 274 FQHSSCSFSCGEGFALVPEVYQCTASGVWTAAPAVCK 312

RESULT 14
PCT-US99-28965-19
Sequence 19, Application PC/TUS9928965
GENERAL INFORMATION:
APPLICANT: Monita, Brett P.
APPLICANT: Xu, Xiaoxing S.
APPLICANT: Isis Pharmaceuticals, Inc.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
FILE REFERENCE: ISPH-0424
CURRENT APPLICATION NUMBER: PCT/US99/28965
CURRENT FILING DATE: 1999-12-08
EARLIER APPLICATION NUMBER: US 09/209,668
EARLIER FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 610
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-28965-19

Query Match 40.7%; Score 862; DB 1; Length 610;
Best Local Similarity 52.0%; Pred. No. 1.6e-66;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps 0;

QY 39 WYHYSEKPMNQARARFCRDNTDLVAIONKAEIEYLEKTLPEFSRYWIGIRKIGIW 98
DB 22 WYHYSTKAVSMWISKYCONRTDVLAIQNKKEIDYLNKLVLYSSYWIIGIRKNNKTW 81
QY 99 TWGTVNKSILTEEAENWGDEPNKKKEDCEVEIYIKRNKDGAKWMDACHKRLKALCYTA 158
DB 82 WYHYSTKAVSMWISKYCONRTDVLAIQNKKEIDYLNKLVLYSSYWIIGIRKNNKTW 141
QY 159 SCQPMSCSGHGECEVETINNHTCNCVDVYGPQCQVLYIOCEPLAPDLGIMNCSHPLAS 218
DB 154 SCQDMSCSKQGECELETIGHYTSCYGPFGYCEVEYREGCELETLPQHVLMNCSHPLGNS 213

DB 142 ACTNCSGHECEVETINNHTCNCVDVYGPQCQVLYIOCEPLAPDLGIMNCSHPLAS 201
QY 219 FSSQCAFSCSEGTNLGIEETTCGPRGNMSSPEPTCOVYIOCEPLAPDLGIMNCSHPLAS 278
DB 202 YNSCSISCDRGYLPSSMETMOCSGEMSAPIPCNVCEADAVTPANGVEYECFONPGS 261
QY 279 FFSFTSACFTICSEGTLEIKKTKTICSSGSIWNSPFIQ 317
DB 262 FFWNTCTCFDCEGFEFLMGAQSLQCTSSGNMNDNEKPTCK 300

RESULT 15
US-08-657-753-2
Sequence 2, Application US/08657753
GENERAL INFORMATION:

APPLICANT: Klimuk, Sandra K.
APPLICANT: Sample, Sean C.
APPLICANT: Scherrier, Peter
APPLICANT: Hope, Michael J.
TITLE OF INVENTION: Enhanced Efficacy of Liposomal Antisense
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,753
FILING DATE: Not yet assigned
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 16303-003600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-657-753-2

Query Match 40.7%; Score 862; DB 10; Length 610;
Best Local Similarity 52.0%; Pred. No. 1.6e-66;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps 0;

QY 39 WYHYSEKPMNQARARFCRDNTDLVAIONKAEIEYLEKTLPEFSRYWIGIRKIGIW 98
DB 22 WYHYSTKAVSMWISKYCONRTDVLAIQNKKEIDYLNKLVLYSSYWIIGIRKNNKTW 81
QY 99 TWGTVNKSILTEEAENWGDEPNKKKEDCEVEIYIKRNKDGAKWMDACHKRLKALCYTA 158
DB 82 WYHYSTKAVSMWISKYCONRTDVLAIQNKKEIDYLNKLVLYSSYWIIGIRKNNKTW 141
QY 159 SCQPMSCSGHGECEVETINNHTCNCVDVYGPQCQVLYIOCEPLAPDLGIMNCSHPLAS 218
DB 142 ACTNCSGHECEVETINNHTCNCVDVYGPQCQVLYIOCEPLAPDLGIMNCSHPLAS 201
QY 219 FSSQCAFSCSEGTNLGIEETTCGPRGNMSSPEPTCOVYIOCEPLAPDLGIMNCSHPLAS 278
DB 202 YNSCSISCDRGYLPSSMETMOCSGEMSAPIPCNVCEADAVTPANGVEYECFONPGS 261

OY 279 FSFTSACTFICSEGTLLIGKKRTICESSGIWSNPICQ 317
| : : ||| | ||| : | ||| | | :
Db 262 FPMWTCTCTFDCEBGFELMGAQSLQCTSSGNMNDNEKPTCK 300

Search completed: October 13, 2001, 02:58:37
Job time: 593 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:54:07 ; Search time 52.07 Seconds

(without alignments)
355.184 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKQSTQORDLNMIFKLMGWTMLCCDFLAHHGTYHSEKPMNQARFCRDN 372

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 329605 seqs, 49716248 residues

Total number of hits satisfying chosen parameters: 329605

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents, AA, New: *
1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2094	99.0	382	5	US-09-760-475-2123
2	2090	98.8	372	1	PCT-US01-26675-3
3	1807	85.4	341	5	US-09-758-449-1158
4	1807	85.4	341	5	US-09-760-443-1328
5	999	47.2	184	5	US-09-760-443-1337
6	999	47.2	184	5	US-09-760-475-3252
7	862	40.7	610	5	US-09-784-356-122
8	473	22.4	196	5	US-09-760-498-916
9	283.5	13.4	355	5	US-09-764-902-1145
10	274.5	13.0	208	5	US-09-760-475-2126
11	270	12.8	207	5	US-09-760-443-1321
12	270	12.8	207	5	US-09-760-498-920
13	270	12.8	207	5	US-09-760-475-3255
14	266	12.6	309	5	US-09-764-875-615
15	246.5	11.6	3571	5	US-09-811-842-2
16	239	11.3	3594	5	US-09-911-842-4
17	222	10.5	138	5	US-09-764-875-938
18	222	10.5	138	5	US-09-764-902-1688
19	183	8.6	326	5	US-09-787-192-11
20	183	8.6	328	5	US-09-787-192-2
21	183	8.6	333	5	US-09-764-870-279
22	172	8.1	1929	1	PCT-US01-08631-30462
23	172	8.1	2039	1	PCT-US01-08631-30466
24	172	8.1	2489	5	US-09-911-842-5
25	170	8.0	404	5	US-09-891-894-1
26	170	8.0	404	6	US-60-300-971-1
27	168	7.9	1139	5	US-09-764-893-102

28	168	7.9	1139	5	US-09-764-853-634	Sequence 634, App
29	168	7.9	1139	5	US-09-764-875-873	Sequence 873, App
30	168	7.9	1139	5	US-09-764-881-99	Sequence 99, App1
31	168	7.9	1139	5	US-09-764-898-204	Sequence 204, App1
32	166	7.8	1184	1	PCT-US01-08631-51085	Sequence 51085, A
33	165.5	7.8	1479	5	US-09-918-715-305	Sequence 305, App
34	164	7.8	330	5	US-09-545-551A-14	Sequence 14, App1
35	162	7.7	1722	5	US-09-194-612A-1	Sequence 1, App1
36	162	7.7	1740	1	PCT-US01-08631-53205	Sequence 53205, A
37	161	7.6	1479	5	US-09-918-715-238	Sequence 238, App
38	160	7.6	130	5	US-09-760-443-870	Sequence 870, App
39	158.5	7.5	470	5	US-09-760-475-2121	Sequence 2121, App
40	158	7.5	497	5	US-09-764-893-125	Sequence 125, App
41	158	7.5	487	5	US-09-764-853-816	Sequence 816, App
42	158	7.5	487	5	US-09-764-875-1154	Sequence 1154, App
43	158	7.5	497	5	US-09-764-881-157	Sequence 157, App
44	158	7.5	497	5	US-09-764-898-276	Sequence 276, App
45	156.5	7.4	1637	1	PCT-US01-08656-9868	Sequence 9868, App

ALIGNMENTS

RESULT 1
US-09-760-475-2123
; Sequence 2123, Application US/09760475
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT249
; CURRENT APPLICATION NUMBER: US/09/760,475
; Prior application data removed - consult PAAI or file wrapper
; NUMBER OF SEQ ID NOS: 4122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2123
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-760-475-2123

Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
1	99.0%	2094	382	99.2%	1.6e-169	1	2	0
11	85.4%	1807	341	85.4%	1.6e-169	1	2	0
61	47.2%	999	184	47.2%	1.6e-169	1	2	0
71	40.7%	862	610	40.7%	1.6e-169	1	2	0
121	22.4%	473	196	22.4%	1.6e-169	1	2	0
131	13.4%	283.5	355	13.4%	1.6e-169	1	2	0
181	8.6%	183	326	8.6%	1.6e-169	1	2	0
241	11.6%	246.5	3571	11.6%	1.6e-169	1	2	0
301	8.1%	172	1929	8.1%	1.6e-169	1	2	0
311	8.1%	172	2039	8.1%	1.6e-169	1	2	0
361	8.0%	170	404	8.0%	1.6e-169	1	2	0
371	7.9%	168	1139	7.9%	1.6e-169	1	2	0

```
RESULT 2
PCT-US01-26675-3
; Sequence 3, Application PCT/US0126675
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Allison E
; APPLICANT: Bieglecki, Katryn M
; APPLICANT: Kilem, Stefanie E
; APPLICANT: Koshiy, Beena
; APPLICANT: Kumar, Anant Madan
; TITLE OF INVENTION: HAPLOTYPES OF THE SELL GENE
; FILE REFERENCE: SELL MWH1116-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/26675
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,262
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-26675-3

Query Match          98.8%; Score 2090; DB 1; Length 372;
Best Local Similarity 98.9%; Pred. No. 3.5e-169;
Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKOSTORDLNNIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRECRDN 60
DB 1 MIFPMKOSTORDLNNIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRECRDN 60
QY 61 YTDLVAIQKAEIEYLEKTLFPSRSYTWIGIRKIGIWTWGTNKSLTBEAENMGDGEFN 120
DB 61 YTDLVAIQKAEIEYLEKTLFPSRSYTWIGIRKIGIWTWGTNKSLTBEAENMGDGEFN 120
QY 121 NKKNKEDCEIYIKRKNKDGKNNDDACHKLAALCTYASCQPMSCSGHGECEIINNHTC 180
DB 121 NKKNKEDCEIYIKRKNKDGKNNDDACHKLAALCTYASCQPMSCSGHGECEIINNHTC 180
QY 181 NCDVGYGPOCOLVIOCEPLEAPELGTMDCTHPFGNFSFSSOCARFSCSGTNTGIEETT 240
DB 181 NCDVGYGPOCOLVIOCEPLEAPELGTMDCTHPFGNFSFSSOCARFSCSGTNTGIEETT 240
QY 241 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTETLIGKKK 300
DB 241 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTETLIGKKK 300
QY 301 TICSESGIMSNSPICQIKDKSFSMTKEGDYNPLFPVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSESGIMSNSPICQIKDKSFSMTKEGDYNPLFPVAVMTAFSGLAFTIWLARLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372

RESULT 3
US-09-758-449-1158
; Sequence 1158, Application US/09758449
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM026
; CURRENT APPLICATION NUMBER: US/09/758,449
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
```

```
; NUMBER OF SEQ ID NOS: 1478
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1158
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-449-1158
```

```
Query Match          85.4%; Score 1807; DB 5; Length 341;
Best Local Similarity 98.7%; Pred. No. 2.9e-145;
Matches 313; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 MIFPMKOSTORDLNNIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRECRDN 60
DB 23 MIFPMKOSTORDLNNIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRECRDN 82
QY 61 YTDLVAIQKAEIEYLEKTLFPSRSYTWIGIRKIGIWTWGTNKSLTBEAENMGDGEFN 120
DB 83 YTDLVAIQKAEIEYLEKTLFPSRSYTWIGIRKIGIWTWGTNKSLTBEAENMGDGEFN 142
QY 121 NKKNKEDCEIYIKRKNKDGKNNDDACHKLAALCTYASCQPMSCSGHGECEIINNHTC 180
DB 143 NKKNKEDCEIYIKRKNKDGKNNDDACHKLAALCTYASCQPMSCSGHGECEIINNHTC 202
QY 181 NCDVGYGPOCOLVIOCEPLEAPELGTMDCTHPFGNFSFSSOCARFSCSGTNTGIEETT 240
DB 203 NCDVGYGPOCOLVIOCEPLEAPELGTMDCTHPFGNFSFSSOCARFSCSGTNTGIEETT 262
QY 241 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTETLIGKKK 300
DB 263 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTETLIGKKK 322
QY 301 TICSESGIMSNSPICQ 317
DB 323 TICSESGIMSNSPICQ 339
```

```
RESULT 4
US-09-760-443-1328
; Sequence 1328, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ212
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1328
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-443-1328
```

```
Query Match          85.4%; Score 1807; DB 5; Length 341;
Best Local Similarity 98.7%; Pred. No. 2.9e-145;
Matches 313; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKOSTORDLNNIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRECRDN 60
DB 23 MIFPMKOSTORDLNNIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRECRDN 82
```

QY	61	YTDVAALONKAEIYELKTLPEFSRXYWIGIRKIGIWTWGTNRKSLTEEAENMGDEPN	120
Db	83	YTDVAALONKAEIYELKTLPEFSRXYWIGIRKIGIWTWGTNRKSLTEEAENMGDEPN	142
QY	121	NKKKKEDCEVEIYIKRNKDAGKWNDDACHLKAALCYTASQCPMSCSGHGECVELIINHTC	180
Db	143	NKKKKEDCEVEIYIKRNKDAGKWNDDACHLKAALCYTASQCPMSCSGHGECVELIINHTC	202
QY	181	NCDDVGYGPOCOALYIOCEPLAEPLGIMDCMHPREGNFSFSOCAFSCSEGNLTGIEETT	240
Db	203	NCDDVGYGPOCOALYIOCEPLAEPLGIMDCMHPREGNFSFSOCAFSCSEGNLTGIEETT	262
QY	241	CGPFGNMSSPEPTQVIOQCEPLASAPDLGIMNCSHPLASFSTSACTPICSEGTGLIGKKK	300
Db	263	CGPFGNMSSPEPTQVIOQCEPLASAPDLGIMNCSHPLASFSTSACTPICSEGTGLIGKKK	322
QY	301	TTCSSGIGWNSPPIQ	317
Db	323	TTCSSGIGWNSPPIQ	339

```

RESULT      5
US-09-760-443-1437
: Sequence 1437, Application US/09760443
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: Pz12
: CURRENT APPLICATION NUMBER: US/09/760,443
: PRIORITY FILING DATE: 2001-01-16
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 2164
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1437
: LENGTH: 184
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-760-443-1437

```

	Query Match	47.2%	Score 999,	DB 55,	length 184,
	Best Local Similarity	99.5%	Pred. No. 3.5e-77,		
	Matches 183;	Conservative	0;	Mismatches 1;	Indels 0; Gaps
QY	189	PQCQVLIQCEPLAEPLGELTMDCTHPFCNFSFSQCAFSCSEGTWLTGIEBTTGCPFGNWS	248		
Db	1	PQCQVLIQCEPLAEPLGELTMDCTHPFCNFSFSQCAFSCSEGTWLTGIEBTTGCPFGNWS	60		
QY	249	SPEETCOVIOCEPLSAPDGLGIMNSHPLASSFSFSACTFLICBETELIGKKTICSSGI	308		
Db	61	SPEETCOVIOCEPLSAPDGLGIMNSHPLASSFSFSACTFLICBETELIGKKTICSSGI	120		
QY	309	WSNPSPICOLKDKSFSMIKEGDVNPLEPIPAVVWYTAFSGLAFITWLRLARKKGKSKRSM	368		
Db	121	WSNPSPICOLKDKSFSMIKEGDVNPLEPIPAVVWYTAFSGLAFITWLRLARKKGKSKRSM	180		
QY	369	NDPY 372			
Db	181	NDPY 184			

```

RESULT      6 45D322
US-09-760-475-3252
: Sequence 3252, Application US/09760475
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PTA49
: CURRENT APPLICATION NUMBER: US/09/760,475
: CURRENT FILING DATE: 2001-01-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 4122
: SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 3252
;
; LENGTH: 184
;
; TYPE: prt
;
; ORGANISM: Homo sapiens
;
US-09-760-475-3252

```

Query Match 47.2%; Score 999; DB 5; Length 184;
Best Local Similarity 99.5%; Pred. No. 3.5e-77;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	189	POCLVATQCEPLAEPLGTMDCTHPFNFSFSSOCASFCEGNNLNGIEETTGCPGNMS	248
Db	1	POCLVATQCEPLAEPLGTMDCTHPNFSFSSOCASFCEGNNLNGIEETTGCPGNMS	60
QY	249	SPEDTCVIOCEPLASPLADLGMNCSHPLASFSFTSACTFICSEGTELIGKKTICESSGI	308
Db	61	SPEDTCVIOCEPLASPLADLGMNCSHPLASFSFTSACTFICSEGTELIGKKTICESSGI	120
QY	309	WSNPSPIQOKLIDKFSKIKEGDYNPLETIPAAVNVTAFSGLAFITLWLRLKCKKSKSRM	368
Db	121	WSNPSPIQOKLIDKFSKIKEGDYNPLETIPAAVNVTAFSGLAFITLWLRLKCKKSKSRM	180
QY	369	NDPY 372	
Db	181	NDPY 184	

```

RESULT      7
US-09-784-356-122
; Sequence 122, Application US/09784356
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glyne, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: Novel Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/09/784,356
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 60/148,425
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 122
; LENGTH: 610
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-784-356-122

```

[illegible]

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

[illegible]

QY 189 PQCQLVTOCEPLAEALGTMCQH-PFGNFSFSSQCAFSCSEGNLTGIBETTCGPFCNW 247
| | : :: | : | : | : | : | : | : | : | : | : | : | : | : |


```

Db      16  PTCE-AVRCAAVHQPRGGLVRCASHPIDGEFTYKSSCAFSCEEGELHSGTQLEOTSGGQW  74
QY      248  SSPEPTQVIOCEPLSAPDUGIMNCS-HPLASETSFTACTFFICSEGTelikKKKTICESS  306
        :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      75  TEEVPSQGVVYKSSLAIPGKIKNNSGEPV-FTGVCKFACPEGWTLNGSAARTGAT  130
QY      307  GIMSNPSPICQKLDKFSMKIEGDIINFLT-----PVAWVTAESGATFIIMLARLTKG  361
        :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      131  GIMSGGLDPTCEAXNTE--SNIPDGSMFLXLDXSGPLA-----PFLIMLRKSLRKA  179
QY      362  KK 363
        :  :
Db      180  KK 181

```

```

RESULT 11
US-09-760-443-1321
: Sequence 1321, Application US/09760443
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PJ212
: CURRENT APPLICATION NUMBER: US/09/760,443
: PRIORITY FILING DATE: 2001-01-16
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 2164
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1321
: LENGTH: 207
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (151)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (185)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (191)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (194)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (198)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: OS-09-760-443-1321

```

Query Match	12.88;	Score 270;	DB 5;	Length 207;
Best Local Similarity	31.68;	Pred. No. 2.1e-15;		
Matches 60; Conservative	26;	Mismatches 64;	Indels 40;	Gaps 7;

QY		189	POCOLVTCQPLEPBLGTJMDCH-PGNFSFSCQAFSCSEGNLTGIBETTCGPGNW	247
	I :	:	:	:
Dd		16	PtCE-AVRCAVAHOPPPGLVRCASHPIGEFTTYSSCAFSCBEGFELHGSLQTECTSGOW	74
QY		248	SSEPPTCOVIQCPELSPADGIMNCS-HPLASFSTACTPICSEGTELIGKRTICESS	306
	:	:	:	:
Dd		75	TDETPSQVWKCSSLAPKGINMSCEPY----FGIVCKFACPBEGLTLNGSAARICGAR	130
QY		307	GIMSNPSPIQOKLDKSFMKEGDYNELT-----PVAVMTAFIGSLAFITW	353
	I :	:	:	:
Dd		131	GHWMSGLLPTC-----EVLPSLPFTGXLDSCWDSSGPLA-----PFLTW	170
QY		354	LARRLKGGK 363	
	I :	:	:	:
Dd		171	LRRSLRAKK 180	

RESULT 12
US-09-760-498-920

```

1 Sequence 920, Application US/09760498
2
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
6 FILE REFERENCE: PC017
7 CURRENT APPLICATION NUMBER: US/09/760,498
8 CURRENT FILING DATE: 2001-01-16
9 Prior application data removed - consult PALM or file wrapper
10 NUMBER OF SEQ ID NOS: 930
11 SOFTWARE: PatentIn Ver. 2.0
12 SEQ ID NO 920
13 LENGTH: 207
14 TYPE: PRT
15 ORGANISM: Homo sapiens
16 FEATURE:
17 NAME/KEY: SITE
18 LOCATION: (111)
19 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
20 NAME/KEY: SITE
21 LOCATION: (185)
22 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
23 NAME/KEY: SITE
24 LOCATION: (191)
25 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
26 NAME/KEY: SITE
27 LOCATION: (194)
28 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
29 NAME/KEY: SITE
30 LOCATION: (198)
31 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
32 US-09-760-498-920

```

Query Match	12.8%;	Score 270;	DB 5;	Length 207;
Best Local Similarity	31.6%;	Pred. No. 2.1e-15;		
Matches 60;	Conservative 26;	Mismatches 64;	Indels 40;	Gaps 7;

```

QY 189 PQCVLTAVICEPLAEPELGTIMCMT-PRGNSEFSQCAFSCSEGNLTGIEETTCGPGN 247
Db 16 PTCE-ARCDVAHNPYPKGLVNCASHPIGEFTLYKSCAFSCBEGFELHGSTQLECTSUGW 74
QY 248 SSPPTGOVIOCEPLASAPDLGIMNC-S-HPLASFSTACTFICSEGTELIGKRTICSS 306
Db 75 TEEVPSQGVVACSSLAIVPGKINMCSGEPV- -FGIVCKFACEDEGWTLNGSAARTGAT 130
QY 307 GIMSNPSPICQKLDKRSFMKEGYNPLT- - -PVAWMTAFESGLAFITW 353
Db 131 GHWGGLLPCTC- - -EVLPSFTPLGXLDFSCMDSSGPIA- - -PFLTW 170
QY 354 LARLRKKGKK 363
Db 171 LRKSLRRAKK 180

```

```

RESULT 13
US-09-760-475-3255
: Sequence 3255, Application US/09/60475
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT249
: CURRENT APPLICATION NUMBER: US/09/760,475
: CURRENT FILING DATE: 2001-01-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 4122
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3255
: LENGTH: 207
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (151)

```

```
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (185)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (191)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (194)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-760-475-3255
```

```
Query Match          12.8%; Score 270; DB 5; Length 207;
Best Local Similarity 31.6%; Pred. No. 2.1e-15;
Matches 60; Conservative 26; Mismatches 64; Indels 40; Gaps 7;
```

```
QY 189 POCQVIOCEPLEABELGTMDCTH-PFGNFSFSSQCAFSCSEGTNLGTIEETTCGPFQMW 247
DB 16 PTCE-AVRCDVAHOPPKGLVRCASHPIGEFTYKSCAFCEGFEHLHGSTOLECTSOQGM 74
QY 248 SSEPTECOVIOCEPLSAPDLGIMNCS-HPLASFSTACTICSEGTTELIGKKTTICESS 306
DB 75 TEVVSQCVKCKSSLAIVPKIKMSSCGEPV----FGTVCKFACPEBWTILNGSAARICGAT 130
QY 307 GIMNSPPIQKIDKSFMSIKEGDYNPLFI-----PVAVMVTAFSGLAFITM 353
DB 131 GIMSGILPFC-----EVPLSPFTLGLDFSCMDSSSGLA-----PFLIM 170
QY 354 LARRLKKGK 363
DB 171 LRKSLRKAKK 180
```

```
RESULT 14
US-09-764-875-615
; Sequence 615, Application US/09764875
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1202
; CURRENT APPLICATION NUMBER: US/09/764,875
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 615
; LENGTH: 309
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-764-875-615
```

```
Query Match          12.6%; Score 266; DB 5; Length 309;
Best Local Similarity 31.5%; Pred. No. 7.6e-15;
Matches 58; Conservative 23; Mismatches 81; Indels 22; Gaps 2;
```

```
QY 195 IOCEPLEABELGTMDCTHPRFGNFSFSSQCAFSCSEGTNLGTIEETTCGPFQNMSSPEPTC 254
DB 119 VCCPALTTGGGTGTCRHHPTGTFGFWTTCYFCGNAGFTLIGDSTLSCRPSGQWTAVTAPAC 178
QY 255 QVIOCEPLSAPDLGIMNCSHPLASFSTACTICSEGTTELIGKKTTICESSGIMNSPSP 314
DB 179 RAVKCESELVNNPRIANMNCNLMGNFSYGISCFHCLGOLLNCSAQTAQENGMHMTYVP 238
QY 315 ICOKIDKSFMSIKEDYNPLFI-----PVAVMVTAFSGLAFITMILARRLKKGKSK 365
DB 239 TCQA-----GPLTIOEALTYFGAVASTIGLIMGSTLALLRKRRROKDDGK 285
QY 366 RSMN 369
```

```
DB 286 CPLN 289
```

```
RESULT 15
US-09-911-842-2
; Sequence 2, Application US/09911842
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; APPLICANT: Elliott, Gary S.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentl version 3.0
; SEQ ID NO 2
; LENGTH: 3571
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-911-842-2
```

```
Query Match          11.6%; Score 246.5; DB 5; Length 3571;
Best Local Similarity 28.9%; Pred. No. 6.4e-12;
Matches 63; Conservative 33; Mismatches 93; Indels 29; Gaps 8;
```

```
QY 138 DAGKMWDACHKIKALCYTASQPMSCSGHGECEVEITNNHNCNDVGY--GPOCQVLI 195
DB 1732 DNGSMNVGSPSCIDVDECAVGS---DCSEHASCINLVDSYSICVPPYTGDKMCAEPI 1787
QY 196 OCEPLEABELGTMDCTHPRGN--FSFSSQCAFSCSEGTNLGTIEETTCGPFQNMSSPEPTC 254
DB 1788 KCKAPGNPENG-----HSGEITYGAEVTFSCQEGYQIMGYKITCLESGERNHLIPYC 1842
QY 255 QVIOCEPLSAPDLGIMNCSHPLASFSTACTICSEGTTELIGKKTTICESSGIMNSPSP 314
DB 1843 KAVSCGRPAIPENG---CIEELA-FTFGSKVYRCNKGYTLADGKRESCSIANSMSHSP 1898
QY 315 ICOKID-KSFMSIKEDYNPLFI-PVAVMVTAFSGLAFI 351
DB 1899 VCEPVKSSPENINNGY-----ILSGLYL 1924
```

```
Search completed: October 13, 2001, 03:00:39
Job time: 392 sec
```